

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:00:45 ; Search time 11.8644 Seconds
(without alignments)
30.459 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query % | | DB | ID | Description |
|------------|---------|--------------|-----|----|-------------------|
| | Score | Match Length | | | |
| 1 | 31 | 100.0 | 7 | 2 | Sequence 23, Appl |
| 2 | 31 | 100.0 | 7 | 2 | Sequence 26, Appl |
| 3 | 31 | 100.0 | 7 | 2 | Sequence 29, Appl |
| 4 | 31 | 100.0 | 7 | 3 | Sequence 23, Appl |
| 5 | 31 | 100.0 | 7 | 3 | Sequence 26, Appl |
| 6 | 31 | 100.0 | 7 | 3 | Sequence 29, Appl |
| 7 | 31 | 100.0 | 113 | 2 | Sequence 6, Appl |
| 8 | 31 | 100.0 | 113 | 2 | Sequence 7, Appl |
| 9 | 31 | 100.0 | 113 | 2 | Sequence 8, Appl |
| 10 | 31 | 100.0 | 113 | 2 | Sequence 96, Appl |
| 11 | 31 | 100.0 | 113 | 2 | Sequence 97, Appl |
| 12 | 31 | 100.0 | 113 | 2 | Sequence 98, Appl |
| 13 | 31 | 100.0 | 113 | 3 | Sequence 6, Appl |
| 14 | 31 | 100.0 | 113 | 3 | Sequence 7, Appl |
| 15 | 31 | 100.0 | 113 | 3 | Sequence 8, Appl |
| 16 | 31 | 100.0 | 113 | 3 | Sequence 104, App |
| 17 | 31 | 100.0 | 113 | 3 | Sequence 108, App |
| 18 | 31 | 100.0 | 113 | 3 | Sequence 112, App |
| 19 | 28 | 90.3 | 7 | 2 | Sequence 20, Appl |
| 20 | 28 | 90.3 | 7 | 3 | Sequence 20, Appl |
| 21 | 28 | 90.3 | 113 | 2 | Sequence 5, Appl |
| 22 | 28 | 90.3 | 113 | 2 | Sequence 95, Appl |
| 23 | 28 | 90.3 | 113 | 3 | Sequence 5, Appl |
| 24 | 28 | 90.3 | 113 | 3 | Sequence 100, App |
| 25 | 28 | 90.3 | 280 | 3 | Sequence 119, App |
| 26 | 27 | 87.1 | 7 | 2 | Sequence 80, Appl |
| 27 | 27 | 87.1 | 7 | 3 | Sequence 80, Appl |

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Query Match      100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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QY 1 LMSTRAS 7
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pB 1 LMSTRAS 7

RESULT 2

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0; Gaps 0;
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; Indels

0. 3e+05; C
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; Pred. N
0; Mism

100.0% derivative

Similarities

Best Local Matches

27

ce 20, Apr
ce 20, Apr

Sequen
SequenC-20
D-2008-672-34
08-214-09

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| US | 2 | 7 |

90.3

480
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170

Sequence 14, Appl
Sequence 18, Appl
Sequence 18, Appl
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Sequence 27521, A
Sequence 32578, A
Sequence 5240838
Patent No. 5240838
Sequence 1003, Ap
Sequence 999, App
Sequence 1007, Ap
Sequence 6926, Ap
Sequence 21143, A
Sequence 24241, A
Sequence 27421, A
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ALIGNMENTS

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28.678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-572-345C-23

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|-----------------------|---------|------------------|-------|---------------|
| Query Match | 100.0%; | Score 31; | DB 2; | Length |
| Best Local Similarity | 100.0%; | Pred. No. 3e+05; | | |
| Matches | 7; | Conservative | 0; | Mismatches 0; |

QY 1 LNSTRAS 7
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DP 1 LNSTRAS 7

RESULT 2

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; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-672-345C-29

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 4
US-09-214-095D-23
; Sequence 23, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-23

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 5
US-09-214-095D-26
; Sequence 26, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-26

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LMSTRAS 7
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Db 1 LMSTRAS 7

RESULT 6

US-09-214-095D-29
; Sequence 29, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-29

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 1 LMSTRAS 7
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Db 1 LMSTRAS 7

RESULT 7

US-08-672-345C-6
; Sequence 6, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-6

Query Match 100.0%; Score 31; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMSTRAS 7
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Db 55 LMSTRAS 61

RESULT 8

US-08-672-345C-7
; Sequence 7, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-7

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||
Db 55 LMSTRAS 61

RESULT 9

US-08-672-345C-8
; Sequence 8, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-8

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 10
US-08-672-345C-96
Sequence 96, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-96

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 11
US-08-672-345C-97
Sequence 97, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-97

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 12
US-08-672-345C-98
Sequence 98, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-98

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred.No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 13
US-09-214-095D-6
; Sequence 6, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCES: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-6

Query Match 100.0%; Score 31; DB 3; Length 113;
Best Local Similarity 100.0%; Pred.No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 14
US-09-214-095D-7
; Sequence 7, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCES: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
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;
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp
US-09-214-095D-7

Query Match 100.0%; Score 31; DB 3; Length 113;
Best Local Similarity 100.0%; Pred.No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 15
US-09-214-095D-8
; Sequence 8, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCES: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-8

Query Match 100.0%; Score 31; DB 3; Length 113;
Best Local Similarity 100.0%; Pred.No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

Search completed: September 30, 2004, 06:38:16
Job time : 12.8644 secs
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Blank sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 9.76271 Seconds
(without alignments)
88.677 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QOLVEYPPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|--------|----|--------|-------------------------|
| 1 | 43 | 89.6 | 383 | 2 | C42622 | ubiquinol-cytochrome b6 |
| 2 | 42 | 87.5 | 74 | 2 | G30538 | Ig kappa chain V r |
| 3 | 42 | 87.5 | 112 | 1 | KVMS16 | Ig kappa chain V r |
| 4 | 42 | 87.5 | 113 | 1 | KVMS1 | Ig kappa chain V r |
| 5 | 37 | 77.1 | 120 | 1 | KVMS67 | Ig kappa chain pre |
| 6 | 37 | 77.1 | 467 | 2 | A85363 | probable calmodulin |
| 7 | 36 | 75.0 | 108 | 2 | S36277 | Ig lambda chain V |
| 8 | 36 | 75.0 | 570 | 2 | T38148 | phosphatidyl synth |
| 9 | 35 | 72.9 | 120 | 2 | B29775 | Ig kappa chain pre |
| 10 | 35 | 72.9 | 480 | 2 | A86371 | hypothetical prote |
| 11 | 34 | 70.8 | 440 | 2 | D82100 | meat protein VC224 |
| 12 | 34 | 70.8 | 586 | 2 | D85903 | hypothetical prote |
| 13 | 34 | 70.8 | 722 | 2 | S76367 | hypothetical prote |
| 14 | 34 | 70.8 | 1074 | 2 | T01906 | hypothetical prote |
| 15 | 33 | 68.8 | 112 | 2 | I26317 | Ig kappa chain V r |
| 16 | 33 | 68.8 | 112 | 2 | D26317 | Ig kappa chain V r |
| 17 | 33 | 68.8 | 277 | 2 | AD3322 | lysosome (EC 3.2.1 |
| 18 | 33 | 68.8 | 315 | 2 | D83163 | hypothetical prote |
| 19 | 33 | 68.8 | 323 | 2 | D90527 | glycerol 3-phospha |
| 20 | 33 | 68.8 | 379 | 1 | S41834 | ubiquinol-cytochrome b6 |
| 21 | 33 | 68.8 | 414 | 2 | AG1614 | B. subtilis YxiO p |
| 22 | 33 | 68.8 | 414 | 2 | A11251 | B. subtilis YxiO p |
| 23 | 33 | 68.8 | 452 | 2 | A25346 | 3',5'-cyclic-nucle |
| 24 | 33 | 68.8 | 561 | 1 | S41589 | long-chain-fatty-a |
| 25 | 33 | 68.8 | 561 | 2 | B90943 | long-chain-fatty-a |
| 26 | 33 | 68.8 | 561 | 2 | F85791 | long-chain-fatty-a |
| 27 | 33 | 68.8 | 561 | 2 | AC0725 | long-chain-fatty-a |
| 28 | 33 | 68.8 | 664 | 2 | F70483 | glycine-tRNA ligase |
| 29 | 33 | 68.8 | 726 | 2 | T21138 | hypothetical prote |

30 33 68.8 816 2 S46268 ataxin-1 - human
31 32 68.8 817 2 T15138 hypothetical prote
32 32 66.7 61 4 I65317 hemoglobin delta c
33 32 66.7 112 2 B49060 Ig light chain V r
34 32 66.7 120 2 A29775 Ig kappa chain pre
35 32 66.7 132 2 S40334 Ig kappa chain - h
36 32 66.7 151 2 G96705 unknown protein, 7
37 32 66.7 180 2 AF2397 hypothetical prote
38 32 66.7 242 2 T45421 probable 2-hydroxy
39 32 66.7 282 2 T49628 biliverdin reducta
40 32 66.7 295 2 A42268 biliverdin reducta
41 32 66.7 296 2 G02066 biliverdin reducta
42 32 66.7 296 2 S62624 biliverdin reducta
43 32 66.7 298 2 T01948 hypothetical prote
44 32 66.7 313 1 F69399 conserved hypotet
45 32 66.7 315 2 A85019 probable bHLH DNA-

ALIGNMENTS

RESULT 1

C42622 ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - honeybee mitochondrion
C:Species: mitochondrion Apis mellifera (honeybee)
A:Variety: ligustica
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 03-Jun-2002
C:Accession: C42622; S52971
R:Crozier, R.H.; Crozier, Y.C.
Mol. Biol. Evol. 9, 474-482, 1992
A:Title: The cytochrome b and ATPase genes of honeybee mitochondrial DNA.
A:Reference number: A42622; MUID:92261310; PMID:1533894
A:Accession: C42622
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <CRO>
A:Cross-references: GB:M87052
R:Crozier, R.H.; Crozier, Y.C.
Genetics 133, 97-117, 1993
A:Title: The mitochondrial genome of the honeybee Apis mellifera: complete sequence and
A:Reference number: S52960; MUID:93114603; PMID:8417993
A:Accession: S52971
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <CR2>
A:Cross-references: EMBL:L06178; NID:G336279; PIDN:AAB96809.1; PID:G552449
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC4
C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol-
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrion;
F:14-340/Domain: cytochrome b homology <CBH>
F:14-211/Domain: cytochrome b6 homology <CB6>
F:223-340/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F:85,184/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F:99,198/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 89.6%; Score 43; DB 2; Length 383;

Best Local Similarity 77.8%; Pred. No. 0.55;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Q/ 1 QOLVEYPPT 9

Db 341 QOLIEYPPT 349

RESULT 2

G30538 Ig kappa chain V region (253.15E2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996

C:Accession: G30538

R:Clafin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988
 A>Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae
 A:Reference number: A30534; MUID:89035545; PMID:3141511

A:Accession: G30538
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-74 <CLIA>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 42; DB 2; Length 74;
 Best Local Similarity 88.9%; Pred. No. 0.15;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
 |||||
 Db 63 QQLVEYPLT 71

RESULT 3

KMS16

Ig kappa chain V region (M167) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
 C:Accession: A01908

R:Rudikoff, S.; Porter, W.
 Biochemistry 17, 2703-2707, 1978
 A>Title: Kappa-Chain variable region from M167, a phosphorylcholine binding myeloma protein
 A:Reference number: A01908; MUID:79000273; PMID:99160

A:Accession: A01908
 A:Molecule type: protein
 A:Residues: 1-112 <RUD>
 C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-95/Domain: immunoglobulin homology <IMM>
 F:23-93/Disulfide bonds: #status predicted

Query Match 87.5%; Score 42; DB 1; Length 112;
 Best Local Similarity 88.9%; Pred. No. 0.24;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
 |||||
 Db 94 QQLVEYPLT 102

RESULT 4

KMS51

Ig kappa chain V region (M511) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
 C:Accession: A01910

R:Appella, E.
 Mol. Immunol. 17, 711-718, 1980
 A>Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine binding myeloma protein
 A:Reference number: A01910; MUID:81052016; PMID:6776396

A:Accession: A01910
 A:Molecule type: protein
 A:Residues: 1-113 <APP>
 C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-95/Domain: immunoglobulin homology <IMM>
 F:23-93/Disulfide bonds: #status predicted

Query Match 87.5%; Score 42; DB 1; Length 113;
 Best Local Similarity 88.9%; Pred. No. 0.24;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
 |||||
 Db 94 QQLVEYPLT 102

RESULT 5

KMS67

Ig kappa chain precursor V region (VK167) - mouse
 C:Species: Mus musculus (house mouse)

C:Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000

C:Accession: A01909

R:Selsing, E.; Storb, U.

Cell 25, 47-58, 1981

A>Title: Somatic mutation of immunoglobulin light-chain variable-region genes.

A:Reference number: A01909; MUID:82002223; PMID:6791832

A:Accession: A01909

A:Molecule type: DNA

A:Residues: 1-120 <SEL>

A>Note: the sequence was determined from the germline gene

C:Genetics:

A:Introns: 17/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>

F:36-115/Domain: immunoglobulin homology <IMM>

F:43-113/Disulfide bonds: #status predicted

Query Match 77.1%; Score 37; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEYP 7
 |||||
 Db 114 QQLVEYP 120

RESULT 6

A85363

Probable calmodulin-binding protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C:Accession: A85363

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory

A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: A85363

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-467 <STO>

A:Cross-references: GB:NC_001268; NID:g7270002; PIDN:CAB79818.1; GSPDB:GN00140

C:Genetics:

A:Gene: At4g31000

A:Map position: 4

Query Match 77.1%; Score 37; DB 2; Length 467;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPPF 8
 |||||
 Db 334 QQLVEYPPF 341

RESULT 7

S36277

Ig lambda chain V region (clone alpha-FOG1-G8) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C:Accession: S36277
 R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMBO J. 12, 725-734, 1993
 A:Title: Human anti-self antibodies with high specificity from phage display libraries.
 A:Reference number: S36256; MUID:193178448; PMID:7679990
 A:Accession: S36277
 A>Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-108 <GRI>
 A:Cross-references: EXBL:Z18829; NID:G33417; PIDN:CAA79281.1; PID:G939910
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-50/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 36; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 4;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||||
 Db 89 QQLISYPLT 97

RESULT 8
 T38148
 phosphatidyl synthase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T38148
 R:Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, September 1997
 A:Reference number: Z11774
 A:Accession: T38148
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-570 <PEA>
 A:Cross-references: EXBL:Z99295; PIDN:CAB16578.1; GSPDB:GN00066; SPDB:SPAC22A12.06c
 A:Experimental source: strain 972h-; cosmid c22A12
 C:Genetics:
 A:Gene: SPDB:SPAC22A12.08c
 A:Map position: 1
 A:Introns: 43/2; 62/2; 227/2; 483/1

Query Match 75.0%; Score 36; DB 2; Length 570;
 Best Local Similarity 77.8%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 :|||||
 Db 547 KQLVEYSPT 555

RESULT 9
 B29775
 Ig kappa chain precursor V region (mouse 24.1) - shrew mouse
 C:Species: Mus pahari
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
 C:Accession: B29775
 R:Jouvin-Marche, E.; Rudikoff, S.
 Immunogenetics 24, 191-201, 1986
 A:Title: Evolution of a V-kappa gene family.
 A:Reference number: A91751; MUID:87006895; PMID:3093373
 A:Accession: B29775
 A:Molecule type: DNA
 A:Residues: 1-120 <JOI>
 A:Cross-references: GB:M15553; NID:G197470; PIDN:AAA39037.1; PID:G197471
 A>Note: this sequence was determined from the germline gene
 C:Genetics:
 A:Introns: 17/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-120/Product: Ig kappa chain V region 24.1 #status predicted <MAT>

F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 35; DB 2; Length 120;
 Best Local Similarity 85.7%; Pred. No. 7.2;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7
 |||||
 Db 114 QQLVEYP 120

RESULT 10
 A86371
 hypothetical protein F508.25 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 C:Accession: A86371
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: A86371
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-480 <STO>
 A:Cross-references: GB:AE005172; NID:G4056452; PIDN:AAC98025.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 72.9%; Score 35; DB 2; Length 480;
 Best Local Similarity 85.7%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQLVEYPP 8
 |||||
 Db 269 QQLVEYPP 275

RESULT 11
 D82100
 mesJ protein VC2242 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Dec-2002
 C:Accession: D82100
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: D82100
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-440 <HEI>
 A:Cross-references: GB:AE004296; GB:AE003852; NID:G9656799; PIDN:AAF95386.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC2242
 A:Map position: 1
 C:Superfamily: Cell cycle protein MesJ

Query Match 70.8%; Score 34; DB 2; Length 440;
 Best Local Similarity 75.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPP 8

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Db      10 QQLARYPF 17
      ||| |||
      ||| |||

RESULT 12
D89903
hypothetical protein Sall31 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89903
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Haramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89903
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-586 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701089; PIDN:BA842384.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: Sall31
C:Superfamily: Halobacterium halobium 2-oxoacid ferredoxin oxidoreductase; 2-oxoacid fer
Query Match      70.8%; Score 34; DB 2; Length 586;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy      2 QQLVEYFP 9
      ||| |||
      ||| |||
Db      109 QQLIEPFT 116

RESULT 13
S76367
hypothetical protein - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
C, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76367
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-722 <KAN>
A:Cross-references: EMBL:D64000; GB:AB001339; NID:gl001484; PIDN:BA010219.1; PID:gl00159
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: glycine-tRNA ligase beta chain
Query Match      70.8%; Score 34; DB 2; Length 722;
Best Local Similarity 85.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy      1 QQLVEYFP 7
      ||| |||
      ||| |||
Db      254 EQVLEYP 260

RESULT 14
T01906
hypothetical protein T12H20.3 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Mar-1999
C:Accession: T01906
R:Cotton, M.; Graves, T.; Sutterer, C.; Modde, T.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of A. thaliana T12H20.
A:Reference number: Z14453
A:Accession: T01906
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1074 <COT>
A:Cross-references: EMBL:AF080119; NID:gl3600029; PID:gl3600033
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Note: T12H20.3
Query Match      70.8%; Score 34; DB 2; Length 1074;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy      2 QQLVEYFP 8
      ||| |||
      ||| |||
Db      853 ELIEYFP 859

RESULT 15
I26317
Ig kappa chain V region (H158-89H4) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a de
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: I26317
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus he
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
P:16-95/Domain: immunoglobulin homology <IMM>
Query Match      68.8%; Score 33; DB 2; Length 112;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy      2 QQLVEYFP 9
      ||| |||
      ||| |||
Db      95 QHLEYPFT 102

Search completed: September 30, 2004, 06:00:35
Job time : 11.7627 secs

```


GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 5.49153 Seconds
(without alignments)
85.337 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVYFPFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|------------|--------------------|
| 1 | 43 | 89.6 | 383 | 1 | CYB APILI | P34845 apis mellif |
| 2 | 42 | 87.5 | 112 | 1 | KV2A MOUSE | P01626 mus musculu |
| 3 | 42 | 87.5 | 113 | 1 | KV2C MOUSE | P01628 mus musculu |
| 4 | 37 | 77.1 | 120 | 1 | KV2B MOUSE | P01627 mus musculu |
| 5 | 36 | 75.0 | 379 | 1 | CYB AKOJE | P21715 akodon jels |
| 6 | 36 | 75.0 | 379 | 1 | CYB AKOTB | P21715 akodon toba |
| 7 | 36 | 75.0 | 379 | 1 | CYB AKOTO | P21721 akodon torq |
| 8 | 36 | 75.0 | 380 | 1 | CYB DELSU | Q9XNV7 delomys sub |
| 9 | 36 | 75.0 | 380 | 1 | CYB MICMS | Q9XNV9 thomasomys |
| 10 | 36 | 75.0 | 380 | 1 | CYB THOIS | Q9XNV9 thomasomys |
| 11 | 36 | 75.0 | 381 | 1 | CYB AULMI | Q9XNV4 auliscomys |
| 12 | 36 | 75.0 | 381 | 1 | CYB ELIMO | Q9XNV3 eligmodonti |
| 13 | 36 | 75.0 | 381 | 1 | CYB PHIXA | Q9ZRF6 phyllotis x |
| 14 | 36 | 75.0 | 381 | 1 | CYB SIGHI | Q9XNU6 sigmodon hi |
| 15 | 36 | 75.0 | 381 | 1 | CYB THODA | Q9XNX1 thomasomys |
| 16 | 34 | 70.8 | 722 | 1 | SYGB SYN3 | Q55690 synechocyst |
| 17 | 33 | 68.8 | 379 | 1 | CYB MARBB | Q9TH45 marmota bob |
| 18 | 33 | 68.8 | 379 | 1 | CYB MARMR | Q9XP34 marmota mar |
| 19 | 33 | 68.8 | 452 | 1 | CYB DICDI | P12019 dictyosteli |
| 20 | 33 | 68.8 | 561 | 1 | LCFA SCOS7 | Q8XDR6 escherichia |
| 21 | 33 | 68.8 | 561 | 1 | LCFA SCOLI | P29212 escherichia |
| 22 | 33 | 68.8 | 561 | 1 | LCFA SALTU | Q8XG98 salmonella |
| 23 | 33 | 68.8 | 664 | 1 | SYGB AQUAE | Q67898 aquifex aeo |
| 24 | 33 | 68.8 | 792 | 1 | ATX1 RAT | Q63540 rattus norv |
| 25 | 33 | 68.8 | 792 | 1 | ATX1 MOUSE | P54254 mus musculu |
| 26 | 33 | 68.8 | 816 | 1 | ATX1 HUMAN | P54253 homo sapien |
| 27 | 32 | 66.7 | 295 | 1 | BIEA RAT | P48644 rattus norv |
| 28 | 32 | 66.7 | 296 | 1 | BIEA HUMAN | P53004 homo sapien |
| 29 | 32 | 66.7 | 332 | 1 | NDPA VIBPA | Q87MV3 vibrio para |
| 30 | 32 | 66.7 | 358 | 1 | YCCF BACSU | Q34478 bacillus su |
| 31 | 32 | 66.7 | 374 | 1 | Y006 BORBU | O51039 borrelia bu |
| 32 | 32 | 66.7 | 379 | 1 | CYB BOLAM | P21722 bolomys amo |
| 33 | 32 | 66.7 | 673 | 1 | Z145_HUMAN | Q05516 homo sapien |

ALIGNMENTS

RESULT 1

| ID | CYB APILI | STANDARD; | PRT; | 383 AA. |
|----|--|-----------|------|---------|
| AC | P34845; | | | |
| DT | 01-FEB-1994 (Rel. 28, Created) | | | |
| DT | 01-FEB-1994 (Rel. 28, Last sequence update) | | | |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) | | | |
| DE | Cytochrome b. | | | |
| GN | MTCTB OR COB OR CYTB. | | | |
| OS | Apis mellifera ligustica (Common honeybee). | | | |
| OG | Mitochondrion. | | | |
| OC | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; | | | |
| OC | Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; | | | |
| OC | Apidae; Apis. | | | |
| OX | NCBI_TaxID=7469; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Thorax; | | | |
| RX | MEDLINE=92261310; PubMed=1533894; | | | |
| RA | Crozier R.H.; Crozier Y.C.; | | | |
| RT | "The cytochrome b and ATPase genes of honeybee mitochondrial DNA."; | | | |
| RL | Mol. Biol. Evol. 9:474-482(1992). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Thorax; | | | |
| RX | MEDLINE=93114603; PubMed=8417993; | | | |
| RA | Crozier R.H.; Crozier Y.C.; | | | |
| RT | "The mitochondrial genome of the honeybee Apis mellifera: complete | | | |
| RL | sequence and genome organization."; | | | |
| RL | Genetics 133:97-117(1993). | | | |
| CC | -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase | | | |
| CC | complex (complex III or cytochrome b-c1 complex), which is a | | | |
| CC | respiratory chain that generates an electrochemical potential | | | |
| CC | coupled to ATP synthesis (By similarity). | | | |
| CC | -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or | | | |
| CC | b562) is low-potential and absorbs at about 562, and heme 2 (or BH | | | |
| CC | or b566) is high-potential and absorbs at about 566 (By | | | |
| CC | similarity). | | | |
| CC | -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, | | | |
| CC | cytochrome c1 and the Rieske protein (By similarity). | | | |
| CC | -!- SIMILARITY: Belongs to the cytochrome b family. | | | |

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modified and this statement is not removed. Usage by and for commercial
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EMBL; L06178; RA096809.1; -;
EMBL; M87052; -; NOT_ANNOTATED_CDS.
PIR; C42622; C42622.
InterPro; IPR005798; Cytb_b6_C.
InterPro; IPR005797; Cytb_b6_N.
Pfam; PF00032; cytochrome_b_C; 1.

Q3cmbl pasteurella
P82047 cervus nipp
P82045 cervus nipp
P82049 cervus nipp
P82048 cervus nipp
P82046 cervus nipp
Q9tlu8 cyanidium c
P05332 bacillus li
Q37931 methanococ
P52708 sorghum bic
Q94zk8 cebus albif
O47922 alces alces

DR Pfam; PF00033; cytochrome_b_n; 1.
 DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
 DR PROSITE; PS00193; CYTOCHROME_B_QO; 1.
 KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
 KW Heme.
 FT METAL 85 85 IRON 1 (HEME B562 AXIAL LIGAND).
 FT METAL 99 99 IRON 2 (HEME B566 AXIAL LIGAND).
 FT METAL 184 184 IRON 1 (HEME B562 AXIAL LIGAND).
 FT METAL 198 198 IRON 2 (HEME B566 AXIAL LIGAND).
 SQ SEQUENCE 383 AA; 45256 MW; A140A05B6053C2D5 CRC64;
 Query Match 89.6%; Score 43; DB 1; Length 383;
 Best Local Similarity 77.8%; Pred. No. 0.36;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQLVEYPT 9
 Db 341 QQLVEYPT 349
 RESULT 2
 KV2A_MOUSE
 ID KV2A_MOUSE STANDARD; PRT; 112 AA.
 AC P01626;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region MOPC 167.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=79000273; PubMed=99160;
 RA Rudikoff S., Potter M.;
 RT "Kappa Chain variable region from M167, a phosphorylcholine binding
 myeloma protein.";
 RL Biochemistry 17:2703-2707(1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY
 CHAIN HAS ALSO BEEN DETERMINED.
 DR PIR; A01908; KWS16.
 DR HSP; P80362; IWL.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG-LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT DOMAIN 40 54
 FT DOMAIN 55 61
 FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON TER 112 112
 SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;
 Query Match 87.5%; Score 42; DB 1; Length 112;
 Best Local Similarity 88.9%; Pred. No. 0.17;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQLVEYPT 9
 Db 94 QQLVEYPT 102
 RESULT 3
 KV2C_MOUSE
 ID KV2C_MOUSE STANDARD; PRT; 113 AA.
 AC P01627;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region V kappa167 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82002223; PubMed=6791832;
 RA Selsing E., Storb U.;
 RT "Somatic mutation of immunoglobulin light-chain variable-region
 genes.";
 RL Cell 25:47-58(1981).
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P01628;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region MOPC 511.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81052016; PubMed=6776396;
 RA Appella E.;
 RT "Amino acid sequence of the light chain variable region of M511, a
 phosphorylcholine-binding murine myeloma protein.";
 RL Mol. Immunol. 17:711-718(1980).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 BINDS PHOSPHORYLCHOLINE.
 DR PIR; A01910; KWS51.
 DR HSP; P80362; IWL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG-LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT DOMAIN 40 54
 FT DOMAIN 55 61
 FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON TER 113 113
 SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;
 Query Match 87.5%; Score 42; DB 1; Length 113;
 Best Local Similarity 88.9%; Pred. No. 0.17;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQLVEYPT 9
 Db 94 QQLVEYPT 102
 RESULT 4
 KV2B_MOUSE
 ID KV2B_MOUSE STANDARD; PRT; 120 AA.
 AC P01627;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region V kappa167 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82002223; PubMed=6791832;
 RA Selsing E., Storb U.;
 RT "Somatic mutation of immunoglobulin light-chain variable-region
 genes.";
 RL Cell 25:47-58(1981).
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CC EMBL; J00562; AAA39032.1; -
CC EMBL; K02415; AAA39051.1; -
CC PIR; A01909; KWS67.
CC HSP; P80362; IWT.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1
CC CHAIN 20
CC DOMAIN 21 120. IG KAPPA CHAIN V-II REGION VKAPPA167.
CC DOMAIN 21 43 FRAMEWORK-1.
CC DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 60 74 FRAMEWORK-2.
CC DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 82 113 FRAMEWORK-3.
CC DOMAIN 114 120 COMPLEMENTARITY-DETERMINING-3.
CC DISULFID 43 113 BY SIMILARITY.
CC SEQUENCE 120 AA; 63B571F0E4DE3E8 CRC64;

Query Match 77.1%; Score 37; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7
DB 114 QQLVEYP 120

RESULT 5
CYB_AKOJE
ID CYB_AKOJE STANDARD; PRT; 379 AA.
AC F21715;
DT 01-MAY-1991 (Rel. 18, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Akodon jelskii (Jelski's South American field mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Abrothrix.
OX NCBI_TaxID=241142;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Smith M.F.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-267 FROM N.A.
RC TISSUE=Liver;
RA Smith M.F., Patton J.L.;
RL "The diversification of South American murid rodents: evidence from mitochondrial DNA sequence data for the akodontine tribe.";
RN [3]
RP SEQUENCE OF 1-133 FROM N.A.
RC STRAIN=Isolate MVZ 173073, Isolate MVZ 173074, Isolate MVZ 173083, and Isolate MVZ 173084;
RC TISSUE=Liver;
RX MEDLINE=91163325; PubMed=2002767;
RA Smith M.F., Patton J.L.;
RL "Variation in mitochondrial cytochrome b sequence in natural populations of South American akodontine rodents (Muridae: Sigmodontinae).";
RL Mol. Biol. Evol. 8:85-103(1991).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-!- CORACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 (By similarity).
-!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.

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EMBL; M35714; AAA16998.2; ALT_TERM.
EMBL; M35715; AAA31630.1; -
EMBL; M35716; AAA31629.1; -
PIR; C41824; C41824.
DR InterPro; IPR005798; Cytb_b6_C.
DR InterPro; IPR005797; Cytb_b6_N.
DR Pfam; PF00032; Cytochrome_b_C; 1.
DR Pfam; PF00033; Cytochrome_b_N; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QQ; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
FT METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
FT VARIANT 118 118 V -> I (in isolates MVZ 173083 and MVZ 173084).
FT VARIANT 122 122 T -> A (in isolates MVZ 173083 and MVZ 173084).
FT SEQUENCE 379 AA; 42529 MW; F9F012A46671D59A CRC64;

Query Match 75.0%; Score 36; DB 1; Length 379;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QQLVEYPPT 9
DB 341 QQLVEYPPT 348

RESULT 6
CYB_AKOTB
ID CYB_AKOTB STANDARD; PRT; 379 AA.
AC Q33887;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Akodon toba (Chaco grass mouse).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Akodon.
OX NCBI_TaxID=29101;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate UMMZ 133965; TISSUE=Liver;
RA Smith M.F., Patton J.L.;
RL "Phylogenetic relationships and the radiation of sigmodontine rodents in South America: evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
RN [2]
RP SEQUENCE OF 1-267 FROM N.A.
RC STRAIN=Isolate UMMZ 133965; TISSUE=Liver;
RA Smith M.F., Patton J.L.;

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```

OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Delonys.
OX NCBI_TaxID=89131;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate MVZ 183075;
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-c1 complex), which is a
respiratory chain that generates an electrochemical potential
coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
b562) is low-potential and absorbs at about 562, and heme 2 (or BH
or b566) is high-potential and absorbs at about 566 (By
similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC
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or send an email to license@isb-sib.ch).
CC
DR EMBL; AF108687; AAD45469.1; -
DR InterPro; IPR005798; Cytb_b6_C.
DR InterPro; IPR005797; Cytb_b6_N.
DR Pfam; PF00032; cytochrome_b_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; 1.
KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 83 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 97 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 182 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 196 IRON 2 (HEME B566 AXIAL LIGAND).
SQ SEQUENCE 380 AA; 42820 MW; DE9A0EDA1D4AE785 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 380;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVPEYPT 9
DB 341 QPVEYPT 348

RESULT 9
ID CYB MICMS STANDARD; PRT; 380 AA.
AC Q9TFX5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Microzomys minutus (Forest small rice rat).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Microzomys.
OX NCBI_TaxID=37025;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=Isolate MVZ 173975;
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-c1 complex), which is a
respiratory chain that generates an electrochemical potential
coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
b562) is low-potential and absorbs at about 562, and heme 2 (or BH
or b566) is high-potential and absorbs at about 566 (By
similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC
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or send an email to license@isb-sib.ch).
CC
DR EMBL; AF108698; AAD45480.1; -
DR InterPro; IPR005798; Cytb_b6_C.
DR InterPro; IPR005797; Cytb_b6_N.
DR Pfam; PF00032; cytochrome_b_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; 1.
KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 83 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 97 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 182 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 196 IRON 2 (HEME B566 AXIAL LIGAND).
SQ SEQUENCE 380 AA; 42930 MW; C8C06F18D6F6DE21 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 380;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVPEYPT 9
DB 341 QPVEYPT 348

RESULT 10
ID CYB THOIS STANDARD; PRT; 380 AA.
AC Q9XNW9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Thomasomys ischyurus (Strong-tailed oldfield mouse).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Thomasomys.
OX NCBI_TaxID=89110;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate MVZ 181999;
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: Evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-c1 complex), which is a

```

```

CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH
CC or b566) is high-potential and absorbs at about 566 (By
CC similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF106675; AAD45457.1; .
CC InterPro; IPR005798; Cytb_b6_C.
CC InterPro; IPR005797; Cytb_b6_N.
CC Pfam; PF00032; cytochrome_b_C; 1.
CC Pfam; PF00033; cytochrome_b_N; 1.
CC PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE; PS00193; CYTOCHROME_B_QO; 1.
CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
CC Heme.
CC FT METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
CC FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
CC FT METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
CC FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
CC SQ SEQUENCE 380 AA; D73B891E41F61438 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 380;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVSEYPT 9
DB 341 QPVEYPT 348

RESULT 11
CYB_AULMI ID CYB_AULMI STANDARD; PRT; 381 AA.
AC Q9XNV4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Auliscomys micropus (Southern big-eared mouse).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Auliscomys.
OC NCBI_TaxID=89122;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
RL in South America: evidence from cytochrome b.";
CC J. Mammal. Evol. 6:189-128(1999).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH
CC or b566) is high-potential and absorbs at about 566 (By
CC similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).

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CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF106690; AAD45472.1; .
CC InterPro; IPR005798; Cytb_b6_C.
CC InterPro; IPR005797; Cytb_b6_N.
CC Pfam; PF00032; cytochrome_b_C; 1.
CC Pfam; PF00033; cytochrome_b_N; 1.
CC PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE; PS00193; CYTOCHROME_B_QO; 1.
CC Mitochondrion; Electron transport; Respiratory chain; Transmembrane;
CC Heme.
CC FT METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
CC FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
CC FT METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
CC FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
CC SQ SEQUENCE 381 AA; 43093 MW; 7DBE9C93338DA2C3 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 381;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVSEYPT 9
DB 341 QPVEYPT 348

RESULT 12
CYB_ELIMO ID CYB_ELIMO STANDARD; PRT; 381 AA.
AC Q9XNV3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Eligmodontia morgani (Morgan's gerbil mouse).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Eligmodontia.
OC NCBI_TaxID=89097;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Isolate MVZ 182670;
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
RL in South America: evidence from cytochrome b.";
CC J. Mammal. Evol. 6:189-128(1999).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH
CC or b566) is high-potential and absorbs at about 566 (By
CC similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC -----
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CC -----

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 CC or send an email to license@isb-sib.ch.

CC EMBL; AF108691; AAD45473.1; -
 CC InterPro; IPR005798; Cytb_b6_C.
 CC InterPro; IPR005797; Cytb_b6_N.
 CC Pfam; PF00032; cytochrome_b_c; 1.
 CC Pfam; PF00033; cytochrome_b_N; 1.
 CC PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
 CC PROSITE; PS00193; CYTOCHROME_B_QO; 1.
 CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
 CC Heme.
 CC METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
 CC METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
 CC METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
 CC METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
 CC SEQUENCE 381 AA; 43035 MW; D43D298BEB59486D CRC64;
 SQ

Query Match 75.0%; Score 36; DB 1; Length 381;
 Best Local Similarity 87.5%; Pred. No. 9.2;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QLVVEPPT 9
 |||||
 DB 341 QPVEPPT 348

RESULT 13

CC CYB_PHYXA STANDARD; PRT; 381 AA.
 CC O92Z6;
 CC 10-OCT-2003 (Rel. 42, Created)
 CC 10-OCT-2003 (Rel. 42, Last sequence update)
 CC 10-OCT-2003 (Rel. 42, Last annotation update)
 CC Cytochrome b.
 CC MTCYB OR COB OR CYTB.
 CC Phyllotis xanthopygus (Yellow-rumped leaf-eared mouse).
 CC Mitochondrion.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 CC Phyllotis.
 CC NCBI_TaxID=59941;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=FMH 133830;
 CC Steppan S.J.;
 CC "Phylogenetic relationships and species limits within Phyllotis
 CC (Rodentia: Sigmodontinae): concordance between mtDNA sequence and
 CC morphology.";
 CC J. Mammal. 79:573-593 (1998).
 CC [2]
 CC REVISIONS.
 CC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
 CC complex (complex III or cytochrome b-c1 complex), which is a
 CC respiratory chain that generates an electrochemical potential
 CC coupled to ATP synthesis (By similarity).
 CC -!- COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
 CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH
 CC or b566) is high-potential and absorbs at about 566 (By
 CC similarity).
 CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
 CC cytochrome c1 and the Rieske protein (By similarity).
 CC -!- SIMILARITY: Belongs to the cytochrome b family.

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CC EMBL; U86931; AAD12358.2; -
 CC InterPro; IPR005798; Cytb_b6_C.
 CC InterPro; IPR005797; Cytb_b6_N.
 CC Pfam; PF00032; cytochrome_b_c; 1.
 CC Pfam; PF00033; cytochrome_b_N; 1.
 CC PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
 CC PROSITE; PS00193; CYTOCHROME_B_QO; 1.
 CC Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
 CC Heme.
 CC METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
 CC METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
 CC METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
 CC METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
 CC SEQUENCE 381 AA; 43076 MW; CC314C640B7246FB CRC64;
 SQ

Query Match 75.0%; Score 36; DB 1; Length 381;
 Best Local Similarity 87.5%; Pred. No. 9.2;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QLVVEPPT 9
 |||||
 DB 341 QPVEPPT 348

RESULT 14

CC CYB_SIGHI STANDARD; PRT; 381 AA.
 CC O9XNU6;
 CC 28-FEB-2003 (Rel. 41, Created)
 CC 28-FEB-2003 (Rel. 41, Last sequence update)
 CC 10-OCT-2003 (Rel. 42, Last annotation update)
 CC Cytochrome b.
 CC MTCYB OR COB OR CYTB.
 CC Sigmodon hispidus (Hispid cotton rat).
 CC Mitochondrion.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 CC Sigmodon.
 CC NCBI_TaxID=42415;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC Smith M.F., Patton J.L.;
 CC "Phylogenetic relationships and the radiation of sigmodontine rodents
 CC in South America: evidence from cytochrome b.";
 CC J. Mammal. Evol. 6:89-128 (1999).
 CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
 CC complex (complex III or cytochrome b-c1 complex), which is a
 CC respiratory chain that generates an electrochemical potential
 CC coupled to ATP synthesis (By similarity).
 CC -!- COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
 CC b562) is low-potential and absorbs at about 562, and heme 2 (or BH
 CC or b566) is high-potential and absorbs at about 566 (By
 CC similarity).
 CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
 CC cytochrome c1 and the Rieske protein (By similarity).
 CC -!- SIMILARITY: Belongs to the cytochrome b family.

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CC EMBL; AF108702; AAD45484.1; -
 CC InterPro; IPR005798; Cytb_b6_C.
 CC InterPro; IPR005797; Cytb_b6_N.
 CC Pfam; PF00032; cytochrome_b_c; 1.
 CC Pfam; PF00033; cytochrome_b_N; 1.
 CC PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
 CC PROSITE; PS00193; CYTOCHROME_B_QO; 1.

KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;

KW Heme: 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
SQ SEQUENCE 381 AA; 42965 MW; 0472259421B38284 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 381;

Best Local Similarity 87.5%; Pred.No. 9.2; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVVEYPFT 9
| | | | |
DB 341 QVVEYPFT 348

RESULT 15

CYB_THODA ID CYB_THODA STANDARD; PRT; 381 AA.
AC Q9XNXL; 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b.
GN MTCYB OR COB OR CYTB.
OS Thomasomys daphne (Daphne's oldfield mouse).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Thomasomys.
OX NCBI_TaxID=89108;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate MVZ 171502;
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents in South America: evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or EL or b562) is low-potential and absorbs at about 562, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 (By similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
CC -----
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CC -----
CC EMBL; AF108673; AAD45455.1; -
CC InterPro; IPR005798; Cytb_b6.C.
CC InterPro; IPR005797; Cytb_b6.N.
CC Pfam; PF00032; cytochrome_b_C; 1.
CC Pfam; PF00033; cytochrome_b_N; 1.
CC PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE; PS00193; CYTOCHROME_B_QQ; 1.
KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 182 182 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 196 196 IRON 2 (HEME B566 AXIAL LIGAND).
SQ SEQUENCE 381 AA; 43035 MW; 351993B27E14502A CRC64;

Query Match 75.0%; Score 36; DB 1; Length 381;
Best Local Similarity 87.5%; Pred.No. 9.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVVEYPFT 9
| | | | |
DB 341 QVVEYPFT 348

Search completed: September 30, 2004, 06:01:18
Job time : 7.49153 secs

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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 29.4407 Seconds
(without alignments)
96.454 Million cell updates/sec

Title: US-09-674-716b-7

Perfect score: 48

Sequence: 1 QQLVEYPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirs:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 40 | 83.3 | 349 | 8 Q85TH4 | Q85th4 melipona bi |
| 2 | 39 | 81.2 | 506 | 16 Q87RR4 | Q87rr4 vibrio para |
| 3 | 37 | 77.1 | 278 | 10 Q8W454 | Q8w454 arabidopsis |
| 4 | 37 | 77.1 | 467 | 10 Q85550 | Q85550 arabidopsis |
| 5 | 37 | 77.1 | 609 | 10 Q8H816 | Q8h816 oryza sativ |
| 6 | 36 | 75.0 | 84 | 8 Q9B313 | Q9b313 neoceratodu |
| 7 | 36 | 75.0 | 247 | 8 Q9W34 | Q9w34 bothriomyrm |
| 8 | 36 | 75.0 | 352 | 8 Q9XNV8 | Q9xnv8 delomyes dor |
| 9 | 36 | 75.0 | 371 | 8 Q8M293 | Q8m293 oxymycteru |
| 10 | 36 | 75.0 | 377 | 8 Q9XNV0 | Q9xnv0 reithrodon |
| 11 | 36 | 75.0 | 377 | 8 Q9XNX5 | Q9xnx5 scapteromys |
| 12 | 36 | 75.0 | 379 | 8 Q8M2A0 | Q8m2a0 oxymycteru |
| 13 | 36 | 75.0 | 379 | 8 Q9TGL4 | Q9tgl4 cervus elap |
| 14 | 36 | 75.0 | 379 | 8 Q8M299 | Q8m299 oxymycteru |
| 15 | 36 | 75.0 | 379 | 8 Q8M296 | Q8m296 oxymycteru |
| 16 | 36 | 75.0 | 379 | 8 Q8M290 | Q8m290 oxymycteru |

| | | | | | |
|----|----|------|-----|----------|--------------------|
| 17 | 36 | 75.0 | 379 | 8 Q9TF12 | Q9tf12 spermophilu |
| 18 | 36 | 75.0 | 379 | 8 Q9TF64 | Q9tf64 spermophilu |
| 19 | 36 | 75.0 | 379 | 8 Q8M294 | Q8m294 oxymycteru |
| 20 | 36 | 75.0 | 379 | 8 Q8M295 | Q8m295 oxymycteru |
| 21 | 36 | 75.0 | 379 | 8 Q8M297 | Q8m297 oxymycteru |
| 22 | 36 | 75.0 | 379 | 8 Q8LU40 | Q8lu40 oxymycteru |
| 23 | 36 | 75.0 | 379 | 8 Q8M292 | Q8m292 oxymycteru |
| 24 | 36 | 75.0 | 379 | 8 Q9TF11 | Q9tf11 spermophilu |
| 25 | 36 | 75.0 | 379 | 8 Q9TF08 | Q9tf08 spermophilu |
| 26 | 36 | 75.0 | 379 | 8 Q33940 | Q33940 bolomy uri |
| 27 | 36 | 75.0 | 379 | 8 Q8H95 | Q8h95 cynocephalu |
| 28 | 36 | 75.0 | 379 | 8 Q94Q8 | Q94q8 carvusi timo |
| 29 | 36 | 75.0 | 379 | 8 Q9Y7J8 | Q9y7j8 salmuri sci |
| 30 | 36 | 75.0 | 380 | 8 Q7I6T9 | Q7i6t9 thomasomys |
| 31 | 36 | 75.0 | 380 | 8 Q35970 | Q35970 thomasomys |
| 32 | 36 | 75.0 | 380 | 8 Q9MNS7 | Q9mns7 calomys lep |
| 33 | 36 | 75.0 | 380 | 8 Q9XNX6 | Q9xnx6 blarinomys |
| 34 | 36 | 75.0 | 380 | 8 Q9XNX0 | Q9xnx0 thomasomys |
| 35 | 36 | 75.0 | 380 | 8 Q9XNW3 | Q9xnw3 rhipidomys |
| 36 | 36 | 75.0 | 380 | 8 Q9MNT3 | Q9mnt3 tapecomys p |
| 37 | 36 | 75.0 | 380 | 8 Q94U29 | Q94uz9 microtus gu |
| 38 | 36 | 75.0 | 380 | 8 Q9MNT5 | Q9mnt5 andalgomy |
| 39 | 36 | 75.0 | 380 | 8 Q94V01 | Q94v01 microtus oa |
| 40 | 36 | 75.0 | 380 | 8 Q9MNT0 | Q9mnt0 graomys dom |
| 41 | 36 | 75.0 | 380 | 8 Q9M7E7 | Q9m7e7 calomys fec |
| 42 | 36 | 75.0 | 380 | 8 Q9XNW8 | Q9xnw8 thomasomys |
| 43 | 36 | 75.0 | 380 | 8 Q9T7L7 | Q9t7l7 microtus ri |
| 44 | 36 | 75.0 | 380 | 8 Q9MHE9 | Q9mhf9 microtus lo |
| 45 | 36 | 75.0 | 380 | 8 Q34853 | Q34853 lenoxus api |

ALIGNMENTS

RESULT 1

| | | | |
|--|--------------|------|---------|
| Q85TH4 | PRELIMINARY; | PRT; | 349 AA. |
| ID Q85TH4 | | | |
| AC Q85TH4; | | | |
| DT 01-JUN-2003 (Tremblrel. 24, Created) | | | |
| DT 01-JUN-2003 (Tremblrel. 24, Last sequence update) | | | |
| DE 01-OCT-2003 (Tremblrel. 25, Last annotation update) | | | |
| DE Cytochrome b. | | | |
| GN CYTB. | | | |
| OS Melipona bicolor. | | | |
| OG Mitochondrion. | | | |
| OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; | | | |
| OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; | | | |
| OC Apidae; Melipona. | | | |
| OX NCBI_taxID=60889; | | | |
| RN [1] | | | |
| RP SEQUENCE FROM N.A. | | | |
| RA Silvestre D., Arias M.C.; | | | |
| RT "The mitochondrial genome of Melipona bicolor (Apidae, Meliponini)."; | | | |
| RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases. | | | |
| DR EMBL; AF466146; AAO18422.1; - | | | |
| DR GO; GO:0016020; C:membrane; IEA. | | | |
| DR GO; GO:0005739; P:oxidoreductase activity; IEA. | | | |
| DR GO; GO:0006118; P:electron transport; IEA. | | | |
| DR InterPro; IPR005798; Cytb_b6_C. | | | |
| DR InterPro; IPR005797; Cytb_b6_N. | | | |
| DR Pfam; PF00032; cytochrome_b_C; 1. | | | |
| DR Pfam; PF00033; cytochrome_b_N; 1. | | | |
| DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1. | | | |
| DR PROSITE; PS00193; CYTOCHROME_B_QQ; 1. | | | |
| KW Mitochondrion. | | | |
| SQ SEQUENCE 349 AA; 41464 MW; 9B1DC3A6927DADD3 CRC64; | | | |

Query Match 83.3%; Score 40; DB 8; Length 349;

Best Local Similarity 75.0%; Pred.No. 5.2;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQLVEYPT 9

RN SEQUENCE FROM N.A.
RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,
RA Currie J., Collura K.;
RT "Rice Genomic Sequence";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AC105364; AN05331.1; -;
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR Pfam; PF00646; F-box; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE; PS0181; PBOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 609 AA; 68105 MW; AEA195731E0BF07C CRC64;

Query Match 77.1%; Score 37; DB 10; Length 609;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLVVEYPFT 9
DB 569 QQLLEIPFT 577

RESULT 6
Q9B313 PRELIMINARY; PRT; 84 AA.
AC Q9B313;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
GN CYTB.
OS Neoceratodus forsteri (Australian lungfish).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus.
OX NCBI_TaxID=7892;
RN 11 SEQUENCE FROM N.A.
RA Frentiu F., Ovenden J.R., Street R.;
RT "Australian lungfish (Neoceratodus forsteri) have low genetic
RT diversity at allozyme and mitochondrial loci: A conservation alert for
RT a living fossil?";
RL Conserv. Genet. 0:0-0 (2001).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF344663; AAK29031.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005798; Cytb_b6_C.
DR Pfam; PF00032; cytochrome_b_c; 1.
DR Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
FT NON TER 1
SQ SEQUENCE 84 AA; 9673 MW; 1E7AFAD921592DAC CRC64;

Query Match 75.0%; Score 36; DB 8; Length 84;
Best Local Similarity 87.5%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPFT 9
DB 27 QPVEYPFT 34

RESULT 7
Q9MP34 PRELIMINARY; PRT; 247 AA.
AC Q9MP34;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
GN CYTB.
OS Bothriomyx meridionalis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Formicidae; Dolichoderinae; Bothriomyrmex.
OX NCBI_TaxID=121499;
RN 11 SEQUENCE FROM N.A.
RA Chiotis M., Jermin L.S., Crozier R.H.;
RT "A molecular framework for the phylogeny of the ant subfamily
RL Dolichoderinae";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF146714; AAF66714.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005798; Cytb_b6_C.
DR InterPro; IPR005797; Cytb_b6_N.
DR Pfam; PF00032; cytochrome_b_c; 1.
DR Pfam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QQ; 1.
DR Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 247 AA; 29263 MW; CC68F8BA0D065B1A CRC64;

Query Match 75.0%; Score 36; DB 8; Length 247;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPFT 9
DB 201 QSIEYPFT 208

RESULT 8
Q9XNV8 PRELIMINARY; PRT; 352 AA.
AC Q9XNV8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome B (Fragment).
GN CYTB.
OS Delomys dorsalis (striped Atlantic forest rat).

OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Delomys.
 OX NCBI_TaxID=89119;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith M.F., Patton J.L.;
 RT "Phylogenetic relationships and the radiation of sigmodontine rodents
 in South America: Evidence from cytochrome b.";
 RL J. Mammal. Evol. 6:189-128(1999).
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CYTOCHROME C1 AND THE RISKS PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
 DR EMBL; AF108686; AAD4548.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR005798; Cytb_b6_C.
 DR InterPro; IPR005797; Cytb_b6_N.
 DR Pfam; PF00033; cytochrome_b_C; 1.
 DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
 DR PROSITE; PS00193; CYTOCHROME_B_QO; 1.
 KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
 KW Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 352 352
 SQ SEQUENCE 352 AA; 39631 MW; AA408DB627140D6C CRC64;
 Query Match 75.0%; Score 36; DB 8; Length 352;
 Best Local Similarity 87.5%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 QLVVEYPPT 9
 Db 341 QPVEYPT 348
 RESULT 9
 ID Q8M293 PRELIMINARY; PRT; 371 AA.
 AC Q8M293;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome b (Fragment).
 GN CYTB.
 OS Oxymycterus quaestor.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Oxymycterus.
 OX NCBI_TaxID=196087;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoffmann F.G., Lessa E.P., Smith M.F.;
 RT "Systematics of Oxymycterus with description of a new species from
 Uruguay.";
 RL J. Mammal. 83:408-420(2002).
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY

CC BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CYTOCHROME C1 AND THE RISKS PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
 DR EMBL; AF454772; AAM33839.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR005798; Cytb_b6_C.
 DR InterPro; IPR005797; Cytb_b6_N.
 DR Pfam; PF00033; cytochrome_b_C; 1.
 DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
 DR PROSITE; PS00193; CYTOCHROME_B_QO; 1.
 KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
 KW Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 371 371
 SQ SEQUENCE 371 AA; 41657 MW; 2B0AC6BAEB2DED16 CRC64;
 Query Match 75.0%; Score 36; DB 8; Length 371;
 Best Local Similarity 87.5%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 QLVVEYPPT 9
 Db 333 QPVEYPT 340
 RESULT 10
 Q8XNV0
 ID Q8XNV0 PRELIMINARY; PRT; 377 AA.
 AC Q8XNV0;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome B (Fragment).
 GN CYTB.
 OS Reithrodon auritus (bunny rat).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Reithrodon.
 OX NCBI_TaxID=56234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith M.F., Patton J.L.;
 RT "Phylogenetic relationships and the radiation of sigmodontine rodents
 in South America: Evidence from cytochrome b.";
 RL J. Mammal. Evol. 6:189-128(1999).
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CYTOCHROME C1 AND THE RISKS PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
 DR EMBL; AF108694; AAD45476.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR005798; Cytb_b6_C.
 DR InterPro; IPR005797; Cytb_b6_N.
 DR Pfam; PF00033; cytochrome_b_C; 1.
 DR Pfam; PF00033; cytochrome_b_N; 1.

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DR PROSITE; PS00192; CYTOCHROME B HEME; 1.
DR PROSITE; PS00193; CYTOCHROME B_QO; 1.
KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
FT Mitochondrion. 1
FT NON_TER 1
SQ SEQUENCE 377 AA; 42533 MW; 618DB37395E5E97 CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 8; Length 377;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 OLVEYPPT 9
DB 338 QPVEYPPT 345

RESULT 11
Q9XNX5 PRELIMINARY; PRT; 377 AA.
AC Q9XNX5;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Cytochrome B (Fragment).
GN CYTB.
OS Scapteromys tumidus (swamp rat).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Scacteromys.
OX NCBI_TaxID=89126;
RN [1]_TaxID=89126;
RP SEQUENCE FROM N.A.
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: Evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
EMBL; AF108669; AAD45451.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:000810; P:transport; IEA.
DR InterPro; IPR005798; Cytb_b6_C.
DR InterPro; IPR005797; Cytb_b6_N.
DR Pfam; PF00032; cytochrome_b_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME B_QO; 1.
DR PROSITE; PS00193; CYTOCHROME B_QO; 1.
KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 377 AA; 42392 MW; 692D67AE20B6F3BB CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 8; Length 377;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 OLVEYPPT 9
DB 337 QPVEYPPT 344
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RESULT 12
Q8M2A0 PRELIMINARY; PRT; 379 AA.
AC Q8M2A0;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
GN CYTB.
OS Oxymycterus amazonicus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Oxymycterus.
OX NCBI_TaxID=196085;
RN [1]_TaxID=196085;
RP SEQUENCE FROM N.A.
RA Hoffmann F.G., Lessa E.P., Smith M.F.;
RT "Systematics of Oxymycterus with description of a new species from
Uruguay.";
RL J. Mammal. 83:408-420(2002).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
EMBL; AF454765; AAM33832.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:000810; P:transport; IEA.
DR InterPro; IPR005798; Cytb_b6_C.
DR InterPro; IPR005797; Cytb_b6_N.
DR Pfam; PF00032; cytochrome_b_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME B_QO; 1.
DR PROSITE; PS00193; CYTOCHROME B_QO; 1.
KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
FT NON_TER 379
FT NON_TER 379
SQ SEQUENCE 379 AA; 42856 MW; E7C010CACE44CE8F CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 8; Length 379;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 OLVEYPPT 9
DB 341 QPVEYPPT 348

RESULT 13
Q9TGL4 PRELIMINARY; PRT; 379 AA.
AC Q9TGL4;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Cervus elaphus (Red deer).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]_TaxID=9860;
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RP SEQUENCE FROM N.A.
RX MEDLINE=20229580; PubMed=10764539;
RA Kuwayama R., Ozawa T.;
RT "Phylogenetic relationships among european red deer, wapiti, and sika
RL deer inferred from mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 15:115-123(2000).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CC EMBL; AB021098; BA83607.1; -.
CC HSP; P00157; IBE3.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005798; Cytb_b6_C.
DR Pfam; PF00032; cytochrome_b6_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_OO; 1.
KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
KW Mitochondrion.
FT NON TER 379
SQ SEQUENCE 379 AA; 42871 MW; 36F71191E46D263B CRC64;

Query Match 75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPT 9
DB 341 QPVEYPT 348

RESULT 14
Q8M299 PRELIMINARY; PRT; 379 AA.
AC Q8M299;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome b (fragment).
GN CYTB.
OS Oxymycterus delator (spy holicudo).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Oxymycterus.
OX NCBI_TaxID=29125;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoffmann F.G., Lessa E.P., Smith M.F.;
RT "Systematics of Oxymycterus with description of a new species from
RL Uruguay.";
RL J. Mammal. 83:408-420(2002).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CC EMBL; AF454766; AM33833.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005798; Cytb_b6_C.
DR Pfam; PF00032; cytochrome_b6_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_OO; 1.
KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
KW Mitochondrion.
FT NON TER 379
SQ SEQUENCE 379 AA; 42802 MW; BFE22C9B4F985AE1 CRC64;

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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005798; Cytb_b6_C.
DR Pfam; PF00032; cytochrome_b6_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_OO; 1.
KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
KW Mitochondrion.
FT NON TER 379
SQ SEQUENCE 379 AA; 42855 MW; 55DD10D7D344D8E3 CRC64;

Query Match 75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPT 9
DB 341 QPVEYPT 348

RESULT 15
Q8M296 PRELIMINARY; PRT; 379 AA.
AC Q8M296;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome b (fragment).
GN CYTB.
OS Oxymycterus dasytrichus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Oxymycterus.
OX NCBI_TaxID=196088;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoffmann F.G., Lessa E.P., Smith M.F.;
RT "Systematics of Oxymycterus with description of a new species from
RL Uruguay.";
RL J. Mammal. 83:408-420(2002).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CC EMBL; AF454769; AM33836.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005798; Cytb_b6_C.
DR Pfam; PF00032; cytochrome_b6_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_OO; 1.
KW Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
KW Mitochondrion.
FT NON TER 379
SQ SEQUENCE 379 AA; 42802 MW; BFE22C9B4F985AE1 CRC64;

```

Query Match 75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 QIVEYDPT 9
DB 341 QIVEYDPT 348

Search completed: September 30, 2004, 05:59:31
Job time : 32.6073 secs

Blank sheet

QM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 43.9322 Seconds
(without alignments)
57.883 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEYFPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Score | Length | DB ID | Description |
|------------|-------------|-------|--------|-------------|---------------------|
| 1 | 48 | 100.0 | 9 | 3 AAY32256 | Aay32256 Light cha |
| 2 | 48 | 100.0 | 116 | 3 AAY32262 | Aay32262 Humanised |
| 3 | 48 | 100.0 | 145 | 3 AAY32261 | Aay32261 Mouse ant |
| 4 | 45 | 93.8 | 19 | 3 AAY70804 | Aay70804 Murine an |
| 5 | 45 | 93.8 | 122 | 3 AAY70790 | Aay70790 Murine an |
| 6 | 45 | 93.8 | 131 | 2 AAY12232 | Aay12232 Mouse Mab |
| 7 | 45 | 93.8 | 132 | 2 AAY122354 | Aay122354 Light lka |
| 8 | 44 | 91.7 | 9 | 2 AAW39823 | Aaw39823 Light cha |
| 9 | 44 | 91.7 | 113 | 2 AAW39882 | Aaw39882 Light cha |
| 10 | 44 | 91.7 | 113 | 2 AAW39804 | Aaw39804 Variable |
| 11 | 37 | 77.1 | 100 | 4 AAE06969 | Aae06969 Mouse ger |
| 12 | 36 | 75.0 | 9 | 2 AAW39817 | Aaw39817 Light cha |
| 13 | 36 | 75.0 | 113 | 2 AAW39803 | Aaw39803 Variable |
| 14 | 36 | 75.0 | 113 | 2 AAW39801 | Aaw39801 Variable |
| 15 | 36 | 75.0 | 241 | 2 AAW24063 | Aaw24063 Human WSX |
| 16 | 36 | 75.0 | 241 | 5 AAU09048 | Aau09048 Insulin/i |
| 17 | 36 | 75.0 | 241 | 7 ADP08951 | Adp08951 Human BLY |
| 18 | 36 | 75.0 | 251 | 5 ABP45299 | Abp45299 Human BLY |
| 19 | 36 | 75.0 | 253 | 5 ABP44925 | Abp44925 Human BLY |
| 20 | 36 | 75.0 | 274 | 2 AAW39899 | Aaw39899 Single ch |
| 21 | 36 | 75.0 | 392 | 3 AAB10863 | Aab10863 Sll-VSGF2 |
| 22 | 36 | 75.0 | 510 | 3 AAB10864 | Aab10864 Sll-scVEG |
| 23 | 35 | 72.9 | 112 | 3 AAY90813 | Aay90813 2G3 hybri |
| 24 | 35 | 72.9 | 126 | 2 AAY36951 | Aay36951 Protein i |
| 25 | 35 | 72.9 | 425 | 6 ABM69120 | Abm69120 Photorhab |

| | | | | | |
|----|----|------|-----|------------|--------------------|
| 26 | 35 | 72.9 | 533 | 3 AAG27700 | Aag27700 Arabidops |
| 27 | 35 | 72.9 | 536 | 3 AAG27699 | Aag27699 Arabidops |
| 28 | 35 | 72.9 | 622 | 3 AAG27698 | Aag27698 Arabidops |
| 29 | 34 | 70.8 | 9 | 3 AAY92171 | Aay92171 Murine l3 |
| 30 | 34 | 70.8 | 113 | 3 AAY92164 | Aay92164 Murine l3 |
| 31 | 34 | 70.8 | 146 | 2 AAW28154 | Aaw28154 Amino aci |
| 32 | 34 | 70.8 | 440 | 6 ABU49487 | Abu49487 Protein e |
| 33 | 34 | 70.8 | 585 | 5 ABP40069 | Abp40069 Staphyloc |
| 34 | 34 | 70.8 | 601 | 6 ABM73103 | Abm73103 Staphyloc |
| 35 | 34 | 70.8 | 604 | 4 AAG81648 | Aag81648 S. epider |
| 36 | 33 | 68.8 | 9 | 2 AAR30450 | Aar30450 C242:11 M |
| 37 | 33 | 68.8 | 82 | 4 ABB36950 | Abb36950 Peptide # |
| 38 | 33 | 68.8 | 107 | 4 AAG93597 | Aag93597 Human ant |
| 39 | 33 | 68.8 | 107 | 6 ABO27404 | AbO27404 Anti-Rh(D |
| 40 | 33 | 68.8 | 108 | 2 AAR34019 | Aar34019 BW 835 VK |
| 41 | 33 | 68.8 | 113 | 2 AAR59513 | Aar59513 Sequence |
| 42 | 33 | 68.8 | 113 | 3 AAY90819 | Aay90819 26OF9 hyb |
| 43 | 33 | 68.8 | 133 | 2 AAR33951 | Aar33951 CTW01 VL |
| 44 | 33 | 68.8 | 133 | 2 AAR33954 | Aar33954 GLI varia |
| 45 | 33 | 68.8 | 133 | 2 AAR59509 | Aar59509 Sequence |

ALIGNMENTS

RESULT 1

AAY32256

ID AAY32256 standard; peptide; 9 AA.

XX AC AAY32256;

XX DT 15-FEB-2000 (first entry)

XX DE Light chain CDR L3 of mouse anti-CD23 Mab C11.

XX KW

CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; rhinitis; eczema; insulinitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.

XX OS Mus musculus.

XX PN WO9958679-A1

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001434.

XX PR 09-MAY-1998; 98GB-00009839.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX DR WPI; 2000-053101/04.

XX DR N-PSDB; AAZ34741.

XX PT Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.

XX PS Claim 1; Page 40; 81pp; English.

XX CC This sequence represents complementarity determining region 3 (CDR L3) of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (see also AAY32262). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble CD23
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
 CC are also useful for studying interactions between CD23 and various
 CC ligands and determining the binding agents
 XX
 XX Sequence 9 AA;

Query Match 100.0%; Score 48; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYDPT 9
 Db 1 QQLVEYDPT 9

RESULT 2
 AAY32262
 ID AAY32262 standard; protein; 116 AA.

XX AAY32262;

XX 15-FEB-2000 (first entry)

XX Humanised anti-CD23 MAB C11 light chain variable region.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 therapy.
 XX
 XX Homo sapiens.
 OS Synthetic.

| Key | Location/Qualifiers |
|-----------|--------------------------------------|
| FT Region | 1..23 /note= "framework region 1" |
| FT Region | 24..39 /note= "CDR 1" |
| FT Region | 40..54 /note= "framework region 2" |
| FT Region | 55..61 /note= "CDR 2" |
| FT Region | 62..93 /note= "framework region 3" |
| FT Region | 94..102 /note= "CDR 3" |
| FT Region | 103..113 /note= "framework region 4" |

XX WO9958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAXO) GLAXO GROUP LTD.

XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPT; 2000-053101/04.
 XX N-PSDB; AAZ34747.
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 XX diabetes, multiple sclerosis and psoriasis.
 XX Claim 9; Fig 3; 8pp; English.

XX This sequence represents the light chain variable region (VL) of
 CC humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human
 CC framework (H5IGKVII) and the light chain complementarity determining
 CC regions (see AAY32254-56) of murine antibody C11. The DNA was constructed
 CC by splice overlap PCR. The invention provides altered antibodies, such as
 CC chimeric or humanised antibodies, which comprise sufficient of the amino
 CC acid sequences of the C11 light and heavy chain complementarity
 CC determining regions to render them capable of binding to the CD23 type II
 CC molecule expressed on haematopoietic cells. The antibodies are used to
 CC block soluble CD23 formation in human therapy. for the treatment of
 CC arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX
 XX Sequence 116 AA;

Query Match 100.0%; Score 48; DB 3; Length 116;
 Best Local Similarity 100.0%; Pred. NO. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYDPT 9
 Db 94 QQLVEYDPT 102

RESULT 3
 AAY32261
 ID AAY32261 standard; protein; 145 AA.

XX AAY32261;

XX 15-FEB-2000 (first entry)

XX Mouse anti-CD23 MAB C11 light chain variable region.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 therapy.
 XX
 XX Mus musculus.

| Key | Location/Qualifiers |
|-----------|--------------------------|
| FT Region | 55..70 /note= "CDR L1" |
| FT Region | 83..92 /note= "CDR L2" |
| FT Region | 125..134 /note= "CDR L3" |

PN WO958679-A1.
 XX 18-NOV-1999.
 XX 07-MAY-1999; 99WO-CB001434.
 XX 09-MAY-1998; 98GB-00009839.
 XX (GLAXO) GLAXO GROUP LTD.
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPI; 2000-053101/04.
 XX N-PSDB; AA234746.
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 XX diabetes, multiple sclerosis and psoriasis.
 XX Claim 8; Fig 2; 81pp; English.
 XX This sequence represents the light chain variable region (VL) of murine
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies (see
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid
 CC sequences of the C11 light and heavy chain complementarity determining
 CC regions (see AAY32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies are
 CC used to block soluble CD23 formation in human therapy, for the treatment
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX
 XX SQ Sequence 145 AA;
 Query Match 100.0%; Score 48; DB 3; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQLVEYPFT 9
 DB 125 QQLVEYPFT 133
 RESULT 4
 AAY70804
 ID AAY70804 standard; peptide; 19 AA.
 XX AAY70804;
 XX 31-JUL-2000 (first entry)
 XX Murine anti-PAB-421 mAb light chain CDR based peptide IDI-1 L3.
 XX Murine; p53 protein; monoclonal antibody; mAb; PAB-421; IDI-1 L3;
 XX light chain variable region; VL; complementarity determining region; CDR;
 XX dermatological; immunosuppressive; antiinflammatory; autoimmune response;
 XX SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
 XX DNA-binding domain; anti-idiotypic antibody.
 XX Mus sp.
 XX WO200023082-A1.
 XX 27-APR-2000.
 XX 19-OCT-1999; 99WO-US024443.

PR 19-OCT-1998; 98US-0104816P.
 XX (VEDA) YEDA RES & DEV CO LTD.
 XX Cohen IR, Rotter V, Erez-Alon N, Herkel J;
 XX WPI; 2000-339512/29.
 XX Treatment of systemic lupus erythematosus by down-regulating the
 PT autoimmune response to the C-terminal DNA-binding domain of the p53
 PT protein by an active compound comprising of antibodies to p53 or
 PT fragments of p53.
 XX Claim 78; Fig 10; 87pp; English.
 XX The patent discloses a method for the treatment of systemic lupus
 CC erythematosus (SLE) by down-regulating the autoimmune response to the C-
 CC terminal DNA-binding domain of p53 protein by an active compound. The
 CC present sequence is a IDI-1 L3 peptide which comprises the
 CC complementarity determining region (CDR) of the light chain of IDI-1
 CC monoclonal antibody (mAb). The IDI-1 mAb is an anti-idiotypic
 CC antibody/Ab2 mAb specific for PAB-421 which is an Ab1 mAb specific to the
 CC C-terminal DNA-binding domain of murine p53 protein. The peptide
 CC corresponds to residues 92-110 of IDI-1 light chain variable region. It
 CC is an example of the active compound useful in the diagnosis, prevention
 CC and treatment of SLE in humans
 XX Sequence 19 AA;
 SQ Query Match 93.8%; Score 45; DB 3; Length 19;
 Best Local Similarity 88.9%; Pred. No. 0.051;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQLVEYPFT 9
 DB 6 QQLVEYPFT 14
 RESULT 5
 AAY70790
 ID AAY70790 standard; protein; 122 AA.
 XX AAY70790;
 XX 31-JUL-2000 (first entry)
 XX Murine anti-PAB-421 IDI-1 mAb light chain variable region.
 XX Murine; p53 protein; PAB-421; monoclonal antibody; mAb; IDI-1;
 XX anti-idiotypic antibody; DNA-binding domain; dermatological;
 XX immunosuppressive; antiinflammatory; autoimmune response; SLE;
 XX systemic lupus erythematosus; diagnosis; treatment; autoantigen;
 XX light chain variable region; VL; complementarity determining region; CDR.
 XX Mus sp.
 XX Key Location/Qualifiers
 XX Region 27..42
 XX /label= CDR
 XX /note= "Complementarity determining region"
 XX Region 58..64
 XX /label= CDR
 XX /note= "Complementarity determining region"
 XX Region 97..105
 XX /label= CDR
 XX /note= "Complementarity determining region"
 XX WO200023082-A1.
 XX 27-APR-2000.
 XX 19-OCT-1999; 99WO-US024443.

PR 19-OCT-1998; 98US-0104816P.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
PI Cohen IR, Rotter V, Erez-Alon N, Herkel J;
XX WPI; 2000-339512/29.
XX
PT Treatment of systemic lupus erythematosus by down-regulating the
PT autoimmune response to the C-terminal DNA-binding domain of the p53
PT protein by an active compound comprising of antibodies to p53 or
PT fragments of p53.
XX
PS Claim 78; Fig 9; 87pp; English.
XX
CC The patent discloses a method for the treatment of systemic lupus
CC erythematosus (SLE) by down-regulating the autoimmune response to the C-
CC terminal DNA-binding domain of p53 protein by an active compound. The
CC present sequence is a light chain variable region of IDI-1 an anti-
CC idiotype antibody/Ab2 monoclonal antibody (mAb) specific for PAb-421
CC which is an Ab1 mAb specific to the C-terminal DNA-binding domain of
CC murine p53 protein. The Ab1 and Ab2 mAbs and peptides based on
CC complementarity determining regions of light and heavy chain variable
CC regions of these antibodies, are examples of active compounds useful in
CC the diagnosis, prevention and treatment of SLE in humans
XX
SQ Sequence 122 AA;
Query Match 93.8%; Score 45; DB 3; Length 122;
Best Local Similarity 88.9%; Pred. No. 0.38;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQLVEYPPT 9
DB 97 QQLVEYPPT 105
RESULT 6
AAR12232
ID AAR12232 standard; protein; 131 AA.
XX
AC AAR12232;
XX
DT 25-MAR-2003 (revised)
DT 19-AUG-1991 (first entry)
XX
DE Mouse MAb 2E12 L chain V region.
XX
KW HIV-1; chimera.
XX
OS Mus sp.
XX
FN WO9107494-A.
XX
PD 30-MAY-1991.
XX
PF 13-NOV-1989; 89US-00433703.
XX
PR 13-NOV-1989; 89US-00433703.
XX
PA (XOMA) XOMA CORP.
XX
PA (GREG) GREEN CROSS CORP.
XX
PA (ZOMA-) ZOMA CORP.
XX
PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
XX WPI; 1991-178106/24.
XX N-PSDB; AAQ12012.
XX
XX New chimeric mouse human antibodies - used in treatment, diagnosis and
PT prophylaxis of HIV infections.
XX
PS Disclosure; Fig 1; 108pp; English.

XX The mouse VL gene product may be used to produce chimeric mouse-human
CC Abs against HIV-1 comprising human Ig constant regions and murine
CC variable regions. These novel sequence are useful in treatment, diagnosis
CC and prophylaxis of HIV infections, and may be produced by a bacterial,
CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 131 AA;
Query Match 93.8%; Score 45; DB 2; Length 131;
Best Local Similarity 88.9%; Pred. No. 0.41;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQLVEYPPT 9
DB 114 QQLVEYPPT 122
RESULT 7
AAR12354
ID AAR12354 standard; protein; 132 AA.
XX
AC AAR12354;
XX
DT 25-MAR-2003 (revised)
DT 15-AUG-1991 (first entry)
XX
DE Light (kappa) chain variable region of murine 2E12 immunoglobulin.
XX
KW Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX
OS Mus musculus.
XX
FN WO9107493-A.
XX
PD 30-MAY-1991.
XX
PF 13-NOV-1989; 89US-00433730.
XX
PR 13-NOV-1989; 89US-00433730.
XX
PA (XOMA) XOMA CORP.
XX
PA (GREG) GREEN CROSS CORP.
XX
PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
XX WPI; 1991-178105/24.
XX N-PSDB; AAQ12056.
XX
PT New chimeric mouse-human antibodies - used to detect, kill and remove HIV
PT -1 antigen from sample.
XX
PS Disclosure; Fig 1; 107pp; English.
XX
CC This is the light (kappa)- chain variable (V) region of a mouse
CC monoclonal antibody (MAb), 2E12, and is specific for an HIV-1 vital
CC antigen. It is used in the construction of a chimeric MAb comprising
CC heavy and light chains having murine V regions and human C regions. The
CC chimeric MAb is more effective than murine MAb 2E12 since they have an
CC increased compatibility in humans. The heavy and light chain V-regions
CC are joined by manipulating their respective joining (J) regions, to
CC generate restriction enzyme recognition sites. The chimeric MAb can be
CC used as immuno- conjugates, in association with e.g. toxins for HIV
CC treatment. They can also be used in diagnosis of HIV. See also AAQ12057-
CC 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003
CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)
XX
SQ Sequence 132 AA;
Query Match 93.8%; Score 45; DB 2; Length 132;
Best Local Similarity 88.9%; Pred. No. 0.41;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

| | | |
|----------|------------------|---|
| DT | 16-JUN-1998 | (first entry) |
| XX | DE | Light chain of the catalytic antibody 2A10. |
| XX | XX | |
| XX | KW | Variable domain; lambda light chain; catalytic antibody; degradation; |
| KW | KW | cocaine; cocaine transition state analogue; TSA; benzoic acid; |
| KW | KW | phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; |
| KW | KW | overdose; addiction. |
| XX | OS | |
| XX | Mus | sp. |
| XX | XX | |
| XX | PN | WO9749800-A1. |
| XX | PD | 31-DEC-1997. |
| XX | XX | |
| XX | PF | 25-JUN-1997; 97WO-US010965. |
| XX | XX | |
| XX | PR | 25-JUN-1996; 96US-00672345. |
| XX | XX | |
| PA | (UYCO) | UNIV COLUMBIA NEW YORK. |
| XX | XX | |
| PI | Landry | DW; |
| XX | XX | |
| XX | DR | WPI; 1998-077166/07. |
| XX | DR | N-PSDB; AAV09789. |
| XX | XX | |
| PT | XX | New catalytic antibodies able to decompose cocaine, single-chain |
| PT | PT | analogues - used to treat cocaine overdose and addiction, required in far |
| PT | PT | smaller doses than antibodies that antagonise cocaine by simply binding. |
| XX | XX | |
| PS | Disclosure; | Fig 21; 147pp; English. |
| XX | XX | |
| CC | CC | The present sequence represents the light chain of a catalytic antibody |
| CC | CC | which is capable of degrading cocaine. A series of cocaine transition |
| CC | CC | state analogues (TSAs) were prepared and used to immunise mice for |
| CC | CC | production of hybridomas. Catalytic antibodies were identified by their |
| CC | CC | capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The |
| CC | CC | antibodies reduce the concentration of cocaine in a subject, and are used |
| CC | CC | particularly for the treatment of an overdose. They are also used for |
| CC | CC | treating addiction (by reducing the in vivo concentration that can be |
| CC | CC | achieved) |
| XX | XX | |
| SQ | Sequence | 113 AA; |
| Query | Match | 91.7%; Score 44; DB 2; Length 113; |
| Best | Local Similarity | 88.9%; Pred. No. 0.55; |
| Matches | 8; Conservative | 0; Mismatches 1; Indels 0; Gaps 0; |
| Qy | 1 | QQQVEVPPT 9 |
| Db | 94 | QQQVEVPPT 102 |
| RESULT | 10 | |
| AAW39804 | | |
| ID | AAW39804 | standard; protein; 113 AA. |
| XX | XX | |
| XX | AAW39804; | |
| XX | XX | |
| DT | 16-JUN-1998 | (first entry) |
| XX | XX | |
| DE | XX | Variable domain of the Kappa light chain of catalytic antibody 2A10. |
| XX | XX | |
| KW | KW | Variable domain; lambda light chain; catalytic antibody; degradation; |
| KW | KW | cocaine; cocaine transition state analogue; TSA; benzoic acid; |
| KW | KW | phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; |
| KW | KW | overdose; addiction. |
| XX | OS | |
| XX | Mus | sp. |
| XX | XX | |
| XX | PN | WO9749800-A1. |
| XX | PD | 31-DEC-1997. |

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Qy 1 QQLVEYPFT 9
Db 114 QQLVEYPFT 122

RESULT 8
AAW39823
ID AAW39823 standard; peptide; 9 AA.
XX AC
XX AAW39823;
XX
XX 16-JUN-1998 (first entry)
XX
XX Light chain CDR3 of catalytic antibody 2A10.
XX
XX Variable domain; lambda light chain; catalytic antibody; degradation;
XX cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX overdose; addiction.
XX
XX Mus sp.
XX WC9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US010965.
XX
XX 25-JUN-1996; 96US-00672345.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
XX WPI; 1998-077166/07.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
XX analogues - used to treat cocaine overdose and addiction, required in far
XX smaller doses than antibodies that antagonise cocaine by simply binding.
XX
XX Claim 15; Page 82; 147pp; English.
XX
XX AAW39821-23 represent the sequences of the light chain complementarity
XX determining regions (CDRs) of the catalytic antibody 2A10, which is able
XX to degrade cocaine. A series of cocaine transition state analogues (TSAs)
XX were prepared and used to immunise mice for production of hybridomas.
XX Catalytic antibodies were identified by their capacity to release 3H-
XX benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
XX using TSA1, which is an immunogenic conjugate of a phosphate monoester
XX transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
XX The antibodies reduce the concentration of cocaine in a subject, and are
XX used particularly for the treatment of an overdose. They are also used
XX for treating addiction (by reducing the in vivo concentration that can be
XX achieved)
XX
XX Sequence 9 AA;
XX
XX Query Match 91.7%; Score 44; DB 2; Length 9;
XX Best Local Similarity 88.9%; Pred No. 1.4e+06;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0
XX
Qy 1 QQLVEYPFT 9
Db 1 QQFVEYPFT 9

RESULT 9
AAW39882
ID AAW39882 standard; protein; 113 AA.
XX AC
XX AAW39882;
XX

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Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T; WPI; 2001-48888/53.

Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin.

Disclosure, Page 151; 183pp; English.

The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherosclerosis and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IGE-mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is mouse germline kappa light chain variable (VK) region, 167/24

Sequence 100 AA;

Query Match 77.1%; Score 37; DB 4; Length 100;
Best Local Similarity 100.0%; Pred.No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 QQLVEYP 7
|||
94 QQLVEYP 100

RESULT 12
AAW39817
ID AAW39817 standard; peptide; 9 AA.
XX AC
XX AAW39817;
AC XX
DT DT
XX 16-JUN-1998 (first entry)
DE Light chain CDR3 of catalytic antibody 3B9.
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
OS Mus sp.
QS WO9749800-Al.
PN 31-DEC-1997.
PD
XX PF
XX 25-JUN-1997; 97WO-US010965.
PR 25-JUN-1996; 96US-00672345.
XX PA
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX PI
XX Landry DW;
XX

DR WPI; 1998-077166/07.
 XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX Claim 11; Page 81; 147pp; English.
 PS
 XX AAW39815-17 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
 CC transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11.
 CC The antibodies reduce the concentration of cocaine in a subject, and are
 CC used particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can be
 CC achieved)
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 75.0%; Score 36; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 QQLVEVPFT 9
 Db 1 QHFVDYDFT 9
 RESULT 13
 AAW39803
 ID AAW39803 standard; protein; 113 AA.
 AC AAW39803;
 XX
 XX 16-JUN-1998 (first entry)
 DT
 DE Variable domain of the Kappa light chain of catalytic antibody 12H1.
 XX
 XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX
 PN WO9749800-A1.
 XX
 XX 31-DEC-1997.
 PD
 XX 25-JUN-1997; 97WO-US010965.
 PF
 XX 25-JUN-1996; 96US-00672345.
 PR
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX Landry DW;
 PI
 XX WPI; 1998-077166/07.
 DR P-PSDB; AAV09802.
 DR
 XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 XX Claim 18; Page 73; 147pp; English.
 PS
 XX AAW39801-05 represent the amino acid sequences of the variable domain of
 CC the Kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were

CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808
 CC represents the heavy chain) was identified using TSA2, and has a per
 CC minute Kcat of 0.016. The antibodies reduce the concentration of cocaine
 CC in a subject, and are used particularly for the treatment of an overdose.
 CC They are also used for treating addiction (by reducing the in vivo
 CC concentration that can be achieved)
 XX
 XX Sequence 113 AA;
 SQ
 Query Match 75.0%; Score 36; DB 2; Length 113;
 Best Local Similarity 66.7%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 QQLVEVPFT 9
 Db 94 QHFVDYDFT 102
 RESULT 14
 AAW39801
 ID AAW39801 standard; protein; 113 AA.
 AC AAW39801;
 XX
 XX 16-JUN-1998 (first entry)
 DT
 DE Variable domain of the Kappa light chain of catalytic antibody 3B9.
 XX
 XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX
 PN WO9749800-A1.
 XX
 XX 31-DEC-1997.
 PD
 XX 25-JUN-1997; 97WO-US010965.
 PF
 XX 25-JUN-1996; 96US-00672345.
 PR
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX Landry DW;
 PI
 XX WPI; 1998-077166/07.
 DR P-PSDB; AAV09791.
 DR
 XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 XX Claim 12; Page 71-72; 147pp; English.
 PS
 XX AAW39801-05 represent the amino acid sequences of the variable domain of
 CC the Kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state analogue.
 CC Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the
 CC concentration of cocaine in a subject, and are used particularly for the
 CC treatment of an overdose. They are also used for treating addiction (by
 CC reducing the in vivo concentration that can be achieved)
 XX
 XX Sequence 113 AA;
 SQ

Query Match 75.0%; Score 36; DB 2; Length 113;
 Best Local Similarity 66.7%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 | : |||
 Db 94 QHEVDYPT 102

QY 1 QQLVEYPFT 9
 | : |||
 Db 223 QQLISYPLT 231

Search completed: September 30, 2004, 06:06:15
 Job time : 46.9322 secs

RESULT 15

AAW24063
 ID AAW24063 standard; protein; 241 AA.

XX AC AAW24063;

XX DT 17-MAR-1998 (first entry)

XX DE Human WSX receptor agonist antibody clone #17.

XX KW Human; WSX receptor; clone #17; identification; purification; ligand;
 KW activator; antibody; agonist; proliferation; obesity; differentiation;
 KW anaemia; treatment; neoplasia; arteriosclerosis; Type II diabetes;
 KW polycystic ovarian disease; cardiovascular disease; osteoarthritis;
 KW dermatological disorder; hypertension; insulin resistance;
 KW hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis.

XX OS Homo sapiens.

XX PN WO9725425-A1.

XX PD 17-JUL-1997.

XX PF 07-JAN-1997; 97WO-US000325.

XX PR 08-JAN-1996; 96US-00585005.

XX PR 20-JUN-1996; 96US-00667197.

XX PA (GETH) GENENTECH INC.

XX PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;

XX PI Rodrigues ML;

XX DR WPI; 1997-372864/34.

XX PT WSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving haematopoiesis or
 PT for treating tumours.

XX PS Example 14; Page 122-123; 219pp; English.

XX CC The present sequence is an agonist antibody clone to the human WSX
 CC receptor, which can be used to identify and purify ligands and
 CC activators. An anti-WSX receptor antibody can be used as an agonist to
 CC activate the WSX receptor, leading to enhanced proliferation or
 CC differentiation of a cell expressing the WSX receptor. It can also be
 CC used to decrease body weight and/or fat-depot weight and/or food intake
 CC in an obese mammal. WSX receptor ligands can be used to enhance
 CC proliferation or differentiation of lymphoid, myeloid or erythroid blood
 CC cell lineages. This is useful when a mammal, especially a human, is
 CC suffering from decreased blood cell levels, i.e. anaemia, caused by
 CC chemotherapy, radiation therapy or bone marrow transplantation therapy.
 CC It can also be used to repopulate blood cells in a mammal. The products
 CC can also be used to treat, e.g. neoplastic disorders, arteriosclerosis,
 CC Type II diabetes, polycystic ovarian disease, cardiovascular diseases,
 CC osteoarthritis, dermatological disorders, hypertension, insulin
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer and
 CC cholelithiasis

XX SQ Sequence 241 AA;

Query Match 75.0%; Score 36; DB 2; Length 241;
 Best Local Similarity 66.7%; Pred. No. 51;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:01:30 ; Search time 151.017 Seconds
(without alignments)
19.178 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEYPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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- 2: /cgn2_6/prodata1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata1/pubpaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/prodata1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 44 | 91.7 | 113 | 10 | US-09-940-727B-8 |
| 3 | 44 | 91.7 | 113 | 10 | US-09-940-727B-108 |
| 4 | 37 | 77.1 | 100 | 9 | US-09-940-459-32 |
| 5 | 37 | 77.1 | 100 | 16 | US-10-766-773-32 |
| 6 | 37 | 77.1 | 100 | 16 | US-10-766-610-32 |
| 7 | 37 | 77.1 | 100 | 16 | US-10-733-563-32 |
| 8 | 37 | 77.1 | 609 | 16 | US-10-437-963-104782 |
| 9 | 36 | 75.0 | 9 | 10 | US-09-940-727B-21 |
| 10 | 36 | 75.0 | 9 | 16 | US-10-632-706-134 |
| 11 | 36 | 75.0 | 113 | 10 | US-09-940-727B-5 |
| 12 | 36 | 75.0 | 113 | 10 | US-09-940-727B-7 |
| 13 | 36 | 75.0 | 113 | 10 | US-09-940-727B-100 |
| 14 | 36 | 75.0 | 113 | 10 | US-09-940-727B-112 |
| 15 | 36 | 75.0 | 241 | 8 | US-08-779-457-50 |

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| 16 | 36 | 75.0 | 251 | 10 | US-09-880-748-1310 | Sequence 1310, Ap |
| 17 | 36 | 75.0 | 251 | 12 | US-10-293-418-1310 | Sequence 1310, Ap |
| 18 | 36 | 75.0 | 253 | 10 | US-09-880-748-936 | Sequence 936, App |
| 19 | 36 | 75.0 | 253 | 12 | US-10-293-418-936 | Sequence 936, App |
| 20 | 36 | 75.0 | 280 | 10 | US-09-940-727B-119 | Sequence 119, App |
| 21 | 35 | 72.9 | 90 | 16 | US-10-767-701-56894 | Sequence 56894, A |
| 22 | 35 | 72.9 | 298 | 12 | US-10-425-114-71736 | Sequence 71736, A |
| 23 | 35 | 72.9 | 569 | 12 | US-10-425-114-72355 | Sequence 72355, A |
| 24 | 34 | 70.8 | 440 | 12 | US-10-282-122A-77411 | Sequence 77411, A |
| 25 | 34 | 70.8 | 1074 | 16 | US-10-389-566-2371 | Sequence 2371, Ap |
| 26 | 33 | 68.8 | 79 | 12 | US-10-425-114-44597 | Sequence 44597, A |
| 27 | 33 | 68.8 | 82 | 9 | US-09-864-761-47635 | Sequence 47635, A |
| 28 | 33 | 68.8 | 82 | 12 | US-10-424-599-280477 | Sequence 280477, A |
| 29 | 33 | 68.8 | 83 | 12 | US-10-424-599-212368 | Sequence 212368, A |
| 30 | 33 | 68.8 | 107 | 10 | US-09-848-798-40 | Sequence 40, Appl |
| 31 | 33 | 68.8 | 199 | 12 | US-10-424-599-246437 | Sequence 246437, A |
| 32 | 33 | 68.8 | 243 | 16 | US-10-437-963-161157 | Sequence 161157, A |
| 33 | 33 | 68.8 | 250 | 16 | US-10-333-235A-55 | Sequence 55, Appl |
| 34 | 33 | 68.8 | 337 | 16 | US-10-437-963-190847 | Sequence 190847, A |
| 35 | 33 | 68.8 | 368 | 16 | US-10-333-235A-58 | Sequence 58, Appl |
| 36 | 33 | 68.8 | 441 | 12 | US-10-282-122A-45037 | Sequence 45037, A |
| 37 | 33 | 68.8 | 465 | 16 | US-10-333-235A-59 | Sequence 59, Appl |
| 38 | 33 | 68.8 | 561 | 15 | US-10-369-493-870 | Sequence 870, App |
| 39 | 33 | 68.8 | 726 | 9 | US-09-973-451-10 | Sequence 10, Appl |
| 40 | 33 | 68.8 | 789 | 14 | US-10-207-706-5 | Sequence 5, Appl |
| 41 | 33 | 68.8 | 792 | 14 | US-10-207-706-4 | Sequence 4, Appl |
| 42 | 33 | 68.8 | 816 | 14 | US-10-207-706-3 | Sequence 3, Appl |
| 43 | 33 | 68.8 | 849 | 16 | US-10-437-963-114890 | Sequence 114890, A |
| 44 | 33 | 68.8 | 899 | 12 | US-10-282-122A-68696 | Sequence 68696, A |
| 45 | 32 | 66.7 | 70 | 12 | US-10-424-599-215810 | Sequence 215810, A |

ALIGNMENTS

RESULT 1

US-09-940-727B-27
; Sequence 27, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-27

Query Match 91.7%; Score 44; DB 10; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9
DB 1 QQLVEYPT 9

RESULT 2

US-09-940-727B-8
; Sequence 8, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:

; APPLICANT: Landry, Donald W
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 0575/51400-B
 ; CURRENT APPLICATION NUMBER: US/09/940,727B
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965
 ; PRIOR FILING DATE: 1997-06-25
 ; PRIOR APPLICATION NUMBER: 08/672,345
 ; PRIOR FILING DATE: 1996-06-25
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 113
 ; TYPE: PRT
 ; ORGANISM: mouse
 US-09-940-727B-8

Query Match 91.7%; Score 44; DB 10; Length 113;
 Best Local Similarity 88.9%; Pred.No. 0.87;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 Db 94 QQFVEYPFT 102

RESULT 3
 US-09-940-727B-108
 ; Sequence 108, Application US/09940727B
 ; Publication No. US2003007793A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald W
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 0575/51400-B
 ; CURRENT APPLICATION NUMBER: US/09/940,727B
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965
 ; PRIOR FILING DATE: 1997-06-25
 ; PRIOR APPLICATION NUMBER: 08/672,345
 ; PRIOR FILING DATE: 1996-06-25
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 108
 ; LENGTH: 113
 ; TYPE: PRT
 ; ORGANISM: mouse
 US-09-940-727B-108

Query Match 91.7%; Score 44; DB 10; Length 113;
 Best Local Similarity 88.9%; Pred.No. 0.87;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 Db 94 QQFVEYPFT 102

RESULT 4
 US-09-840-459-32
 ; Sequence 32, Application US/09840459
 ; Patent No. US20020150576A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Larosa, Gregory J.
 ; APPLICANT: Horvath, Christopher
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: O'Brien, Siobhan H.
 ; APPLICANT: O'Keefe, Theresa
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; TITLE OF INVENTION: METHODS OF USE THEREFOR
 ; FILE REFERENCE: 1855.1052-012
 ; CURRENT APPLICATION NUMBER: US/09/840,459
 ; CURRENT FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: PCT/US01/03537
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/497,625
 ; PRIOR FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/359,193
 ; PRIOR FILING DATE: 1999-07-22
 ; PRIOR APPLICATION NUMBER: 09/121,781
 ; PRIOR FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-840-459-32

Query Match 77.1%; Score 37; DB 9; Length 100;
 Best Local Similarity 100.0%; Pred.No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7
 Db 94 QQLVEYP 100

RESULT 5
 US-10-766-773-32
 ; Sequence 32, Application US/10766773
 ; Publication No. US20040126851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Larosa, Gregory J.
 ; APPLICANT: Horvath, Christopher
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: O'Brien, Siobhan H.
 ; APPLICANT: O'Keefe, Theresa
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 ; TITLE OF INVENTION: METHODS OF USE THEREFOR
 ; FILE REFERENCE: 1855.1052-028
 ; CURRENT APPLICATION NUMBER: US/10/766,773
 ; CURRENT FILING DATE: 2004-01-27
 ; PRIOR APPLICATION NUMBER: 09/497,625
 ; PRIOR FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/359,193
 ; PRIOR FILING DATE: 1999-07-22
 ; PRIOR APPLICATION NUMBER: 09/121,781
 ; PRIOR FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-766-773-32

Query Match 77.1%; Score 37; DB 16; Length 100;
 Best Local Similarity 100.0%; Pred.No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7
 Db 94 QQLVEYP 100

RESULT 6
 US-10-766-610-32
 ; Sequence 32, Application US/10766610
 ; Publication No. US20040132980A1
 ; GENERAL INFORMATION:

APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 1855.1052-029
CURRENT APPLICATION NUMBER: US/10/766,610
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: 09/840,459
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-10-766-610-32

Query Match 77.1%; Score 37; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7
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DB 94 QQLVEYP 100

RESULT 7
US-10-733-563-32
Sequence 32, Application US/10733563
Publication No. US20040151721A1
GENERAL INFORMATION:
APPLICANT: O'Keefe, Theresa
APPLICANT: Ponath, Paul
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 10448-213001
CURRENT APPLICATION NUMBER: US/10/733,563
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US 10/272,899
PRIOR FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 60/392,364
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/350,166
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-10-733-563-32

Query Match 77.1%; Score 37; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7
|||
DB 94 QQLVEYP 100

RESULT 8

US-10-437-963-104782
Sequence 104782, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 104782
LENGTH: 609
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_102083C.1.pep
US-10-437-963-104782

Query Match 77.1%; Score 37; DB 16; Length 609;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
|||
DB 569 QQLVEYPFT 577

RESULT 9

US-09-940-727B-21
Sequence 21, Application US/09940727B
Publication No. US2003007793A1
GENERAL INFORMATION:
APPLICANT: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR FILING DATE: 1997-06-25
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 9
TYPE: PRT
ORGANISM: mouse
US-09-940-727B-21

Query Match 75.0%; Score 36; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
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DB 1 QHFDVYPT 9

RESULT 10

US-10-632-706-134
Sequence 134, Application US/10632706
Publication No. US20040175385A1

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; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 134
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-134

Query Match 75.0%; Score 36; DB 16; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 1 QQLISYPLT 9

RESULT 11
US-09-940-727B-5
; Sequence 5, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-5

Query Match 75.0%; Score 36; DB 10; Length 113;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 94 QHFVDYDFT 102

RESULT 12
US-09-940-727B-7
; Sequence 7, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
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; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-7

Query Match 75.0%; Score 36; DB 10; Length 113;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 94 QHFVDYDFT 102

RESULT 13
US-09-940-727B-100
; Sequence 100, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-100

Query Match 75.0%; Score 36; DB 10; Length 113;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 94 QHFVDYDFT 102

RESULT 14
US-09-940-727B-112
; Sequence 112, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
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NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-112

Query Match 75.0%; Score 36; DB 10; Length 113;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
Db 94 QHFDYPT 102

RESULT 15
US-08-779-457-50
; Sequence 50, Application US/08779457
; Publication No. US20020193571A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodrigues, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-779-457-50

Query Match 75.0%; Score 36; DB 8; Length 241;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
Db 223 QQLISYPLT 231

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Job time : 152.017 secs

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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:00:45 ; Search time 15.2542 Seconds
(without alignments)
30.459 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEYPPT 9

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Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pap:*
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- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 44 | 91.7 | 113 | 2 | US-08-672-345C-8 |
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| 6 | 44 | 91.7 | 113 | 3 | US-09-214-095D-108 |
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| 8 | 36 | 75.0 | 9 | 3 | US-09-214-095D-21 |
| 9 | 36 | 75.0 | 113 | 2 | US-08-672-345C-5 |
| 10 | 36 | 75.0 | 113 | 2 | US-08-672-345C-7 |
| 11 | 36 | 75.0 | 113 | 2 | US-08-672-345C-95 |
| 12 | 36 | 75.0 | 113 | 2 | US-08-672-345C-97 |
| 13 | 36 | 75.0 | 113 | 3 | US-09-214-095D-5 |
| 14 | 36 | 75.0 | 113 | 3 | US-09-214-095D-7 |
| 15 | 36 | 75.0 | 113 | 3 | US-09-214-095D-100 |
| 16 | 36 | 75.0 | 113 | 3 | US-09-214-095D-112 |
| 17 | 36 | 75.0 | 280 | 3 | US-09-214-095D-119 |
| 18 | 35 | 72.9 | 112 | 3 | US-08-483-749A-4 |
| 19 | 34 | 70.8 | 9 | 4 | US-09-406-532-20 |
| 20 | 34 | 70.8 | 113 | 4 | US-09-406-532-14 |
| 21 | 34 | 70.8 | 585 | 4 | US-09-134-001C-4914 |
| 22 | 33 | 68.8 | 9 | 1 | US-08-438-123-3 |
| 23 | 33 | 68.8 | 11 | 1 | US-08-438-123-11 |
| 24 | 33 | 68.8 | 107 | 3 | US-09-240-274-40 |
| 25 | 33 | 68.8 | 108 | 1 | US-08-468-661-3 |
| 26 | 33 | 68.8 | 108 | 1 | US-08-466-272A-3 |
| 27 | 33 | 68.8 | 108 | 1 | US-08-478-857-3 |

28 33 68.8 108 2 US-08-471-771-3 Sequence 3, Appli
29 33 68.8 108 3 US-09-130-783-3 Sequence 3, Appli
30 33 68.8 113 3 US-08-483-749A-16 Sequence 16, Appli
31 33 68.8 113 5 PCT-US93-11611-5 Sequence 5, Appli
32 33 68.8 133 1 US-08-253-877C-10 Sequence 10, Appli
33 33 68.8 133 1 US-08-253-877C-28 Sequence 28, Appli
34 33 68.8 133 2 US-08-452-164A-10 Sequence 10, Appli
35 33 68.8 133 2 US-08-452-164A-28 Sequence 28, Appli
36 33 68.8 133 3 US-08-603-024-4 Sequence 4, Appli
37 33 68.8 133 3 US-08-603-024-27 Sequence 27, Appli
38 33 68.8 133 4 US-08-450-809-23 Sequence 23, Appli
39 33 68.8 133 5 PCT-US93-11611-2 Sequence 2, Appli
40 33 68.8 133 5 PCT-US93-11611-9 Sequence 9, Appli
41 33 68.8 141 1 US-08-438-123-7 Sequence 7, Appli
42 33 68.8 437 4 US-09-252-991A-20209 Sequence 20209, A
43 33 68.8 442 4 US-09-328-352-5748 Sequence 5748, Ap
44 33 68.8 584 4 US-09-489-039A-14137 Sequence 14137, A
45 33 68.8 598 4 US-09-252-991A-25875 Sequence 25875, A

ALIGNMENTS

RESULT 1
US-08-672-345C-27
; Sequence 27, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-27

Query Match 91.7%; Score 44; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e-05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QQLVEYPPT 9

Db 1 QQFVEYPT 9

RESULT 2

US-09-214-095D-27
; Sequence 27, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-27

Query Match 91.7%; Score 44; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 38+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOLVEYPFT 9
||| |||||

Db 1 QQFVEYPFT 9

RESULT 3

US-08-672-345C-8
; Sequence 8, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-8

Query Match 91.7%; Score 44; DB 2; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOLVEYPFT 9
||| |||||

Db 94 QQFVEYPFT 102

RESULT 4
US-08-672-345C-98
; Sequence 98, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-98

Query Match 91.7%; Score 44; DB 2; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOLVEYPFT 9
||| |||||

Db 94 QQFVEYPFT 102

RESULT 5

US-09-214-095D-8
; Sequence 8, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-8

Query Match 91.7%; Score 44; DB 3; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 75.0%; Score 36; DB 2; Length 9;

US-08-672-345C-5

Query Match 75.0%; Score 36; DB 2; Length 113;
 Best Local Similarity 66.7%; Pred. No. 8.5;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9
 | : : : :
 Db 94 QHFVDYPT 102

RESULT 10

US-08-672-345C-7
 ; Sequence 7, Application US/08672345C
 ; Patent No. 5948658

; GENERAL INFORMATION:
 ; APPLICANT: Landry Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York

; COUNTRY: USA
 ; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/672,345C

; FILING DATE: 24-JUN-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/51400

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-278-0400

; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 113 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-672-345C-7

Query Match

75.0%; Score 36; DB 2; Length 113;
 Best Local Similarity 66.7%; Pred. No. 8.5;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9
 | : : : :
 Db 94 QHFVDYPT 102

RESULT 11

US-08-672-345C-95

; Sequence 95, Application US/08672345C
 ; Patent No. 5948658

; GENERAL INFORMATION:

; APPLICANT: Landry Donald, W.

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-672-345C-95

Query Match

75.0%; Score 36; DB 2; Length 113;
 Best Local Similarity 66.7%; Pred. No. 8.5;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9
 | : : : :
 Db 94 QHFVDYPT 102

RESULT 12

US-08-672-345C-97

; Sequence 97, Application US/08672345C
 ; Patent No. 5948658

; GENERAL INFORMATION:

; APPLICANT: Landry Donald, W.

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; US-08-672-345C-97

Query Match      75.0%; Score 36; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 94 QHFVDYPFT 102

RESULT 13
US-09-214-095D-5
; Sequence 5, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-5

Query Match      75.0%; Score 36; DB 3; Length 113;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 94 QHFVDYPFT 102

Search completed: September 30, 2004, 06:38:17
Job time : 16.2542 secs
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Blank sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model
Run on: September 30, 2004, 05:55:56 ; Search time 5.42373 Seconds
(without alignments)
88.677 Million cell updates/sec

Title: US-09-674-716B-9
Perfect score: 33
Sequence: 1 GYWS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 33 | 100.0 | 67 | 2 A84376 | hypothetical prote |
| 2 | 33 | 100.0 | 117 | 1 GZMSU1 | Ig heavy chain V r |
| 3 | 33 | 100.0 | 444 | 2 S09681 | citrate transport |
| 4 | 33 | 100.0 | 1043 | 2 F97302 | hypothetical prote |
| 5 | 30 | 90.9 | 86 | 2 T42185 | conserved hypothet |
| 6 | 30 | 90.9 | 298 | 2 AE1752 | hypothetical prote |
| 7 | 30 | 90.9 | 298 | 2 AH1728 | AbiD phage protein |
| 8 | 30 | 90.9 | 315 | 2 H86836 | carbamate kinase (|
| 9 | 30 | 90.9 | 348 | 2 G69142 | GDP-D-mannose dehy |
| 10 | 30 | 90.9 | 358 | 2 H83554 | hypothetical prote |
| 11 | 30 | 90.9 | 375 | 2 E83163 | hypothetical prote |
| 12 | 30 | 90.9 | 417 | 2 T08724 | hypothetical prote |
| 13 | 30 | 90.9 | 448 | 2 B9249 | PTS system, IIC co |
| 14 | 30 | 90.9 | 448 | 2 G98113 | conserved hypothet |
| 15 | 30 | 90.9 | 452 | 2 T00113 | undecaprenyl-phosp |
| 16 | 30 | 90.9 | 464 | 2 T28818 | hypothetical prote |
| 17 | 30 | 90.9 | 475 | 2 T46745 | arginine/ornithine |
| 18 | 30 | 90.9 | 476 | 2 D84505 | probable membrane |
| 19 | 30 | 90.9 | 480 | 2 S39978 | scRA protein - Sta |
| 20 | 30 | 90.9 | 480 | 2 D90038 | PTS system, sucros |
| 21 | 30 | 90.9 | 490 | 2 C86879 | arginine/ornithine |
| 22 | 30 | 90.9 | 518 | 1 G69804 | multidrug-efflux t |
| 23 | 30 | 90.9 | 535 | 2 S78598 | D-ribulokinase (BC |
| 24 | 30 | 90.9 | 583 | 2 C72544 | probable glycol-tr |
| 25 | 30 | 90.9 | 592 | 1 IKBBCA | colicin A - Citrob |
| 26 | 30 | 90.9 | 592 | 2 T15600 | hypothetical prote |
| 27 | 30 | 90.9 | 608 | 2 QJ4462 | phosphoenolpyruvat |
| 28 | 30 | 90.9 | 667 | 1 VCUJGL | env polyprotein.pr |
| 29 | 30 | 90.9 | 847 | 2 JC4836 | alpha-glucuronidas |

| | | | | | |
|----|----|------|------|----------|--------------------|
| 30 | 30 | 90.9 | 851 | 2 T47495 | hypothetical prote |
| 31 | 30 | 90.9 | 1063 | 2 A33830 | cation efflux syst |
| 32 | 30 | 90.9 | 1063 | 2 JC4700 | cadmium, zinc, cob |
| 33 | 30 | 90.9 | 1215 | 2 A85595 | SWI/SNF family hel |
| 34 | 30 | 90.9 | 1215 | 2 B72029 | helicase, Snf2/Rad |
| 35 | 30 | 90.9 | 1502 | 2 T42216 | multidrug resistan |
| 36 | 29 | 87.9 | 71 | 2 AFO683 | hypothetical prote |
| 37 | 29 | 87.9 | 101 | 2 S13692 | Ig heavy chain V r |
| 38 | 29 | 87.9 | 102 | 2 B72742 | hypothetical prote |
| 39 | 29 | 87.9 | 111 | 2 S13693 | Ig heavy chain V r |
| 40 | 29 | 87.9 | 112 | 2 S13690 | Ig heavy chain V r |
| 41 | 29 | 87.9 | 115 | 2 S13694 | Ig heavy chain V r |
| 42 | 29 | 87.9 | 116 | 2 S13691 | Ig heavy chain V r |
| 43 | 29 | 87.9 | 122 | 2 A83756 | hypothetical prote |
| 44 | 29 | 87.9 | 137 | 2 S03326 | Ig heavy chain pre |
| 45 | 29 | 87.9 | 152 | 2 D84436 | hypothetical prote |

ALIGNMENTS

RESULT 1

A84376
hypothetical protein Vng2253h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84376
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jurg, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebbardt, H.; Lowe, T.M.; Lie
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: A84376
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-67 <STO>
A;Cross-references: GB:AE004437; NID:g10581666; PIDN:AG20373.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG2253H

Query Match 100.0%; Score 33; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
| | | | |
Db 59 GYWS 63

RESULT 2

GZMSU1
Ig heavy chain V region (UPC10) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 23-Mar-2001
C;Accession: A02081
R;Auffray, C.; Slikav, J.L.; Ollo, R.; Rougeon, F.
Ann. Immunol. (Paris) 132D, 77-88, 1981
A;Title: Correlation between D region structure and antigen-binding specificity: evidences
A;Reference number: A02081; MUID:83021113; PMID:6181731
A;Accession: A02081
A;Molecule type: mRNA
A;Residues: 1-117 <AUF>
C;Comment: This chain was isolated from an Ig gamma-2a myeloma protein binding 2,6-levan.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMW>
F;22-96/Disulfide bonds: #status predicted
Query Match 100.0%; Score 33; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
|||||
Db 31 GYWS 35

RESULT 3

S09681 citrate transport protein - Klebsiella pneumoniae plasmid pES1

N;Alternate names: citrate carrier

C;Species: Klebsiella pneumoniae

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999

C;Accession: S09681

R;van der Rest, M.E.; Schwarz, E.; Oesterheld, D.; Konings, W.N.

Eur. J. Biochem. 189, 401-407, 1990

A;Title: DNA sequence of a citrate carrier of Klebsiella pneumoniae.

A;Reference number: S09681; MUID:90249385; PMID:2186908

A;Accession: S09681

A;Molecule type: DNA

A;Residues: 1-444 <RES>

A;Cross-references: EMBL:X51479; NID:G43800; PIDN:CAA35944.1; PID:G43801

C;Genetics:

A;Genome: plasmid pES1

C;Superfamily: citrate utilization determinant

C;Keywords: membrane protein

Query Match 100.0%; Score 33; DB 2; Length 444;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5

|||||

Db 415 GYWS 419

RESULT 4

F97302

hypothetical protein CAC3275 [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C;Accession: F97302

R;Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: F97302

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1043 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK81209.1; PID:g15026351; GSPDB:GN00168

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC3275

Query Match

Best Local Similarity 100.0%; Score 33; DB 2; Length 1043;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5

|||||

Db 580 GYWS 584

RESULT 5

T42185

conserved hypothetical protein L7085 - Escherichia coli plasmid pO157

C;Species: Escherichia coli

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T42185

R;Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.

Nucleic Acids Res. 26, 4196-4204, 1998

A;Title: The complete DNA sequence and analysis of the large virulence plasmid of Escher

A;Reference number: Z22068; MUID:98391744; PMID:9722640

A;Accession: T42185

A;Status: preliminary; translated from GB/EMBL/DBU

A;Molecule type: DNA

A;Residues: 1-86 <EUR>

A;Cross-references: EMBL:AF074613; PIDN:AACT0153.1

A;Experimental source: strain EDL933; serotype O157:H7

C;Genetics:

A;Genome: plasmid pO157

A;Note: L7085

Query Match

Best Local Similarity 90.9%; Score 30; DB 2; Length 86;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5

|||||

Db 72 GYWS 76

RESULT 6

AE1752

hypothetical protein homolog lin2562 [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C;Accession: AE1752

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,

J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat

ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A;Title: Comparative Genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AE1752

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-298 <GLA>

A;Cross-references: GB:AL592022; PIDN:CAC97789.1; PID:g16415084; GSPDB:GN00178

A;Experimental source: strain Clip11262

C;Genetics:

A;Gene: lin2562

Query Match

Best Local Similarity 90.9%; Score 30; DB 2; Length 298;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5

|||||

Db 45 GYWS 49

RESULT 7

AB1728

AbiD phage protein homolog lin2373 [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C;Accession: AB1728

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,

J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat

ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A;Title: Comparative Genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AB1728

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-298 <GLA>

A;Cross-references: GB:AL592022; PIDN:CAC97600.1; PID:g16414896; GSPDB:GN00178

A;Experimental source: strain Clip11262

C;Genetics:

A;Gene: lin2373

Query Match 90.9%; Score 30; DB 2; Length 298;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
Db 45 GYWS 49

RESULT 8

H86836
carbamate kinase (EC 2.7.2.2) [imported] - Lactococcus lactis subsp. lactis (strain IL14)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: H86836
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86836
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315 <STO>
A;Cross-references: GB:AE005176; PID:gl2724712; PIDN:AAK05794.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: arcC3
C;Superfamily: carbamate kinase
C;Keywords: phosphotransferase

Query Match 90.9%; Score 30; DB 2; Length 315;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
Db 88 GYWS 92

RESULT 9

G69142
GDP-D-mannose dehydratase - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Accession: G69142
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qi, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: G69142
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-348 <MTH>
A;Cross-references: GB:AE000818; GB:AE000666; NID:g2621384; PIDN:AA84839.1; PID:g262138
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH333
C;Superfamily: GDP-D-mannose dehydratase

Query Match 90.9%; Score 30; DB 2; Length 348;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
Db 156 GYWS 160

RESULT 10

H83554

hypothetical protein PA0736 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83554
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83554
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <STO>
A;Cross-references: GB:AE004508; GB:AE004091; NID:g9946611; PIDN:AAG04125.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0736

Query Match 90.9%; Score 30; DB 2; Length 358;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
Db 203 GYWS 207

RESULT 11

E83163
hypothetical protein PA3863 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83163
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83163
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-375 <STO>
A;Cross-references: GB:AE004803; GB:AE004091; NID:g9950035; PIDN:AAG07250.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3863

Query Match 90.9%; Score 30; DB 2; Length 375;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
Db 19 GYWS 23

RESULT 12

T08724
hypothetical protein DKFZp566D213.1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08724
R;Koehler, K.; Beyer, A.; Mewes, H.W.; Cassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16468
A;Accession: T08724
A;Molecule type: mRNA
A;Residues: 1-417 <KOE>
A;Cross-references: EMBL:AL050275
A;Experimental source: fetal kidney; clone DKFZp566D213

C;Genetics:
A;Note: DKFp566D213.1

Query Match 90.9%; Score 30; DB 2; Length 417;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||:
Db 402 GYWLS 406

RESULT 13

B95249
PTS system, IIC component, probable [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: B95249
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapf, P.
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: B95249
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK76187.1; PID:gl4973641; GSPDB:GN00164; TIGR.SP4
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP2123

Query Match 90.9%; Score 30; DB 2; Length 448;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||:
Db 186 GYWLS 190

RESULT 14

G98113
conserved hypothetical protein spr1938 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: G98113
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: G98113
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 <KUR>
A;Cross-references: GB:AE007317; PIDN:AA00740.1; PID:gl5459636; GSPDB:GN00174
C;Genetics:
A;Gene: spr1938

Query Match 90.9%; Score 30; DB 2; Length 448;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||:
Db 186 GYWLS 190

RESULT 15

T00113
undecaprenyl-phosphate galactosephosphotransferase homolog - Actinobacillus actinomycetec
C;Species: Actinobacillus actinomycetecommittans
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C;Accession: T00113
R;Nakano, Y.; Yoshida, Y.; Yanashita, Y.; Koga, T.
Biochim. Biophys. Acta 1442, 409-414, 1998
A;Title: A gene cluster for 6-deoxy-L-talan synthesis in Actinobacillus actinomycetecomm
A;Reference number: Z14111; MUID:99023768; PMID:9805002
A;Accession: T00113
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-452 <NAK>
A;Cross-references: EMBL:AB010415; NID:g3132248; PIDN:BAA28142.1; PID:g3132265
A;Experimental source: strain NCTC 9710
C;Superfamily: xps2A protein

Query Match 90.9%; Score 30; DB 2; Length 452;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||:
Db 11 GYWLS 15

Search completed: September 30, 2004, 06:00:37
Job time : 7.42373 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 3.05085 Seconds
(without alignments)
85.337 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|---------------|---------------------|
| 1 | 33 | 100.0 | 117 | 1 HV41_MOUSE | P01811 mus musculus |
| 2 | 33 | 100.0 | 444 | 1 CITI1_KLEPN | P16482 klebsiella |
| 3 | 30 | 90.9 | 214 | 1 CAPA_KLJLA | O74232 kluyveromyc |
| 4 | 30 | 90.9 | 292 | 1 AMPR_PROST | O69772 providencia |
| 5 | 30 | 90.9 | 309 | 1 ARCI_ENTFA | P35836 enterococcu |
| 6 | 30 | 90.9 | 475 | 1 ARCD_LACSK | O53092 lactobacill |
| 7 | 30 | 90.9 | 478 | 1 ARCD_CLOPE | O46170 clostridium |
| 8 | 30 | 90.9 | 480 | 1 PTSE_STAXY | P51184 staphylococ |
| 9 | 30 | 90.9 | 583 | 1 SYG_AERPE | O9ybf8 aeropyrum p |
| 10 | 30 | 90.9 | 592 | 1 CEA_CITFR | P01480 citrobacter |
| 11 | 30 | 90.9 | 608 | 1 PPCK_NEOPR | P22130 neocallinas |
| 12 | 30 | 90.9 | 667 | 1 ENV_GALV | P21415 gibbon ape |
| 13 | 30 | 90.9 | 847 | 1 AGUA_TRIRE | O99024 trichoderma |
| 14 | 30 | 90.9 | 936 | 1 CAPP_RHOMR | O59757 rhodothermu |
| 15 | 30 | 90.9 | 1063 | 1 CZCA_ALCEU | P13511 alcaligenes |
| 16 | 30 | 90.9 | 1063 | 1 CZCA_ALCSP | P94177 alcaligenes |
| 17 | 30 | 90.9 | 1502 | 1 MRPE_RAT | O88269 rattus norv |
| 18 | 30 | 90.9 | 1503 | 1 MRPE_HUMAN | O95255 homo sapien |
| 19 | 29 | 87.9 | 252 | 1 PRIO_ATEPA | P51446 ateles pani |
| 20 | 29 | 87.9 | 252 | 1 PRIO_RABIT | O95211 oryctolagus |
| 21 | 29 | 87.9 | 270 | 1 GPR1_YARLI | P41943 yarrowia li |
| 22 | 29 | 87.9 | 271 | 1 YAB8_SCHPO | O09834 schizosacch |
| 23 | 29 | 87.9 | 287 | 1 LEF4_LEGPN | O68433 legionella |
| 24 | 29 | 87.9 | 305 | 1 F334_HUMAN | O9rnw3 homo sapien |
| 25 | 29 | 87.9 | 313 | 1 ARCC_OBNOE | O8vw54 oenococcus |
| 26 | 29 | 87.9 | 314 | 1 ARCC_LACSK | O53090 lactobacill |
| 27 | 29 | 87.9 | 318 | 1 ARCC_LACHI | O8g997 lactobacill |
| 28 | 29 | 87.9 | 363 | 1 MPG1_SCHPO | O74484 schizosacch |
| 29 | 29 | 87.9 | 388 | 1 TSQA_BUCAL | P57601 buchnera ap |
| 30 | 29 | 87.9 | 394 | 1 AR22_DROME | P45888 drosophila |
| 31 | 29 | 87.9 | 482 | 1 ARCD_FSEAE | P18275 pseudomonas |
| 32 | 29 | 87.9 | 494 | 1 AMY1_SACFI | P21567 saccharomyc |
| 33 | 29 | 87.9 | 503 | 1 PR19_YEAST | P22523 saccharomyc |

ALIGNMENTS

RESULT 1

| ID | HV41_MOUSE | STANDARD; | PRT; | 117 AA. |
|----|---|-----------|------|---------|
| AC | P01811; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) | | | |
| DE | ig heavy chain V region UPC10. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=83021113; PubMed=6181731; | | | |
| RA | Auffray C., Sikorav J.L., Olio R., Rougeon F.; | | | |
| RT | "Correlation between D region structure and antigen-binding specificity: evidences from the comparison of closely related immunoglobulin VH sequences." | | | |
| RL | Ann. Immunol. (Paris) 132D:77-88(1981) | | | |
| CC | -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG GAMMA-2A MYELOMA | | | |
| CC | PROTEIN BINDING 2.6-LEVAN. | | | |
| CC | -!- SIMILARITY: Contains 1 immunoglobulin-like domain. | | | |
| CC | ----- | | | |
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| CC | ----- | | | |
| DR | EMBL; M36531; AAA38078.1; - | | | |
| DR | PIR; A02081; G2MSU. | | | |
| DR | HSP; P01810; 2FBJ. | | | |
| DR | InterPro; IPR007110; Ig-like. | | | |
| DR | InterPro; IPR003596; Ig_v. | | | |
| DR | Pfam; PF00047; Ig; 1. | | | |
| DR | SMART; SM00406; IGv; 1. | | | |
| DR | PROSITE; PS50835; IG-LIKE; 1. | | | |
| KW | Immunoglobulin V region. | | | |
| FT | DOMAIN 1 116 IG-LIKE. | | | |
| FT | NON TER 117 | | | |
| SQ | SEQUENCE 117 AA; B20A1074F8E99E7F CRC64; | | | |

Query Match 100.0%; Score 33; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 12; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0;

Qy 1 GYWMS 5

Db 31 GYWMS 35

RESULT 2

CITI1_KLEPN

```

ID CIT1_KLPPN STANDARD; PRT; 444 AA.
AC P16482;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Citrate-proton symporter (Citrate transporter) (Citrate carrier
DE protein).
GN CITH OR CIT.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13882;
RX MEDLINE=90249385; PubMed=2186908;
RA van der Rest M.E., Schwarz E., Oesterhelt D., Konings W.N.;
RT "DNA sequence of a citrate carrier of Klebsiella pneumoniae.";
RL Eur. J. Biochem. 189:401-407(1990)
CC -!- FUNCTION: UPTAKE OF CITRATE ACROSS THE BOUNDARY MEMBRANE WITH
CC THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
CC -!- PATHWAY: Allows the utilization of citrate as a sole source of
CC carbon and energy.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- SIMILARITY: TO CIT IN TN3411 AND PWR60 FOUND IN E. COLI AND TO
CC CIT IN CITROBACTER AMALONATICS.
CC -!- SIMILARITY: Belongs to the sugar transporter family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X51479; CAA35844.1; -.
CC PIR; S09681; S09681.
CC InterPro; IPR004736; Cit_H_sympor.
CC InterPro; IPR007114; MFS.
CC InterPro; IPR005828; Sub_transporter.
CC InterPro; IPR005829; Sug_transporter.
CC Pfam; PF00083; sugar_tr; 1.
CC TIGRFAMs; TIGR00883; 2A0106; 1.
CC PROSITE; PS50850; MFS; 1.
CC PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.
CC PROSITE; PS00317; SUGAR_TRANSPORT_2; 1.
CC
CC Transport; Transmembrane; Inner membrane; Citrate utilization;
CC Symport.
KW DOMAIN 1 41 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 62 1 (POTENTIAL).
FT TRANSMEM 63 72 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 73 93 2 (POTENTIAL).
FT TRANSMEM 94 114 3 (POTENTIAL).
FT DOMAIN 115 135 4 (POTENTIAL).
FT TRANSMEM 136 158 5 (POTENTIAL).
FT DOMAIN 159 177 6 (POTENTIAL).
FT TRANSMEM 178 198 7 (POTENTIAL).
FT DOMAIN 199 220 8 (POTENTIAL).
FT TRANSMEM 221 251 9 (POTENTIAL).
FT DOMAIN 252 272 10 (POTENTIAL).
FT TRANSMEM 273 289 11 (POTENTIAL).
FT DOMAIN 290 310 12 (POTENTIAL).
FT TRANSMEM 311 318 1 (POTENTIAL).
FT DOMAIN 319 339 2 (POTENTIAL).
FT TRANSMEM 340 340 3 (POTENTIAL).
FT DOMAIN 341 361 4 (POTENTIAL).
FT TRANSMEM 362 379 5 (POTENTIAL).
FT DOMAIN 380 400 6 (POTENTIAL).
FT TRANSMEM 401 411 7 (POTENTIAL).
FT DOMAIN 412 432 8 (POTENTIAL).
FT TRANSMEM 413 432 9 (POTENTIAL).

FT DOMAIN 433 444 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 444 AA; 48142 MW; D431F732EDA3EC2 CRC64;

Query Match 100.0%; Score 33; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 415 GYWMS 419

RESULT 3
CAPA_KLUJA STANDARD; PRT; 214 AA.
AC 074232;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE F-actin capping protein alpha subunit (Fragment).
GN CAP1.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RA Banfield D.K.;
RT "DNA sequence of the SFT1 gene from Kluyveromyces lactis.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: F-actin capping proteins bind in a Ca(2+)-independent
CC manner to the fast growing ends of actin filaments (barbed end)
CC thereby blocking the exchange of subunits at these ends. Unlike
CC other capping proteins (such as gelsolin and severin), these
CC protein do not sever actin filaments (By similarity).
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit (By
CC similarity).
CC -!- SIMILARITY: Belongs to the F-actin capping protein alpha subunit
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF072674; AAC24885.1; -.
CC InterPro; IPR002189; F-actin_cap_A.
CC Pfam; PF01267; F-actin_cap_A; 1.
CC PRINTS; PR00191; F-actinCAPA.
CC PRODOM; PD006960; F-actin_cap_A; 1.
CC PROSITE; PS00748; F-actin_CAPPING_A; 1.
CC PROSITE; PS00749; F-actin_CAPPING_A_2; 1.
CC KW Actin-binding; Actin capping.
CC FT NON TER 1
CC SQ SEQUENCE 214 AA; 24380 MW; 31851D6573630C02 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 214;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 111 GYWMS 115

RESULT 4
AMPR_PROST STANDARD; PRT; 292 AA.
ID AMPR_PROST
AC O69772;
DT 30-MAY-2000 (Rel. 39, Created)

```

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE HTH-type transcriptional activator ampR.
 GN AMPR.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Providencia.
 ON NCBI_TaxID=588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VDG 96;
 RA Koeck J.L., Basmaciogullari S., Parzy D., Barnaud G., Teyssou R.,
 RA Buissou V., Philippot A., Arlet G.J.;
 RT Cloning and sequencing of ampC and ampR genes from Providencia
 RT stuartii.;
 RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RL FUNCTION: THIS PROTEIN IS A POSITIVE REGULATOR OF GENE EXPRESSION
 CC OF BETA-LACTAMASE (AMPC).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Contains 1 HTH lysr-type DNA-binding domain.
 CC
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 CC
 CC EMBL; Y17315; CAA76738.1; -
 CC InterPro; IPR000847; HTH_LysR.
 CC InterPro; IPR005119; LysR_subst.
 CC Pfam; PF00126; HTH_1; 1.
 CC Pfam; PF03466; LysR_substrate; 1.
 CC PRINTS; PR00039; HTHLYSR.
 CC PROSITE; PS05931; HTH_LysR; 1.
 CC Transcription regulation; DNA-binding; Activator.
 CC DOMAIN 9 66 HTH_LysR-TYPE.
 CC FT DNA BIND 26 45 H-T-H MOTIF (POTENTIAL).
 CC FT SEQUENCE 292 AA; 32741 MW; 982CEFF667E112F0 CRC64;
 CC
 CC Query Match 90.9%; Score 30; DB 1; Length 292;
 CC Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 CC Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 GYVMS 5
 CC |||||
 CC Db 264 GYVLS 268
 CC
 CC RESULT 5
 CC ID -ARCI ENTFA STANDARD; PRT; 309 AA.
 CC AC P35836; OS4531;
 CC DT 01-JUN-1994 (Rel. 29, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Carbamate kinase 1 (EC 2.7.2.2).
 CC GNCARCC1 OR ARCC-1 OR ARCC OR EF0106.
 CC OS Enterococcus faecalis (Streptococcus faecalis), and
 CC OS Enterococcus faecium (Streptococcus faecium).
 CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 CC NCBI_TaxID=1351, 1352;
 CC [1]
 CC SEQUENCE FROM N.A.; CHARACTERIZATION, AND MASS SPECTROMETRY.
 CC SPECIES=E.faecalis, and E.faecium; STRAIN=ATCC 29212, and D10;
 CC MEDLINE=98237599; PubMed=9578487;
 RA Marina A., Uriarte M., Barcelona B., Fresquet V., Cervera J.,
 RA Rubio V.;
 RT "Carbamate kinase from Enterococcus faecalis and Enterococcus faecium.
 RT Cloning of the genes, studies on the enzyme expressed in Escherichia
 RT coli, and sequence similarity with N-acetyl-L-glutamate kinase.";
 DR Eur. J. Biochem. 253:280-291(1998).

RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.faecalis; STRAIN=ATCC 29212;
 RX MEDLINE=2286540; PubMed=12399499;
 RA Barcelona-Andres B., Marina A., Rubio V.;
 RT "Gene structure, organization, expression, and potential regulatory
 RT mechanisms of arginine catabolism in Enterococcus faecalis.";
 J. Bacteriol. 184:6289-6300(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.faecalis; STRAIN=V583 / ATCC 700802;
 RX MEDLINE=22550857; PubMed=12663927;
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
 RA Tetzelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
 RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
 RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
 RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
 RT "Role of mobile DNA in the evolution of vancomycin-resistant
 RT Enterococcus faecalis.";
 RL Science 299:2071-2074(2003).
 RN [4]
 RP SEQUENCE OF 1-32 AND 158-168, AND CHARACTERIZATION.
 RC SPECIES=E.faecium; STRAIN=D10;
 RX MEDLINE=94141928; PubMed=8308697;
 RA Marina A., Bravo J., Fita I., Rubio V.;
 RT "Crystallization, characterization and preliminary crystallographic
 RT studies of carbamate kinase of Streptococcus faecium.";
 RL J. Mol. Biol. 235:1345-1347(1994).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND MUTAGENESIS OF GLU-135;
 RP GLU-137; LYS-139; GLU-140; ASP-207 AND ASP-209.
 RC SPECIES=E.faecium; STRAIN=D10;
 RX MEDLINE=99226823; PubMed=10211841;
 RA Marina A., Alzari P.M., Bravo J., Uriarte M., Barcelona B., Fita I.,
 RA Rubio V.;
 RT "Carbamate kinase: new structural machinery for making carbamoyl
 RT phosphate, the common precursor of pyrimidines and arginine.";
 RL Protein Sci. 8:934-940(1999).
 CC -1- FUNCTION: Catalyzes the reversible synthesis of carbamate and ATP
 CC from carbamoyl phosphate and ADP. Can also catalyze, although with
 CC low efficiency, the phosphorylation of bicarbonate, leading to the
 CC formation of carboxyphosphate, an unstable intermediate found in
 CC the reactions catalyzed by carbamoyl-phosphate synthase and biotin
 CC carboxylase. Can also use acetate.
 CC -1- CATALYTIC ACTIVITY: ATP + NH(3) + CO(2) = ADP + carbamoyl
 CC phosphate.
 CC -1- ENZYME REGULATION: Inhibited by
 CC adenosine(5')pentaphospho(5')adenosine (ApsA), ApsA and to a much
 CC lower extent by Ap4A.
 CC -1- PATHWAY: Arginine degradation via arginine deiminase; third step.
 CC -1- SUBUNIT: Homodimer (predominantly) and homotetramer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- INDUCTION: By arginine.
 CC -1- MASS SPECTROMETRY: MW=32803; MW ERR=10; METHOD=Electrospray.
 CC -1- SIMILARITY: Belongs to the carbamate kinase family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AJ223331; CAA11270.1; -
 CC EMBL; AJ223332; CAA11271.1; -
 CC EMBL; AJ312276; CAC41343.1; -
 CC EMBL; AE016947; AAC79981.1; -
 CC PIR; S44002; S44002.
 CC DR PDB; 1B7B; 26-SEP-01.
 CC TIGR; EF0106; -
 CC InterPro; IPR001048; Aa_Kinase.

DR InterPro; IPR003964; Bac_carb_kinase.
 DR Pfam; PF00696; aakinasase; 1.
 DR PRINTS; PRO1469; CARYOTKINASE.
 DR TIGRFAMs; TIGR00746; arcC; 1.
 KW Transferase; Kinase; Arginine metabolism; 3D-structure;
 KW Complete proteome.
 FT INIT MET 0
 FT MUTAGEN 135 135 E->A: NO CHANGE IN ACTIVITY; WHEN
 FT MUTAGEN 137 137 ASSOCIATED WITH A-137, A-139 AND A-140.
 FT MUTAGEN 137 137 E->A: NO CHANGE IN ACTIVITY; WHEN
 FT MUTAGEN 139 139 ASSOCIATED WITH A-135, A-139 AND A-140.
 FT MUTAGEN 139 139 K->A: NO CHANGE IN ACTIVITY; WHEN
 FT MUTAGEN 140 140 ASSOCIATED WITH A-135, A-137 AND A-140.
 FT MUTAGEN 140 140 E->A: NO CHANGE IN ACTIVITY; WHEN
 FT MUTAGEN 207 207 ASSOCIATED WITH A-135, A-137 AND A-139.
 FT MUTAGEN 209 209 D->A: ALMOST NO ACTIVITY; WHEN ASSOCIATED
 FT MUTAGEN 209 209 WITH A-209.
 FT CONFLICT 168 168 I -> D (IN REF. 4).
 SQ SEQUENCE 309 AA; 32795 MW; 50145147FEED290 CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 309;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYVWS 5
 DB 86 GYVLS 90
 RESULT 6
 ARCD_CLOPE STANDARD; PRT; 475 AA.
 ID ARCD_LACSK
 AC O53092;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Arginine/ornithine antiporter.
 GN ARCD.
 OS Lactobacillus sakei.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1599;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98361904; PubMed=9696763;
 RA Zuniga M., Champomier-Verges M., Zagorec M., Perez-Martinez G.;
 RT "Structural and functional analysis of the gene cluster encoding the
 enzymes of the arginine deiminase pathway of Lactobacillus sake.";
 RL J. Bacteriol. 180:4154-4159(1998).
 CC -!- FUNCTION: Catalyzes an electroneutral exchange between arginine
 and ornithine to allow high-efficiency energy conversion in the
 arginine deiminase pathway (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the amino acid permease family.
 CC Arcd/cadB/lysi subfamily.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AJ001330; CAA04686.1; -
 CC PIR; T46745; T46745.
 CC InterPro; IPR002293; AA/rel_permease1.
 CC InterPro; IPR004841; Permease_region.
 CC Pfam; PF00324; aa_permeases; 1.
 CC TIGRFAMs; TIGR00905; 2A0302; 1.

KW Transport; Antiport; Amino-acid transport; Transmembrane.
 FT TRANSMEM 10 30 POTENTIAL.
 FT TRANSMEM 42 62 POTENTIAL.
 FT TRANSMEM 74 94 POTENTIAL.
 FT TRANSMEM 101 121 POTENTIAL.
 FT TRANSMEM 157 177 POTENTIAL.
 FT TRANSMEM 205 225 POTENTIAL.
 FT TRANSMEM 238 258 POTENTIAL.
 FT TRANSMEM 283 303 POTENTIAL.
 FT TRANSMEM 333 353 POTENTIAL.
 FT TRANSMEM 361 381 POTENTIAL.
 FT TRANSMEM 397 417 POTENTIAL.
 FT TRANSMEM 451 471 POTENTIAL.
 SQ SEQUENCE 475 AA; 51881 MW; 8E91A01F6A2203CC CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 475;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYVWS 5
 DB 94 GYVLS 98
 RESULT 7
 ARCD_CLOPE STANDARD; PRT; 478 AA.
 ID ARCD_CLOPE
 AC Q46170;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Arginine/ornithine antiporter.
 GN ARCD OR CPE0170.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97199138; PubMed=90533381;
 RA Ohtani K., Bando M., Swe T., Banu S., Oe M., Hayashi H., Shimizu T.;
 RT "Collagenase gene (cola) is located in the 3'-flanking region of the
 perfringolysin O (pfoA) locus in Clostridium perfringens.";
 RL FEMS Microbiol. Lett. 146:155-159(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=13 / Type A;
 RX MEDLINE=21664373; PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 flesh-eater".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 CC -!- FUNCTION: Catalyzes an electroneutral exchange between arginine
 and ornithine to allow high-efficiency energy conversion in the
 arginine deiminase pathway (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the amino acid permease family.
 CC Arcd/cadB/lysi subfamily.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X97768; CAA66366.1; -
 CC EMBL; AF003185; BAB79876.1; -
 CC InterPro; IPR002293; AA/rel_permease1.
 CC InterPro; IPR004841; Permease_region.

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EMBL; X69800; CAA49461.1; -

PIR; S39978; S39978; Ptrans_EIIB.

InterPro; IPR001996; Ptrans_EIIB.

InterPro; IPR003352; Ptrans_EIIC.

Pfam; PF00367; PTS_EIIB; 1.

Pfam; PF02378; PTS_EIIC; 1.

ProDom; PD001476; PTS_EIIB; 1.

TIGRfams; TIGR00826; EIIB_glc; 1.

PROSITE; PS01035; PTS_EIIB_CVS; 1.

Phosphotransferase system; Sugar transport; Transferase;

KW Transmembrane; Inner membrane; Phosphorylation.

FT DOMAIN ? EIIB.

FT MOD_RES 26 26 PHOSPHORYLATION (BY SIMILARITY).

FT MOD_RES 325 325 PHOSPHORYLATION (BY SIMILARITY).

SQ SEQUENCE 480 AA; 51326 MW; AB4E1D9785D84E47 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 480;

Best Local Similarity 80.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYWMS 5
|||
DB 290 GYLWS 294

RESULT 9

ID SVG AERPE STANDARD; PRT; 583 AA.

AC Q9YEF8;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glycyl-tRNA synthetase (EC 6.1.1.14) [Glycine-tRNA ligase] (GLYS)

GN GLYS OR APE1639.

OS Aeropyrum pernix.

OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;

CC Desulfurococccaceae; Aeropyrum.

OX NCBI_TaxID=58636;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K1.

RX MEDLINE=99310339; PubMed=10382966;

RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix K1.";

RL RNA Res. 6:83-101(1999).

CC -!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate + glycyI-tRNA(Gly).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.

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EMBL; AP000062; BAA80640.1; -

PIR; C72544; C72544.

HSSP; P56206; 1ARI.

HMAP; MF 00253; -; 1.

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EMBL; X69800; CAA49461.1; -

PIR; S39978; S39978; Ptrans_EIIB.

InterPro; IPR001996; Ptrans_EIIB.

InterPro; IPR003352; Ptrans_EIIC.

Pfam; PF00367; PTS_EIIB; 1.

Pfam; PF02378; PTS_EIIC; 1.

ProDom; PD001476; PTS_EIIB; 1.

TIGRfams; TIGR00826; EIIB_glc; 1.

PROSITE; PS01035; PTS_EIIB_CVS; 1.

Phosphotransferase system; Sugar transport; Transferase;

KW Transmembrane; Inner membrane; Phosphorylation.

FT DOMAIN ? EIIB.

FT MOD_RES 26 26 PHOSPHORYLATION (BY SIMILARITY).

FT MOD_RES 325 325 PHOSPHORYLATION (BY SIMILARITY).

SQ SEQUENCE 480 AA; 51326 MW; AB4E1D9785D84E47 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 480;

Best Local Similarity 80.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYWMS 5
|||
DB 290 GYLWS 294

RESULT 9

ID SVG AERPE STANDARD; PRT; 583 AA.

AC Q9YEF8;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glycyl-tRNA synthetase (EC 6.1.1.14) [Glycine-tRNA ligase] (GLYRS).

GN GLYS OR APE1639.

OS Aeropyrum pernix.

OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;

CC Desulfurococccaceae; Aeropyrum.

OX NCBI_TaxID=58636;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K1.

RX MEDLINE=99310339; PubMed=10382966;

RA Kawarayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix K1.";

RL RNA Res. 6:83-101(1999).

CC -!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate + glycyI-tRNA(Gly).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.

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EMBL; AP000062; BAA80640.1; -

PIR; C72544; C72544.

HSSP; P56206; 1ARI.

HMAP; MF 00253; -; 1.

DR InterPro: IPR004154; HGTP anticodon.
 DR InterPro: IPR002314; tRNA-synt 2b.
 DR InterPro: IPR002315; tRNA-synt_gly.
 DR InterPro: IPR006195; tRNA_ligase_II.
 DR Pfam: PF03129; HGTP-anticodon; 1.
 DR Pfam: PF00567; tRNA-synt 2b; 1.
 DR PRINTS; PR01043; TRNASYNTHGLY.
 DR TIGRFAMs; TIGR00389; GLYS dimeric; 1.
 DR PROSITE; PS00862; AA tRNA LIGASE II; 1.
 KW Aminocyl-tRNA synthetase; Protein biosynthesis, Ligase; ATP-binding;
 KW Complete proteome.
 SQ SEQUENCE 583 AA; 66395 MW; 7D75DE7B5AA3F999 CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 583;
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 Db 277 GYWS 281
 RESULT 10
 CEA_CITFR
 ID_CEA_CITFR STANDARD; PRT; 592 AA.
 AC P04180;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Colicin A.
 GN CAA.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84036205; PubMed=6313941;
 RA Morlon J., Lioubes R., Varenne S., Chartier M., Lazdunski C.;
 RT "Complete nucleotide sequence of the structural gene for colicin A, a
 RT gene translated at non-uniform rate.";
 RL J. Mol. Biol. 170:271-285(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88174422; PubMed=2832701;
 RA Morlon J., Chartier M., Bidaud M., Lazdunski C.;
 RT "The complete nucleotide sequence of the colicinogenic plasmid ColA.
 RT High extent of homology with ColE1.";
 RL Mol. Gen. Genet. 211:231-243(1988).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 389-592.
 RX MEDLINE=92233820; PubMed=1273773;
 RA Parker M.W., Postma J.P.M., Pattus F., Tucker A.D., Tsernoglou D.;
 RT "Refined structure of the pore-forming domain of colicin A at 2.4-A
 RT resolution.";
 RL J. Mol. Biol. 224:639-657(1992).
 CC -!- FUNCTION: This colicin is a channel-forming colicin. This class of
 CC transmembrane toxins depolarize the cytoplasmic membrane, leading
 CC to dissipation of cellular energy.
 CC -!- FUNCTION: COLICINS ARE POLYPEPTIDE TOXINS PRODUCED BY AND ACTIVE
 CC AGAINST ESCHERICHIA COLI AND CLOSELY RELATED BACTERIA.
 CC -!- SIMILARITY: Belongs to the channel forming colicin family.
 CC
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 CC
 CC EMBL; X01008; CAA25503.1; -

DR EMBL; M37402; AAA72879.1; -.
 DR PIR; I40784; IKEBCA.
 DR PUB; LCOL; 15-JUL-93.
 DR InterPro: IPR000293; Channel_colicin.
 DR Pfam: PF01024; Colicin; 1.
 DR PRINTS; PR00280; CHANCOLICIN.
 DR PRODOM; PD002657; Channel_colicin; 1.
 DR PROSITE; PS00276; CHANNEL COLICIN; 1.
 KW Antibiotic; Bacteriocin; Plasmid; Transmembrane; 3D-structure.
 KW TRANSMEM 528 548
 FT TRANSMEM 555 575
 FT HELIX 396 418
 FT HELIX 420 434
 FT TURN 435 435
 FT TURN 437 438
 FT HELIX 444 455
 FT TURN 456 456
 FT HELIX 458 460
 FT HELIX 464 475
 FT TURN 476 476
 FT HELIX 479 489
 FT HELIX 491 493
 FT TURN 496 497
 FT HELIX 498 515
 FT TURN 519 530
 FT TURN 531 532
 FT HELIX 535 552
 FT HELIX 557 575
 FT TURN 577 577
 FT HELIX 578 586
 FT TURN 587 588
 SQ SEQUENCE 592 AA; 62992 MW; B80FAIP52A8CFC5D CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 592;
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 Db 136 GYWS 140
 RESULT 11
 PCKK_NEOFR
 ID_PCKK_NEOFR STANDARD; PRT; 608 AA.
 AC P22130;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphoenolpyruvate carboxylase [GTP] (EC 4.1.1.32)
 DE (Phosphoenolpyruvate carboxylase) (PEPCK).
 OS Neocallimastix frontalis (Rumen fungus).
 OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
 OC Neocallimastixaceae; Neocallimastix.
 OX NCBI_TaxID=4757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92164115; PubMed=1339359;
 RA Raymond P., Gecurjon C., Roux B., Durand R., Fevre M.;
 RT "Sequence of the phosphoenolpyruvate carboxylase-encoding cDNA from
 RT the rumen anaerobic fungus Neocallimastix frontalis: comparison of
 RT the amino acid sequence with animals and yeast.";
 RL Gene 110:57-63(1992).
 CC -!- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
 CC + CO(2).
 CC -!- PATHWAY: Rate-limiting gluconeogenic enzyme.
 CC -!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxylase [GTP]
 CC family.
 CC
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 CC -----

DR EMBL; M59372; AAA33553.1; -;
 DR PIR; JQ1462; JQ1462; PEP_carboxykin.
 DR InterPro; IPR008209; PEP_carboxykin.
 DR InterPro; IPR008210; PEPCK_N.
 DR Pfam; PF00821; PEPCK; 1.
 DR ProDom; PD004738; PEPCK_N; 1.
 DR ProSITE; PS00505; PEPCK_GTP; 1.
 KW Glucuronogenesis; Lyase; Decarboxylase; GTP-binding.
 FT NP_BIND 217 224 GTP (POTENTIAL).
 FT ACT_SITE 269 269 POTENTIAL.
 SQ SEQUENCE 608 AA; 66904 MW; C4D2B249A92B7D26 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 608;
 Best Local Similarity 80.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 DB 478 GYWS 482

RESULT 12
 ID ENV_GALV STANDARD; PRT; 667 AA.
 AC 21415;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ENV polyprotein precursor (Contains: Knob protein GP70; Spike protein
 DE P15E).
 GN ENV.
 OS Gibbon ape leukemia virus.
 OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
 OX NCBI_TaxID=11840;
 RN [1]
 RP MEDLINE=90051069; PubMed=2683360;
 RX Delassus S., Sonigo P., Wain-Hobson S.;
 RT "Genetic organization of gibbon ape leukemia virus.";
 RL Virology 173:205-213(1989).

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 CC -----

DR EMBL; M26927; AAA46811.1; -;
 DR PIR; C32595; VCLJGL.
 DR HSP; P03385; 1MOP.
 DR InterPro; IPR002050; Env polyprotein.
 DR InterPro; IPR008951; F_MuLV bind.
 DR Pfam; PF00429; ENV_polyprotein; 1.
 KW Coat protein; Glycoprotein; Polyprotein; Transmembrane; Signal.
 FT SIGNAL 1 42
 FT CHAIN 43 489 KNOB PROTEIN GP70.
 FT CHAIN 490 667 SPIKE PROTEIN P15E.
 FT TRANSMEM 637 653 POTENTIAL.
 FT TRANSMEM 637 653 POTENTIAL.
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 667 AA; 73729 MW; 5FEB32F00D8631BE CRC64;

Query Match 90.9%; Score 30; DB 1; Length 667;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 DB 180 GYWS 184

RESULT 13
 ID AGUA_TRIRE STANDARD; PRT; 847 AA.
 AC Q99024;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alpha-glucuronidase precursor (EC 3.2.1.139) (Alpha-glucosiduronase)
 DE (GLR).
 OS Trichoderma reesei (Hypocrea jecorina).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 OX NCBI_TaxID=51453;
 RN [1]
 RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
 RC STRAIN=QM9414 / Rut C-30;
 RX MEDLINE=96257277; PubMed=8654984;
 RA Margolles-Clark E., Saloheimo M., Siika-Aho M., Penttilae M.;
 RT "The alpha-glucuronidase-encoding gene of Trichoderma reesei.";
 RL Gene 172:171-172(1996).
 CC -1- FUNCTION: RELEASES 4-O-METHYLGLUCURONIC ACID FROM XYLAN.
 CC -1- CATALYTIC ACTIVITY: An alpha-D-glucuronoside + H(2)O = an alcohol
 CC + D-glucuronate.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO FAMILY 67 OF GLYCOSYL HYDROLASES.

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 CC -----

DR EMBL; Z68706; CAA92949.1; -;
 DR PIR; JC4836; JC4836.
 DR InterPro; IPR005154; Glyco_hydro_67.
 DR Pfam; PF03648; Glyco_hydro_67; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 847 ALPHA-GLUCURONIDASE.
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 586 586 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 692 692 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 740 740 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 767 767 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA; 93424 MW; 214AAE487382FDB4 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 847;
 Best Local Similarity 80.0%; Pred. No. 3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 DB 119 GYWS 123

RESULT 14
 ID CAPP_RHOMR STANDARD; PRT; 936 AA.
 AC Q59757;

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Enophenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
 GN PPC OR PEPC.
 OS Rhodothermus marinus (Rhodothermus obamensis).
 CC Bacteria; Bacteroidetes; Sphingobacteriales;
 CC Crenotrichaceae; Rhodothermus.
 OX NCBI_TaxID=29549;
 RN [1]_TaxID=29549;
 RP SEQUENCE FROM N.A.
 RC STRAIN=OKD7;
 RX MEDLINE=97420683; PubMed=9276668;
 RA Takai K., Sako Y., Uchida A., Ishida Y.;
 RT "Extremely thermostable phosphoenolpyruvate carboxylase from an
 extreme thermophile, Rhodothermus obamensis.";
 RL J. Biochem. 122:32-40 (1997).
 CC -!- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
 CC it forms oxaloacetate, a four-carbon dicarboxylic acid source for
 CC the tricarboxylic acid cycle.
 CC -!- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
 CC phosphoenolpyruvate + CO(2).
 CC -!- COFACTOR: Absolute requirement for divalent cations.
 CC -!- ENZYME REGULATION: Exhibits positive allosteric property with
 CC acetyl-CoA and fructose 1,6-bisphosphate, and a negative one with
 CC L-aspartate and L-malate.
 CC -!- PATHWAY: Tricarboxylic acid cycle.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- MISCELLANEOUS: The optimum temperature for activity is 75 degrees
 CC Celsius. The enzyme exhibits a pH optimum of 8.0.
 CC -!- SIMILARITY: Belongs to the PEPCase family.
 CC
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 CC
 CC EMBL; X99379; CAA67760.1; --
 CC HSP; P00864; 1FTY.
 CC HAMAP; MF 00595; -; 1.
 CC InterPro; IPR001449; PEPCase.
 CC Pfam; PF00311; PEPCase; 1.
 CC PRINTS; PR00150; PEPCARXLA.
 CC PROSITE; PS00393; PEPCASE 2; 1.
 CC PROSITE; PS00781; PEPCASE 1; 1.
 CC Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle;
 KW Allosteric enzyme. 155
 FT ACT_SITE 155 BY SIMILARITY.
 FT ACT_SITE 595 BY SIMILARITY.
 FT ACT_SITE 595
 SQ SEQUENCE 936 AA; 107886 MW; C9AA94C3F26C345A CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 936;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 |||||
 Db 598 GYWSA 602
 RESULT 15
 CZCA_ALCEU STANDARD; PRT; 1063 AA.
 ID CZCA_ALCEU
 AC P13511; P94142;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cobalt-zinc-cadmium resistance protein czca (Cation efflux system
 DE protein czca).
 GN CZCA.

OS Alkaligenes eutrophus (Ralstonia eutropha).
 OG Plasmid pMO30.
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 CC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CH34;
 RX MEDLINE=90017477; PubMed=2678100;
 RA Nies D.H., Nies A., Chu L., Silver S.;
 RT "Expression and nucleotide sequence of a plasmid-determined divalent
 RT cation efflux system from Alkaligenes eutrophus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7351-7355 (1989).
 RN [2]
 RP REVISIONS TO 318 AND 959-960.
 RC STRAIN=CH34;
 RA van der Lelie D., Schwuchow T., Wuerz S., Schwidetzky U.,
 RA Baeyens W., Scheel P.O., Nies D.H.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: HAS A LOW CATION TRANSPORT ACTIVITY FOR CO(2+). IT IS
 CC ESSENTIAL FOR THE EXPRESSION OF COBALT, ZINC, AND CADMIUM
 CC RESISTANCE. CZCA AND CZCB TOGETHER WOULD ACT IN ZN(2+) EFFLUX
 CC NEARLY AS EFFECTIVELY AS THE COMPLETE CZC EFFLUX SYSTEM (CZCABC).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -!- INDUCTION: By cadmium, copper and zinc.
 CC -!- SIMILARITY: BELONGS TO THE ACRB/ACRD/ACRF FAMILY.
 CC
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 CC
 CC EMBL; X38451; CAA67084.1; --
 CC PIR; A33830; A33830.
 CC InterPro; IPR001036; Acrflvin_res.
 CC InterPro; IPR004763; Czca.
 CC Pfam; PF00873; ACR tran; 1.
 CC PRINTS; PR00702; ACRIFLAVINRP.
 CC TIGRfam; TIGR00914; 2A0601.1
 KW Plasmid; Transport; Zinc; Cobalt; Cadmium resistance; Transmembrane.
 FT TRANSMEM 14 29 POTENTIAL.
 FT TRANSMEM 350 370 POTENTIAL.
 FT TRANSMEM 452 472 POTENTIAL.
 FT TRANSMEM 487 507 POTENTIAL.
 FT TRANSMEM 534 554 POTENTIAL.
 FT TRANSMEM 883 903 POTENTIAL.
 FT TRANSMEM 906 926 POTENTIAL.
 FT TRANSMEM 937 957 POTENTIAL.
 FT TRANSMEM 982 1004 POTENTIAL.
 FT TRANSMEM 1013 1033 POTENTIAL.
 SQ SEQUENCE 1063 AA; 115668 MW; 1E95B7923996AEBB CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 1063;
 Best Local Similarity 80.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 |||||
 Db 862 GYWS 865

Search completed: September 30, 2004, 06:01:20
 Job time : 5.05085 secs

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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 16.3559 Seconds
(without alignments)
96.454 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 33 | 100.0 | 67 | 17 | Q9HN48 |
| 2 | 33 | 100.0 | 73 | 16 | Q8PR71 |
| 3 | 33 | 100.0 | 85 | 16 | Q8PB4 |
| 4 | 33 | 100.0 | 285 | 16 | Q8W52 |
| 5 | 33 | 100.0 | 377 | 13 | Q9IAF9 |
| 6 | 33 | 100.0 | 377 | 13 | Q9IAE9 |
| 7 | 33 | 100.0 | 377 | 13 | Q9IAH4 |
| 8 | 33 | 100.0 | 377 | 13 | Q9IAF0 |
| 9 | 33 | 100.0 | 377 | 13 | Q9IAH2 |
| 10 | 33 | 100.0 | 377 | 13 | Q9I87 |
| 11 | 33 | 100.0 | 377 | 13 | Q9IAG1 |
| 12 | 33 | 100.0 | 377 | 13 | Q9IAF4 |
| 13 | 33 | 100.0 | 377 | 13 | Q9IAD8 |
| 14 | 33 | 100.0 | 377 | 13 | Q9IAH1 |
| 15 | 33 | 100.0 | 377 | 13 | Q9IAE0 |
| 16 | 33 | 100.0 | 377 | 13 | Q9IAF6 |

ALIGNMENTS

RESULT 1

Q9HN48
ID Q9HN48 PRELIMINARY; PRT; 67 AA.
AC Q9HN48;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Vng2253h.
GN VNG2253H.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
CX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2050483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jabloncki P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Beck R.F., Pohlbroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Oner A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
EMBL: AE005110; AAG20373.1; -;
DR PIR; A84376; A84376.
KW Complete proteome.
SQ SEQUENCE 67 AA; 6601 MW; A8BAP23FCBBB648 CRC64;

Query Match 100.0%; Score 33; DB 17; Length 67;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 GYMS 5

Db 59 GYMS 63

17 33 100.0 377 13 Q9IAD9
18 33 100.0 377 13 Q9IAH0
19 33 100.0 377 13 Q9IAE1
20 33 100.0 377 13 Q9IAG4
21 33 100.0 377 13 Q9IAF5
22 33 100.0 377 13 Q9IAE6
23 33 100.0 377 13 Q9IAG3
24 33 100.0 377 13 Q9IAD5
25 33 100.0 377 13 Q9IAF7
26 33 100.0 377 13 Q9IAG6
27 33 100.0 377 13 Q9IAD7
28 33 100.0 377 13 Q9IAG2
29 33 100.0 377 13 Q9IAD6
30 33 100.0 377 13 Q9IAF8
31 33 100.0 377 13 Q9IAG7
32 33 100.0 377 13 Q9IAG9
33 33 100.0 377 13 Q9IAH3
34 33 100.0 377 13 Q9IAH6
35 33 100.0 377 13 Q8AWR8
36 33 100.0 396 13 Q7SY78
37 33 100.0 721 10 Q9FRN4
38 33 100.0 721 10 Q7XB20
39 33 100.0 1028 5 Q8XA6
40 33 100.0 1043 16 Q97E41
41 33 100.0 1254 5 Q9VF51
42 33 100.0 1254 5 Q8GNS1
43 30 90.9 77 2 Q9S4W3
44 30 90.9 79 2 Q9WTF7
45 30 90.9 79 16 Q9JMR3

Q9IAD9 pollimyrus
Q9IAH0 campylonorm
Q9IAE1 pollimyrus
Q9IAG4 hippopotamy
Q9IAF5 marcusenius
Q9IAE6 paramomyro
Q9IAG3 hippopotamy
Q9IAD5 stomatorhin
Q9IAF7 marcusenius
Q9IAG6 gnathonemus
Q9IAD7 stomatorhin
Q9IAG2 hippopotamy
Q9IAD6 stomatorhin
Q9IAF8 marcusenius
Q9IAG7 genomyrus
Q9IAG9 campylonorm
Q9IAH3 brienyomyrus
Q9IAH6 boulengerom
Q8AWR8 pollimyrus
Q7SY78 xenopus lae
Q9FRN4 cryza sativ
Q7XB20 cryza sativ
Q8XA6 drosophila
Q97E41 clostridium
Q9VF51 drosophila
Q8GNS1 drosophila
Q9S4W3 escherichia
Q9WTF7 escherichia
Q9JMR3 escherichia

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RESULT 2
Q8PR71 PRELIMINARY; PRT; 73 AA.
AC Q8PR71;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein XAC0095.
GN XAC0095.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE011632; AAM34987.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 73 AA; 8296 MW; 89C3771680F46C3D CRC64;

Query Match 100.0%; Score 33; DB 16; Length 73;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 6 GYWS 10

RESULT 3
Q8PEB4 PRELIMINARY; PRT; 85 AA.
AC Q8PEB4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein XCC0067.
GN XCC0067.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=2022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE011632; AAM34987.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 85 AA; 8296 MW; 89C3771680F46C3D CRC64;

Query Match 100.0%; Score 33; DB 16; Length 73;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 6 GYWS 10

RESULT 4
Q88W52 PRELIMINARY; PRT; 285 AA.
AC Q88W52;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Integral membrane protein.
GN LP 1809.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCF81;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCF81."
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935257; CAD64219.1; -.
DR InterPro; IPR007163; DUF368.
DR Pfam; PF04018; DUF368; 1.
KW Complete proteome.
SQ SEQUENCE 285 AA; 30888 MW; D93DB9353EA9D881 CRC64;

Query Match 100.0%; Score 33; DB 16; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 274 GYWS 278

RESULT 5
Q9IAF9 PRELIMINARY; PRT; 377 AA.
AC Q9IAF9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (fragment).
OS Iivindomyrus opdenboschi.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012100; AAM39386.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 85 AA; 9609 MW; C6FDC29D07155274 CRC64;

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Query Match 100.0%; Score 33; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GYWS 5
DB 18 GYWS 22

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OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Iivindomyrus.
 OX NCBI_TaxID=91727;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20115608; PubMed=10648209;
 RX Sullivan J.P., Lavoue S., Hopkins C.D.;
 RA "Molecular systematics of the African electric fishes (Mormyroidea;
 RT Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201635; AAF43346.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 DR NON_TER 377 377
 FT NON TER 1
 SQ SEQUENCE 377 AA; 41428 MW; B60EDE613EAFDDE CRC64;
 Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 Db 368 GYWS 372
 RESULT 6
 Q9IAE9 PRELIMINARY; PRT; 377 AA.
 AC Q9IAE9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Mormyrus rume.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Mormyrus.
 OX NCBI_TaxID=91731;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20115608; PubMed=10648209;
 RX Sullivan J.P., Lavoue S., Hopkins C.D.;
 RA "Molecular systematics of the African electric fishes (Mormyroidea;
 RT Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201645; AAF43356.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 DR NON_TER 377 377
 FT NON TER 1
 SQ SEQUENCE 377 AA; 41364 MW; D59BAC6D739AEE56 CRC64;
 Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 Db 368 GYWS 372
 RESULT 7
 Q9IAH4 PRELIMINARY; PRT; 377 AA.
 AC Q9IAH4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Brienomyrus hopkinsi.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Brienomyrus.
 OX NCBI_TaxID=112141;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20115608; PubMed=10648209;
 RX Sullivan J.P., Lavoue S., Hopkins C.D.;
 RA "Molecular systematics of the African electric fishes (Mormyroidea;
 RT Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201618; AAF43329.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 DR NON_TER 377 377
 FT NON TER 1
 SQ SEQUENCE 377 AA; 41403 MW; 0A4599C6604C8123 CRC64;
 Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 Db 368 GYWS 372
 RESULT 8
 Q9IAFO PRELIMINARY; PRT; 377 AA.
 AC Q9IAFO;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Mormyrus ovis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Mormyrus.
 OX NCBI_TaxID=112155;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20115608; PubMed=10648209;
 RX Sullivan J.P., Lavoue S., Hopkins C.D.;
 RA "Molecular systematics of the African electric fishes (Mormyroidea;
 RT Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201644; AAF43355.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 DR NON_TER 377 377
 FT NON TER 1
 SQ SEQUENCE 377 AA; 41431 MW; 7EB7C6C644E569DB CRC64;
 Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 Db 368 GYWS 372

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RESULT 9
Q9IAH2
ID Q9IAH2 PRELIMINARY; PRT; 377 AA.
AC Q9IAH2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Brienomyrus niger.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Brienomyrus.
OX NCBI_TaxID=42637;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the African electric fishes (Mormyroidea;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201620; AAF43331.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON_TER 1
FT NON_TER 377
SQ SEQUENCE 377 AA; 41522 MW; 2E93DC79A8B6EC4A CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 368 GYWS 372

RESULT 10
Q9I867
ID Q9I867 PRELIMINARY; PRT; 377 AA.
AC Q9I867;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Campylomormyrus tamandua.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Campylomormyrus.
OX NCBI_TaxID=91719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the African electric fishes (Mormyroidea;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201625; AAF43336.1; -.
DR EMBL; AF201624; AAF43335.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON_TER 1
FT NON_TER 377
SQ SEQUENCE 377 AA; 41387 MW; D52A9E361A56AB43 CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 368 GYWS 372

RESULT 11
Q9IAG1
ID Q9IAG1 PRELIMINARY; PRT; 377 AA.
AC Q9IAG1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Hyperolius bebe.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Hyperolius.
OX NCBI_TaxID=91725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the African electric fishes (Mormyroidea;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201633; AAF43344.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON_TER 1
FT NON_TER 377
SQ SEQUENCE 377 AA; 41324 MW; C3C5A2BEBE34EF6FC CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 368 GYWS 372

RESULT 12
Q9IAF4
ID Q9IAF4 PRELIMINARY; PRT; 377 AA.
AC Q9IAF4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Marcusenius senegalensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Marcusenius.
OX NCBI_TaxID=42650;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the African electric fishes (Mormyroidea;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201640; AAF43351.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON_TER 1
FT NON_TER 377
SQ SEQUENCE 377 AA; 41324 MW; C3C5A2BEBE34EF6FC CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 368 GYWS 372

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DR GO: 0006310; P:DNA recombination; IEA.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1 377
 FT NON_TER 377 377
 SQ SEQUENCE 377 AA; 41475 MW; 735853EEA67408FE CRC64;
 Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 Db 368 GYWS 372

RESULT 13
 Q9IAD8 PRELIMINARY; PRT; 377 AA.
 ID Q9IAD8;
 AC Q9IAD8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Stomatolobus walkeri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Stomatolobus.
 OX NCBI_TaxID=112160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the African electric fishes (Mormyroidae: Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201656; AAF43367.1; -;
 DR GO: 0005634; C:nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR GO: 0006310; P:DNA recombination; IEA.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1 377
 FT NON_TER 377 377
 SQ SEQUENCE 377 AA; 41529 MW; 4FD1CC06990F0E2F CRC64;
 Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 Db 368 GYWS 372

RESULT 14
 Q9IAH1 PRELIMINARY; PRT; 377 AA.
 ID Q9IAH1;
 AC Q9IAH1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Brienomyrus sp. CU79740.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Brienomyrus.
 OX NCBI_TaxID=112278;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the African electric fishes (Mormyroidae: Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201621; AAF43332.1; -;
 DR GO: 0005634; C:nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.

RESULT 15
 Q9IAE0 PRELIMINARY; PRT; 377 AA.
 ID Q9IAE0;
 AC Q9IAE0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Pollimyrus isidori.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Pollimyrus.
 OX NCBI_TaxID=91713;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the African electric fishes (Mormyroidae: Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201654; AAF43365.1; -;
 DR GO: 0005634; C:nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR GO: 0006310; P:DNA recombination; IEA.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1 377
 FT NON_TER 377 377
 SQ SEQUENCE 377 AA; 41457 MW; 393E1B1FA938E9C8 CRC64;
 Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 Db 368 GYWS 372

Search completed: September 30, 2004, 05:59:33
 Job time : 18.5226 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 24.4068 Seconds
(without alignments)
57.883 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYMVS

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 33 | 100.0 | 5 | 3 AAY32257 | Aay32257 Light cha |
| 2 | 33 | 100.0 | 137 | 3 AAY32260 | Aay32260 Mouse ant |
| 3 | 33 | 100.0 | 163 | 7 ABM73967 | Abm73967 DNA clone |
| 4 | 33 | 100.0 | 345 | 7 ABM73656 | Abm73656 DNA clone |
| 5 | 33 | 100.0 | 444 | 3 AAY32263 | Aay32263 Humanised |
| 6 | 33 | 100.0 | 1254 | 4 ABB62006 | Abb62006 Drosophil |
| 7 | 30 | 90.9 | 40 | 4 AEG07533 | Aeg07533 Novel hum |
| 8 | 30 | 90.9 | 43 | 2 AAR95472 | Aar95472 V39, mono |
| 9 | 30 | 90.9 | 63 | 6 ABR48102 | Abr48102 Human sec |
| 10 | 30 | 90.9 | 63 | 6 ABR00271 | Abr00271 Human gen |
| 11 | 30 | 90.9 | 63 | 7 ADB91793 | Adb91793 Human sec |
| 12 | 30 | 90.9 | 63 | 7 ADC74531 | Adc74531 Human sec |
| 13 | 30 | 90.9 | 64 | 2 AAY07813 | Aay07813 Human sec |
| 14 | 30 | 90.9 | 181 | 2 AAY35482 | Aay35482 Chlamydia |
| 15 | 30 | 90.9 | 210 | 4 AAU17327 | Aau17327 Novel sig |
| 16 | 30 | 90.9 | 210 | 7 ADB94035 | Adb94035 Human nov |
| 17 | 30 | 90.9 | 242 | 3 AAY76114 | Aay76114 Rat HT gl |
| 18 | 30 | 90.9 | 242 | 4 AAB56053 | Aab56053 Skin cell |
| 19 | 30 | 90.9 | 242 | 5 ABB72253 | Abb72253 Rat prote |
| 20 | 30 | 90.9 | 242 | 5 ABB72301 | Abb72301 Rat prote |
| 21 | 30 | 90.9 | 242 | 5 ABB72290 | Abb72290 Rat prote |
| 22 | 30 | 90.9 | 243 | 5 ABP39269 | Abp39269 Staphyloc |
| 23 | 30 | 90.9 | 287 | 6 ABM72990 | Abm72990 Staphyloc |
| 24 | 30 | 90.9 | 310 | 4 AAU35317 | Aau35317 Enterococ |
| 25 | 30 | 90.9 | 310 | 4 AAB19867 | Aab19867 GALV retr |

ALIGNMENTS

RESULT 1

AAY32257

ID AAY32257 standard; peptide; 5 AA.

XX

AC AAY32257;

DT 15-FEB-2000 (first entry)

XX

DE Light chain CDR H1 of mouse anti-CD23 MAB C11.

XX

KW CD23; FCER1I; IGE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinis;
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
KW therapy.

XX

OS Mus musculus.

XX

PN WO9558679-A1.

XX

PD 18-NOV-1999.

XX

PP 07-MAY-1999; 99WO-CB001434.

XX

PR 09-MAY-1998; 98GB-00009839.

XX

PA (GLAX) GLAXO GROUP LTD.

XX

PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX

DR WPI; 2000-053101/04.

XX

DR N-PSDB; AAZ34742.

XX

PT Cell receptor specific antibodies useful for treating e.g. arthritis,

XX

PS diabetes, multiple sclerosis and psoriasis.

XX

PS Claim 1; Page 40; 81pp; English.

XX

XX This sequence represents complementarity determining region 1 (CDR H1)

CC of the heavy chain of murine anti-CD23 (FCER1I) monoclonal antibody C11

CC (see also AAY32263). The invention provides altered antibodies, such as

CC chimeric or humanised antibodies, which comprise sufficient of the amino

CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC

render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type 1 diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents

Sequence 5 AA;

Query Match 100.0%; Score 33; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
| | | | |
DB 1 GYWS 5

RESULT 2

AAV32260 standard; protein; 137 AA.

QY 1 GYWS 5
| | | | |
DB 1 GYWS 5

QY 1 GYWS 5
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DB 1 GYWS 5

QY 1 GYWS 5
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DB 1 GYWS 5

QY 1 GYWS 5
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DB 1 GYWS 5

QY 1 GYWS 5
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DB 1 GYWS 5

PS Claim 8; Fig 1; 81pp; English.
XX This sequence represents the heavy chain variable region (VH) of murine anti-CD23 (PCERII) monoclonal antibody C11. The invention provides altered antibodies, such as chimeric or humanised antibodies (see CC AAY32262 and AAY32263), which comprise sufficient of the amino acid CC regions of the C11 light and heavy chain complementarity determining CC sequences (see AAY32254-59) to render them capable of binding to the CD23 CC type II molecule expressed on haematopoietic cells. The antibodies are CC used to block soluble CD23 formation in human therapy, for the treatment CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma, CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft- CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell CC malignancies (claimed). They are also useful for studying interactions CC between CD23 and various ligands and determining the binding agents CC
XX Sequence 137 AA;
SQ

Query Match 100.0%; Score 33; DB 3; Length 137;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
| | | | |
DB 59 GYWS 63

RESULT 3

ABM73967

ID ABM73967 standard; protein; 163 AA.

QY 1 GYWS 5
| | | | |
DB 59 GYWS 63

QY 1 GYWS 5
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DB 59 GYWS 63

QY 1 GYWS 5
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DB 59 GYWS 63

QY 1 GYWS 5
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DB 59 GYWS 63

QY 1 GYWS 5
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QY 1 GYWS 5
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QY 1 GYWS 5
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QY 1 GYWS 5
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DB 59 GYWS 63

Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of barley varieties and production of barley transformants with desired characteristics.
Disclosure; SEQ ID XX; 284pp; Japanese.
The present invention relates to oligonucleotide clones originating in barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley

CC varieties, identification of particular varieties and genotype-phenotype
 CC analysis, isolation of specific genes and creation of new varieties by
 CC transformation of barley varieties with them and production of new barley
 CC varieties with desired properties. The present sequence represents an
 CC oligonucleotide clone sequence featured in the specification. The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published-pct-sequences
 XX
 SQ Sequence 163 AA;

Query Match 100.0%; Score 33; DB 7; Length 163;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 |||||
 DB 84 GYWS 88

RESULT 4
 ABM73656
 ID ABM73656 standard; protein; 345 AA.

XX AC ABM73656;
 XX 17-OCT-2003 (first entry)

XX DNA clone originating in barley containing SNP sequence #66.

XX Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.

XX Hordeum vulgare.

XX WO2003057877-A1.

XX 17-JUL-2003.

XX 16-DEC-2002; 2002WO-IB005403.

XX 20-DEC-2001; 2001JP-00387059.

XX 20-DEC-2001; 2001JP-00387131.

XX 20-DEC-2001; 2001JP-00403299.

XX 20-DEC-2001; 2001JP-00403300.

XX 27-SEP-2002; 2002JP-00327515.

XX (UNIV-) UNIV JAPAN OKAYAMA.

XX Sato K, Takeda K, Kohara Y;

XX WPI; 2003-587127/55.

XX Single nucleotide polymorphism sites in barley varieties and DNA

XX sequences containing them for analysis and identification of barley

XX varieties and production of barley transformants with desired

XX characteristics.

XX Disclosure; SEQ ID XX; 284pp; Japanese.

XX The present invention relates to oligonucleotide clones originating in

XX barley (Hordeum vulgare) which contain single nucleotide polymorphisms

XX (SNP). The oligonucleotides may be used for analysis of SNPs among barley

XX varieties, identification of particular varieties and genotype-phenotype

XX analysis, isolation of specific genes and creation of new varieties by

XX transformation of barley varieties with them and production of new barley

XX varieties with desired properties. The present sequence represents an

XX oligonucleotide clone sequence featured in the specification. The

XX sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published-pct-sequences

XX Sequence 345 AA;

Query Match 100.0%; Score 33; DB 7; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 |||||
 DB 266 GYWS 270

RESULT 5
 AAY32263
 ID AAY32263 standard; protein; 444 AA.

XX AC AAY32263;

XX 15-FEB-2000 (first entry)

XX Humanised anti-CD23 MAb C11 heavy chain.

XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;
 XX monoclonal antibody; chimeric antibody; humanised antibody;
 XX complementarity determining region; CDR; autoimmune disease;
 XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 XX urticaria; nephrotic syndrome; glomerulonephritis;
 XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 XX graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 XX therapy.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX 1..30 /note= "framework region 1"

XX 31..35 /note= "CDR 1"

XX 36..49 /note= "framework region 2"

XX 50..68 /note= "CDR 2"

XX 69..100 /note= "framework region 3"

XX 101..103 /note= "CDR 3"

XX 104..111 /note= "framework region 4"

XX 112..444 /note= "constant region"

XX WO9556679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX) GLAXO GROUP LTD.

XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

XX N-PSDB; AAZ34748.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,

XX diabetes, multiple sclerosis and psoriasis.

XX Claim 9; Fig 4; 8pp; English.

XX This amino acid sequence represents the heavy chain of humanised anti-

XX CD23 (FCERII) monoclonal antibody C11, composed of a human framework

XX CC

CC (HSIGKVII) and the heavy chain complementarity determining regions. (see
 CC AAY32257-59) of murine antibody C11. The DNA was constructed by splice
 CC overlap PCR. The invention provides altered antibodies, such as chimeric
 CC or humanised antibodies, which comprise sufficient of the amino acid
 CC sequences of the C11 light and heavy chain complementarity determining
 CC regions to render them capable of binding to the CD23 type II molecule
 CC expressed on haematopoietic cells. The antibodies are used to block
 CC soluble CD23 formation in human therapy, for the treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, urveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,
 CC glomerulonephritis, inflammatory bowel disease, ulcerative colitis,
 CC Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute aschmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX
 XX Sequence 444 AA;

Query Match 100.0%; Score 33; DB 3; Length 444;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |||||
 Db 31 GYWMS 35

RESULT 6
 ABB62006
 ID ABB62006 standard; protein; 1254 AA.
 XX
 AC ABB62006;
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 12810.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 ER 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 XX WPI; 2001-656860/75.
 DR N-FSDB; ABL06109.
 XX

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PT
 XX Disclosure; SEQ ID NO 12810; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-

CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1254 AA;

Query Match 100.0%; Score 33; DB 4; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |||||
 Db 1139 GYWMS 1143

RESULT 7
 ABBG07533
 ID ABBG07533 standard; protein; 40 AA.

XX
 AC ABBG07533;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #7524.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS71720.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 37892; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABBG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pt_sequences
XX
SQ Sequence 40 AA;

Query Match 90.9%; Score 30; DB 4; Length 40;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 33 GYMLS 37
|||:|
|||:|

RESULT 8
AAR95472
ID AAR95472 standard; peptide; 43 AA.
XX
AC
XX AAR95472;
DT 05-NOV-1996 (first entry)
XX
XX V39, monoclonal antibody SM-3 derived antigen binding peptide.
DE
XX
XX Abtide; prostate specific mucin antigen; human prostate cancer; LNCaP;
KW diagnostic; detection; imaging; tumour; phage; peptide library; breast;
KW polymorphic; epithelial.
XX
XX Synthetic.
OS
XX
XX WO9609411-A1.
FN
XX
XX
PD 28-MAR-1996.
XX
XX
PF 20-SEP-1995; 95WO-US011934.
XX
XX 21-SEP-1994; 94US-00310192.
PR 07-JUN-1995; 95US-00488161.
XX
XX (CYTO-) CYTOGEN CORP.
PA
XX
XX Alvarez VL;
PI
XX
XX WPI; 1996-188471/19.
DR
XX
XX New isolated peptide(s) with specific binding activities - obtd. by
PT screening random peptide libraries, for use in diagnostic and therapeutic
PT compsns.
PT
XX
PS Claim 38; Page 75; 106pp; English.
XX
XX AAR95459-R95509 are antigen binding peptides ("abtides") derived from the
CC monoclonal antibody SM-3 which recognises a specific polymorphic
CC epithelial mucin tumour antigen found on human breast cancer cells. The
CC abtides are identified from random peptide libraries using specific
CC ligand binding. Abtides mimic the binding specificity of large molecules
CC such as antibodies and receptors but have a much smaller size allowing
CC their production at a lower cost and reducing the extent of their
CC immunogenicity aiding in vivo delivery. The abtides are useful for the
CC diagnosis, detection, imaging and treatment of disease, e.g. tumours,
CC prostate cancer and breast cancer
XX
SQ Sequence 43 AA;

Query Match 90.9%; Score 30; DB 2; Length 43;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 6 GYMLS 10
|||:|
|||:|

RESULT 9

ABR48102
ID ABR48102 standard; protein; 63 AA.
XX
AC ABR48102;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human secreted protein, SEQ ID 993.
XX
XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
KW vulnery; antiinflammatory; noctropic; neuroprotective;
KW antiparkinsonian; gene therapy; human; cardiovascular disorder.
XX
XX Homo sapiens.
XX
XX WO200295010-A2.
XX
PD 28-NOV-2002.
XX
XX 19-MAR-2002; 2002WO-US009785.
XX
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM;
PI
XX
XX WPI; 2003-129429/12.
DR
XX
XX Novel human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
PT disorders such as arrhythmia.
XX
XX
PS Claim 13; SEQ ID NO 993; 1881pp; English.
XX
XX The present invention relates to novel human secreted proteins (ABR47633-
CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
CC and their coding sequences are useful for the preparation of a diagnostic
CC or pharmaceutical composition for diagnosing or treating a cardiovascular
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, renal disorders,
CC proliferative disorders and/or cancerous diseases and conditions, for
CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism. Note: The sequence data for this patent was published in
CC electronic format and is available from WIPO at
CC ftp.wipo.int/pub/published_pt_sequences
XX
SQ Sequence 63 AA;

Query Match 90.9%; Score 30; DB 6; Length 63;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 45 GYMLS 49
|||:|
|||:|

RESULT 10

KW antianemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
 KW antidyslipidemic; immunosuppressive; dermatological; nephrotropic;
 KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;
 KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;
 KW haemopoietic; haematologic; anaemia; autoimmune disorder;
 KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
 KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
 KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
 KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
 KW human.
 XX Homo sapiens.
 OS
 PN WO2003038063-A2.
 XX
 XX 08-MAY-2003.
 PD
 XX 19-MAR-2002; 2002WO-US008277.
 PF
 XX 21-MAR-2001; 2001US-0277340P.
 PR
 XX 19-JUL-2001; 2001US-0306171P.
 PR
 XX 13-NOV-2001; 2001US-0331287P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Ruben SM;
 PI WPI; 2003-430516/40.
 XX N-PSDB; ADC73916.
 DR
 XX New human secreted polypeptide for diagnosing, preventing or treating
 PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
 PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
 PT atherosclerosis).
 XX Claim 16; SEQ ID NO 1164; 2272pp; English.
 PS
 XX The invention relates to a novel human secreted polypeptide comprising a
 CC defined sequence given in the specification. The polypeptide, nucleic
 CC acid molecule, antibody, agonist or antagonist of the invention may be
 CC useful for preparing a composition for diagnosing or treating a
 CC hematopoietic or hematologic disorder such as anaemia, autoimmune
 CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
 CC diabetes, systemic lupus erythematosus or glomerulonephritis.
 CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
 CC disease, wounds and hyperproliferative disorders including
 CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
 CC parasitic infections. The polypeptide may also be used during gene
 CC therapy procedures and for identifying a binding partner by contacting
 CC the polypeptide with a binding partner and determining whether the
 CC binding partner increases or decreases the activity of the polypeptide.
 CC The current sequence is that of the human secreted protein of the
 CC invention.
 XX
 SQ Sequence 63 AA;
 Query Match 90.9%; Score 30; DB 7; Length 63;
 Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWNWS 5
 DB 45 GYWLIS 49
 RESULT 13
 AAY07813
 ID AAY07813 standard; protein; 64 AA.
 XX
 AC AAY07813;
 XX
 DT 06-JUL-1999 (first entry)
 XX

DE Human secreted protein fragment encoded from gene 70.
 XX
 KW Human; secreted protein; prevention; cancer; tumour; neurodegenerative disorder;
 KW gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder;
 KW developmental abnormality; foetal deficiency; blood disorder; lymphoma;
 KW leukemia; immune system disorder; autoimmune disease; hepatic disease;
 KW renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS;
 KW Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis;
 KW arthritis; psoriasis; digestive; endocrine; infection.
 XX
 OS Homo sapiens.
 XX
 PN WO9909155-A1.
 XX
 XX 25-FEB-1999.
 PD
 XX 18-AUG-1998; 98WO-US017044.
 PF
 XX 19-AUG-1997; 97US-0056368P.
 PR
 XX 19-AUG-1997; 97US-0056369P.
 PR
 XX 19-AUG-1997; 97US-0056535P.
 PR
 XX 19-AUG-1997; 97US-0056555P.
 PR
 XX 19-AUG-1997; 97US-0056558P.
 PR
 XX 19-AUG-1997; 97US-0056628P.
 PR
 XX 19-AUG-1997; 97US-0056629P.
 PR
 XX 19-AUG-1997; 97US-0056726P.
 PR
 XX 19-AUG-1997; 97US-0056728P.
 PR
 XX 16-JUN-1998; 98US-0089510P.
 PR
 XX 15-JUL-1998; 98US-0092956P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ruben SM, Young PE, Brewer LA, Ebner R, Olsen HS, Florence KA;
 PI Rosen CA, Duan R, Moore PA, Shi Y, Lafleur DW, Florence C;
 PI Soppet DR, Endress GA, Feng P, Komatsoulis GA;
 XX WPI; 1999-190160/16.
 DR
 XX N-PSDB; AAX37438.
 DR
 XX New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders.
 XX
 PS Claim 1b; Page 264; 280pp; English.
 XX
 CC This invention describes novel isolated human secreted proteins and their
 CC encoding nucleic acid sequences. The products of the invention are useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. Also pathological conditions can be diagnosed by
 CC determining the presence or amount of expression of the new polypeptides
 CC in a sample or by determining the presence or absence of mutations in the
 CC new polynucleotides. Specific uses are described for each of the 70
 CC polynucleotides, based on which tissues they are most highly expressed
 CC in, and include developing products for the diagnosis or treatment of
 CC cancer, tumours, neurodegenerative disorders, developmental abnormalities
 CC and foetal deficiencies, blood disorders, leukemias, diseases of the
 CC immune system, autoimmune diseases, hepatic and renal diseases, lymphomas,
 CC inflammation, allergies, asthma, sepsis, diabetes, Alzheimer's and
 CC cognitive disorders, schizophrenia, osteoporosis, arthritis, psoriasis,
 CC digestive/endocrine disorders, infections and AIDS. The human secreted
 CC proteins of the invention are represented in AAY07744-Y07850 and the
 CC encoding nucleic acids are represented in AAX37369-X37441
 XX
 SQ Sequence 64 AA;
 Query Match 90.9%; Score 30; DB 2; Length 64;
 Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWNWS 5
 DB 45 GYWLIS 49

RESULT 14
 AAY35482
 ID AAY35482 standard; protein; 181 AA.
 XX
 AC AAY35482;
 XX
 DT 17-OCT-2003 (revised)
 DT 13-SEP-1999 (first entry)
 XX
 DE Chlamydia pneumoniae transmembrane protein sequence.
 XX
 KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope.
 XX
 OS Chlamydia pneumoniae.
 XX
 PN WO9927105-A2.
 XX
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-IB001890.
 XX
 PR 21-NOV-1997; 97FR-00014673.
 PR 04-NOV-1998; 98US-0107078P.
 XX
 PA (GEST) GENSET.
 XX
 PI Griffais R;
 XX
 DR WPI; 1999-357842/30.
 XX
 PT Genome sequence of Chlamydia pneumoniae.
 XX
 PS Page 1244; Disclosure; 1912pp; English.
 XX
 CC AAY34584-Y35879 represent the proteins encoded by all the open reading
 CC frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
 CC pneumoniae causes respiratory disease such as pneumonia and bronchitis.
 CC and is thought to be a contributing factor in heart disease, sarcoidosis,
 CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The
 CC polypeptides encoded by the open reading frames of the C. pneumoniae
 CC genome (see AAY34584-Y35879) can be used in immunogenic compositions as
 CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also
 CC be used as immunogenic compositions, especially where the vector directs
 CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17
 CC -OCT-2003 to standardise OS field)
 XX
 SQ Sequence 181 AA;
 Query Match 90.9%; Score 30; DB 2; Length 181;
 Best Local Similarity 80.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWMS 5
 DB 48 GYWLS 52
 RESULT 15
 AAU17327
 ID AAU17327 standard; protein; 210 AA.
 XX
 AC AAU17327;
 XX
 DT 07-NOV-2001 (first entry)
 DT
 DE Novel signal transduction pathway protein, Seq ID 892.
 XX
 KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
 KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
 KW immune system disorder; rheumatoid arthritis; inflammatory condition;

KW organ transplant rejection; infection; hepatitis C; blood disorder;
 KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
 KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
 KW reproductive system; gastrointestinal; liver disorder; AIDS;
 XX acquired immune deficiency syndrome.
 XX Homo sapiens.
 OS
 PN WO200154733-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001312.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
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 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
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 PR 14-AUG-2000; 2000US-0224518P.
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 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
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 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
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 PR 05-SEP-2000; 2000US-0229509P.
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 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
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 PR 12-SEP-2000; 2000US-0231968P.
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PR 14-SEP-2000; 2000US-0233063P.
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PR 21-SEP-2000; 2000US-0234223P.
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PR 25-SEP-2000; 2000US-0234997P.
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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
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PR 12-OCT-2000; 2000US-0237040P.
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PR 20-OCT-2000; 2000US-0240960P.
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PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.

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PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUYA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-465460/50.
DR N-PSDB; AAS27244.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders.
XX
PS Claim 1; SEQ ID NO 892; 880pp; English.
XX
XX The invention relates to novel isolated polypeptides (I), and
XX polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders, in wound healing,
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC disease), reproductive system disorders, gastrointestinal disorders
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
CC AAU17683 represent novel signal transduction pathway protein, amino acid
CC sequences of the invention
XX

Query Match 90.9%; Score 30; DB 4; Length 210;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYWMS 5
Db 68 GYWLS 72
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Job time : 29.4068 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:01:30 ; Search time 83.8983 Seconds
(without alignments)
19.178 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYVMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799131 residues

Total number of hits satisfying chosen parameters: 1351062

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | Score | Match | Length | DB | ID | Description |
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| 1 | 33 | 100.0 | 10 | 15 | US-10-327-598-450 | | Sequence 450, App |
| 2 | 33 | 100.0 | 73 | 15 | US-10-418-861B-57 | | Sequence 57, Appl |
| 3 | 33 | 100.0 | 103 | 16 | US-10-437-963-178878 | | Sequence 178878, |
| 4 | 33 | 100.0 | 504 | 16 | US-10-437-963-128079 | | Sequence 128079, |
| 5 | 33 | 100.0 | 721 | 16 | US-10-437-963-144813 | | Sequence 144813, |
| 6 | 30 | 90.9 | 64 | 14 | US-10-144-929-162 | | Sequence 162, App |
| 7 | 30 | 90.9 | 64 | 15 | US-10-144-929-162 | | Sequence 162, App |
| 8 | 30 | 90.9 | 77 | 12 | US-10-424-599-231107 | | Sequence 231107, |
| 9 | 30 | 90.9 | 88 | 16 | US-10-767-701-41902 | | Sequence 41902, A |
| 10 | 30 | 90.9 | 95 | 16 | US-10-767-701-53836 | | Sequence 53836, A |
| 11 | 30 | 90.9 | 167 | 12 | US-10-424-599-178190 | | Sequence 178190, |
| 12 | 30 | 90.9 | 181 | 15 | US-10-289-762-900 | | Sequence 900, App |
| 13 | 30 | 90.9 | 210 | 9 | US-09-764-868-892 | | Sequence 892, App |
| 14 | 30 | 90.9 | 229 | 12 | US-10-424-599-210785 | | Sequence 210785, |
| 15 | 30 | 90.9 | 242 | 10 | US-09-866-050A-393 | | Sequence 393, App |

ALIGNMENTS

RESULT 1

US-10-327-598-450
; Sequence 450, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Hongliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 450
; LENGTH: 10
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-450

Query Match 100.0%; Score 33; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYVMS 5
|
|
|
|
|
Db 6 GYVMS 10

RESULT 2

US-10-418-861B-57
; Sequence 57, Application US/10418861B
; Publication No. US20040010131A1
; GENERAL INFORMATION:

Sequence 502, App
Sequence 625, App
Sequence 10910, A
Sequence 57347, A
Sequence 18477, A
Sequence 1130, Ap
Sequence 149574,
Sequence 180, App
Sequence 156, App
Sequence 180, App
Sequence 828, App
Sequence 141970,
Sequence 109, App
Sequence 109, App
Sequence 109, App
Sequence 109, App
Sequence 109, App
Sequence 109, App
Sequence 109, App
Sequence 86, Appl
Sequence 109, App
Sequence 109, App
Sequence 103, App
Sequence 109, App

242 10 US-09-866-050A-502
242 10 US-09-866-050A-625
310 9 US-09-815-242-10910
310 12 US-10-282-122A-57347
315 15 US-10-369-493-18477
348 15 US-10-359-493-1130
381 16 US-10-437-963-149574
392 14 US-10-050-704-180
392 14 US-10-144-929-156
392 15 US-10-144-929-156
392 16 US-10-798-512-180
414 12 US-10-087-192-828
419 16 US-10-437-963-141970
420 9 US-09-909-320-109
420 9 US-09-909-088B-109
420 9 US-09-903-291A-109
420 9 US-09-902-853-109
420 9 US-09-907-824-109
420 9 US-09-907-841-109
420 10 US-09-904-011-109
420 10 US-09-906-742-109
420 10 US-09-906-838-109
420 10 US-09-907-613-109
420 10 US-09-907-942-109
420 10 US-09-796-753-84
420 10 US-09-796-753-86
420 10 US-09-904-859-109
420 10 US-09-903-204-109
420 10 US-09-904-820-109
420 10 US-09-904-786-109

```

; APPLICANT: da Silva, Ana Claudia Raseira
; APPLICANT: Farah, Shaker Chuck
; APPLICANT: Quaggio, Ronaldo Bento
; APPLICANT: Reinach, Fernando de Castro
; APPLICANT: Ferro, Jesus Aparecido
; APPLICANT: De Oliveira, Julio Cezar Franco
; APPLICANT: De Laia, Marcelo Luiz
; APPLICANT: Setubal Joao C.
; APPLICANT: Furlan, Luiz Roberto
; TITLE OF INVENTION: Isolated xanthomonas nucleic acid molecules, proteins encoded the
; FILE REFERENCE: FAPESP 205.1 US
; CURRENT APPLICATION NUMBER: US/10/418,861B
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/374,620
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 57
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Xanthomonas
; FEATURE:
US-10-418-861B-57

Query Match      100.0%; Score 33; DB 15; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      6 GYWS 10

RESULT 3
US-10-437-963-178878
; Sequence 178878, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 178878
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(103)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT4530_76394C.1.pep
US-10-437-963-178878

Query Match      100.0%; Score 33; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      15 GYWS 19

RESULT 4
US-10-437-963-128079
; Sequence 128079, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128079
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(504)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30468C.1.pep
US-10-437-963-128079

Query Match      100.0%; Score 33; DB 16; Length 504;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      4 GYWS 8

RESULT 5
US-10-437-963-144813
; Sequence 144813, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 144813
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45593C.1.pep
US-10-437-963-144813

Query Match      100.0%; Score 33; DB 16; Length 721;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      15 GYWS 19

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Db 319 GYWMS 323

RESULT 6

US-10-144-929-162

; Sequence 162, Application US/10144929

; Publication No. US20030069405A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 70 Human Secreted Proteins

; FILE REFERENCE: P2014P1

; CURRENT APPLICATION NUMBER: US/10/144,929

; CURRENT FILING DATE: 2002-05-15

; PRIOR APPLICATION NUMBER: US/09/251,329

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: PCT/US98/17044

; PRIOR FILING DATE: 1998-08-18

; NUMBER OF SEQ ID NOS: 257

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 162

; LENGTH: 64

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (64)

; OTHER INFORMATION: Xaa equals stop translation

US-10-144-929-162

Query Match 90.9%; Score 30; DB 14; Length 64;

Best Local Similarity 80.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db 45 GYWLS 49

RESULT 7

US-10-144-929-162

; Sequence 162, Application US/10144929

; Publication No. US20040014954A9

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 70 Human Secreted Proteins

; FILE REFERENCE: P2014P1

; CURRENT APPLICATION NUMBER: US/10/144,929

; CURRENT FILING DATE: 2002-05-15

; PRIOR APPLICATION NUMBER: US/09/251,329

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: PCT/US98/17044

; PRIOR FILING DATE: 1998-08-18

; NUMBER OF SEQ ID NOS: 257

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 162

; LENGTH: 64

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (64)

; OTHER INFORMATION: Xaa equals stop translation

US-10-144-929-162

Query Match 90.9%; Score 30; DB 15; Length 64;

Best Local Similarity 80.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db 45 GYWLS 49

RESULT 8

US-10-424-599-231107

; Sequence 231107, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 231107

; LENGTH: 77

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_50710C.1.pep

US-10-424-599-231107

Query Match 90.9%; Score 30; DB 12; Length 77;

Best Local Similarity 80.0%; Pred. No. 6.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db 36 GYWLS 40

RESULT 9

US-10-767-701-41902

; Sequence 41902, Application US/10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 41902

; LENGTH: 88

; TYPE: PRT

; ORGANISM: Sorghum bicolor

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(88)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3478-024-P1-K1-P2.pep

US-10-767-701-41902

Query Match 90.9%; Score 30; DB 16; Length 88;

Best Local Similarity 80.0%; Pred. No. 7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db 70 GYWLS 74

RESULT 10

US-10-767-701-53836

; Sequence 53836, Application US/10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

```
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 53836
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 13586731.pep
US-10-767-701-53836

Query Match          90.9%; Score 30; DB 16; Length 95;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 16 GYWS 20

RESULT 11
US-10-424-599-178190
; Sequence 178190, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 178190
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131921C.1.pep
US-10-424-599-178190

Query Match          90.9%; Score 30; DB 12; Length 167;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 89 GYWS 93

RESULT 12
US-10-289-762-900
; Sequence 900, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 900
; LENGTH: 181
; TYPE: PRT
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; ORGANISM: Chlamydia pneumoniae
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...181
; OTHER INFORMATION: Xaa=unknown or other
US-10-289-762-900
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Query Match          90.9%; Score 30; DB 15; Length 181;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GYWS 5
Db 48 GYWS 52
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RESULT 13
US-09-764-868-892
; Sequence 892, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 892
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-892
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Query Match          90.9%; Score 30; DB 9; Length 210;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GYWS 5
Db 68 GYWS 72
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RESULT 14
US-10-424-599-210785
; Sequence 210785, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 210785
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32366C.1.pep
US-10-424-599-210785
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Query Match          90.9%; Score 30; DB 12; Length 229;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GYWS 5
Db 68 GYWS 72
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Db 109 GYWLS 113

RESULT 15

US-09-866-050A-393
; Sequence 393, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 393
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Rat
US-09-866-050A-393

Query Match 90.9%; Score 30; DB 10; Length 242;
Best Local Similarity 80.0%; Pred. No. 1.7e-03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5

Db 224 GYWLS 228

Search completed: September 30, 2004, 06:54:52
Job time : 83.8983 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:00:45 ; Search time 8.47458 Seconds
(without alignments)

30.459 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWS 5

Scoring table: BLOSUM62

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 33 | 100.0 | 466 | 4 | US-09-489-039A-14325 |
| 2 | 30 | 90.9 | 43 | 2 | US-08-488-161-39 |
| 3 | 30 | 90.9 | 43 | 3 | US-09-273-685-39 |
| 4 | 30 | 90.9 | 43 | 5 | PCT-US95-11934-39 |
| 5 | 30 | 90.9 | 181 | 4 | US-09-198-452A-900 |
| 6 | 30 | 90.9 | 242 | 4 | US-09-312-283C-393 |
| 7 | 30 | 90.9 | 243 | 4 | US-09-134-001C-4114 |
| 8 | 30 | 90.9 | 334 | 4 | US-09-134-000C-6029 |
| 9 | 30 | 90.9 | 383 | 4 | US-09-252-991A-29457 |
| 10 | 30 | 90.9 | 396 | 4 | US-09-252-991A-20263 |
| 11 | 30 | 90.9 | 408 | 4 | US-09-107-532A-6992 |
| 12 | 30 | 90.9 | 420 | 4 | US-09-907-794A-109 |
| 13 | 30 | 90.9 | 420 | 4 | US-09-908-125A-109 |
| 14 | 30 | 90.9 | 420 | 4 | US-09-902-775A-109 |
| 15 | 30 | 90.9 | 478 | 4 | US-09-107-532A-6868 |
| 16 | 30 | 90.9 | 484 | 4 | US-09-634-238-216 |
| 17 | 30 | 90.9 | 534 | 4 | US-09-107-532A-6549 |
| 18 | 30 | 90.9 | 538 | 4 | US-09-489-039A-8363 |
| 19 | 30 | 90.9 | 667 | 4 | US-09-315-127-5 |
| 20 | 30 | 90.9 | 667 | 4 | US-09-315-127-6 |
| 21 | 30 | 90.9 | 685 | 4 | US-09-489-039A-12981 |
| 22 | 29 | 87.9 | 5 | 2 | US-08-480-434-22 |
| 23 | 29 | 87.9 | 5 | 2 | US-08-480-434-31 |
| 24 | 29 | 87.9 | 5 | 2 | US-08-053-451B-22 |
| 25 | 29 | 87.9 | 5 | 2 | US-08-053-451B-31 |
| 26 | 29 | 87.9 | 14 | 1 | US-08-204-658B-11 |
| 27 | 29 | 87.9 | 14 | 1 | US-08-470-702-11 |

Sequence 11, Appl
Sequence 114, Appl
Sequence 125, Appl
Sequence 29, Appl
Sequence 28, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 7742, Appl
Sequence 32, Appl
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Sequence 6217, Appl
Sequence 7475, Appl
Sequence 8223, Appl
Sequence 18697, A
Sequence 23790, A

14 1 US-08-467-831-11
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526 4 US-09-489-039A-8223
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563 4 US-09-252-991A-23790

ALIGNMENTS

RESULT 1

US-09-489-039A-14325
; Sequence 14325, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14325
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14325

Query Match 100.0%; Score 33; DB 4; Length 466;
Best Local Similarity 100.0%; Pred. No. 28+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
Db 437 GYWS 441

RESULT 2

US-08-488-161-39
; Sequence 39, Application US/08488161
; Patent No. 5885577
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/488,161
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 436
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Misrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-176
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 39:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 43 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-488-161-39

Query Match 90.9%; Score 30; DB 2; Length 43;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||:
Db 6 GYWLS 10

RESULT 3
US-09-273-685-39
; Sequence 39, Application US/09273685
; Patent No. 6015561
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/273,685
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,161
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-273-685-39

Query Match 90.9%; Score 30; DB 3; Length 43;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||:
Db 6 GYWLS 10

RESULT 4
PCT-US95-11934-39
; Sequence 39, Application PC/TUS9511934
; GENERAL INFORMATION:
; APPLICANT: Cytogen Corporation
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11934
; FILING DATE: 20-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-196-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-11934-39

Query Match 90.9%; Score 30; DB 5; Length 43;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||:
Db 6 GYWLS 10

RESULT 5
US-09-198-452A-900
; Sequence 900, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 900
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...181
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-900

Query Match 90.9%; Score 30; DB 4; Length 181;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 48 GYWS 52

RESULT 6

US-09-312-283C-393
; Sequence 393, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Marison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 393
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-393

Query Match 90.9%; Score 30; DB 4; Length 242;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 224 GYWS 228

RESULT 7

US-09-134-001C-4114
; Sequence 4114, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4114
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4114

Query Match 90.9%; Score 30; DB 4; Length 243;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 52 GYWS 56

RESULT 8

US-09-134-000C-6029
; Sequence 6029, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6029
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6029

Query Match 90.9%; Score 30; DB 4; Length 334;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 111 GYWS 115

RESULT 9

US-09-252-991A-29457
; Sequence 29457, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29457
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29457

Query Match 90.9%; Score 30; DB 4; Length 383;
Best Local Similarity 80.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 228 GYWS 232

RESULT 10

US-09-252-991A-20263
; Sequence 20263, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20263
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20263

Query Match 90.9%; Score 30; DB 4; Length 396;
Best Local Similarity 80.0%; Pred. No. 5.5e-02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 40 GYWS 44

RESULT 11
US-09-107-532A-6992
; Sequence 6992, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6992:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES

ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...408
; SEQUENCE DESCRIPTION: SEQ ID NO: 6992:
US-09-107-532A-6992

Query Match 90.9%; Score 30; DB 4; Length 408;
Best Local Similarity 80.0%; Pred. No. 5.6e-02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 263 GYWT 267

RESULT 12
US-09-907-794A-109
; Sequence 109, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Feng, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; ACIDS ENCODING THE SAME
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 109
 ; LENGTH: 420
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-907-794A-109

Query Match 90.9%; Score 30; DB 4; Length 420;
 Best Local Similarity 80.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 Db 402 GYWS 406

RESULT 13
 US-09-905-125A-109
 ; Sequence 109, Application US/09905125A
 ; Patent No. 6664376
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/905,125A
 ; CURRENT FILING DATE: 2001-07-12
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 109
 ; LENGTH: 420
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-905-125A-109

Query Match 90.9%; Score 30; DB 4; Length 420;
 Best Local Similarity 80.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 Db 402 GYWS 406

RESULT 14
 US-09-902-775A-109
 ; Sequence 109, Application US/09902775A
 ; Patent No. 666451
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/902,775A
 ; CURRENT FILING DATE: 2001-07-12
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594

FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 109
LENGTH: 420
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-109

Query Match 90.9%; Score 30; DB 4; Length 420;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
Db 402 GYWS 406

RESULT 15

US-09-107-532A-6868
Sequence 6868, Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6868:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...478
SEQUENCE DESCRIPTION: SEQ ID NO: 6868:
US-09-107-532A-6868

Query Match 90.9%; Score 30; DB 4; Length 478;
Best Local Similarity 80.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
Db 98 GYWS 102

Search completed: September 30, 2004, 06:39:18
Job time : 9.47458 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: September 30, 2004, 05:55:56 ; Search time 20.6102 Seconds
(without alignments)
88.677 Million cell updates/sec

Title: US-09-674-716B-11
Perfect score: 98
Sequence: 1 EIRLSDNYATHVAESVKG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283365

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|-------|--------|--------|----|--------------------|
| 1 | 98 | 100.0 | 101 | 2 | S26460 | | Ig heavy chain V r |
| 2 | 98 | 100.0 | 115 | 2 | S38714 | | Ig heavy chain V r |
| 3 | 93 | 94.9 | 106 | 2 | S24521 | | Ig heavy chain V r |
| 4 | 93 | 94.9 | 115 | 1 | AVMS06 | | Ig heavy chain V-I |
| 5 | 91 | 92.9 | 113 | 1 | AVMSAB | | Ig heavy chain V-I |
| 6 | 91 | 92.9 | 113 | 1 | AVMS61 | | Ig heavy chain V-I |
| 7 | 91 | 92.9 | 113 | 1 | AVMS09 | | Ig heavy chain V-I |
| 8 | 91 | 92.9 | 113 | 1 | AVMSB7 | | Ig heavy chain V-I |
| 9 | 91 | 92.9 | 115 | 1 | AVMS82 | | Ig heavy chain V-I |
| 10 | 89 | 90.8 | 115 | 2 | A25803 | | Ig heavy chain V r |
| 11 | 86 | 87.8 | 113 | 1 | AVMS57 | | Ig heavy chain V-I |
| 12 | 85 | 86.7 | 113 | 1 | HVMSAM | | Ig heavy chain V-I |
| 13 | 75.5 | 77.0 | 111 | 1 | MEMS76 | | Ig heavy chain pre |
| 14 | 73 | 74.5 | 139 | 2 | PC1213 | | Ig heavy chain V r |
| 15 | 68 | 69.4 | 64 | 2 | I77394 | | Ig heavy chain V-D |
| 16 | 68 | 69.4 | 121 | 2 | S09958 | | Ig heavy chain V r |
| 17 | 67 | 68.4 | 100 | 2 | S26462 | | Ig heavy chain V r |
| 18 | 67 | 68.4 | 110 | 2 | PH1091 | | Ig heavy chain V r |
| 19 | 67 | 68.4 | 110 | 2 | PH1092 | | Ig heavy chain V r |
| 20 | 67 | 68.4 | 119 | 2 | A27630 | | Ig heavy chain pre |
| 21 | 67 | 68.4 | 121 | 2 | A41940 | | Ig heavy chain V r |
| 22 | 67 | 68.4 | 141 | 2 | I32513 | | Ig heavy chain pre |
| 23 | 66 | 67.3 | 125 | 2 | S67945 | | Ig heavy chain pre |
| 24 | 65 | 66.3 | 139 | 2 | G29380 | | Ig heavy chain pre |
| 25 | 64 | 65.3 | 110 | 2 | PH1093 | | Ig heavy chain V r |
| 26 | 63 | 64.3 | 220 | 2 | S68211 | | Ig heavy chain (Ma |
| 27 | 63 | 64.3 | 444 | 2 | PC4436 | | monoclonal antibod |
| 28 | 61 | 62.2 | 119 | 2 | PH1293 | | Ig heavy chain pre |
| 29 | 61 | 62.2 | 137 | 2 | S42467 | | Ig heavy chain V r |

| | | | | | | |
|----|----|------|-----|---|--------|--------------------|
| 30 | 58 | 59.2 | 55 | 2 | S46466 | Ig heavy chain V r |
| 31 | 58 | 59.2 | 100 | 2 | PL0122 | Ig heavy chain V-I |
| 32 | 58 | 59.2 | 126 | 2 | S44107 | Ig heavy chain V-D |
| 33 | 58 | 59.2 | 132 | 2 | PH1289 | Ig heavy chain pre |
| 34 | 57 | 58.2 | 116 | 2 | H29380 | Ig heavy chain pre |
| 35 | 57 | 58.2 | 118 | 2 | A31485 | Ig heavy chain V r |
| 36 | 57 | 58.2 | 137 | 2 | B34903 | Ig heavy chain pre |
| 37 | 57 | 58.2 | 137 | 2 | F34903 | Ig heavy chain pre |
| 38 | 57 | 58.2 | 137 | 2 | D34903 | Ig heavy chain pre |
| 39 | 57 | 58.2 | 137 | 2 | A34903 | Ig heavy chain pre |
| 40 | 57 | 58.2 | 142 | 1 | EVTR2 | Ig heavy chain pre |
| 41 | 56 | 57.1 | 127 | 2 | S58213 | Ig heavy chain V r |
| 42 | 56 | 57.1 | 133 | 2 | PH1288 | Ig heavy chain pre |
| 43 | 55 | 56.1 | 100 | 2 | S26926 | Ig heavy chain V r |
| 44 | 55 | 56.1 | 119 | 2 | S00981 | Ig heavy chain pre |
| 45 | 55 | 56.1 | 119 | 2 | PH1290 | Ig heavy chain pre |

ALIGNMENTS

RESULT 1

S26460
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26460
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26460
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-101 <KAV>
A:Cross-references: EMBL:X59106; NID:G51707; PIDN:CAA41832.1; PID:G51708
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 98; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHVAESVKG 19

Db 32 EIRLSDNYATHVAESVKG 50

RESULT 2

S38714
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S38714
R:Climanis, A.V.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38713
A:Accession: S38714
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <CIM>
A:Cross-references: EMBL:X76014; NID:G416092; PIDN:CAA53601.1; PID:G1334076
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-99/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 98; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHVAESVKG 19

Db 49 EIRLSDNYATHVAESVKG 67

```

RESULT 3
S24521
IG heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S24521
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24521
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <KAA>
A:Cross-references: EMBL:X66664; NID:G51247; PIDN:CAA47226.1; PID:G51248
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-106/Domain: immunoglobulin homology <IMM>

Query Match 94.9%; Score 93; DB 2; Length 106;
Best Local Similarity 94.7%; Pred. No. 7.4e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
|||||:|||||:|||||
Db 56 EIRLKSNHYATHYAESVKG 74

RESULT 4
AVMS06
IG heavy chain V-III region (J606) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: C92811; A02072
R:Johnson, N.; Slankard, J.; Paul, L.; Hood, L.
J. Immunol. 128, 302-307, 1982
A:Title: The complete V domain amino acid sequences of two myeloma inulin-binding proteins
A:Reference number: A92811; MUID:82099361; PMID:6798111
A:Accession: C92811
A:Molecule type: protein
A:Residues: 1-115 <JOH>
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 8.1e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
|||||:|||||:|||||
Db 50 EIRLKSNHYATHYAESVKG 68

RESULT 5
AVMSAB
IG heavy chain V-III region (A4) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 31-Mar-1997
C:Accession: A93818; A02072
R:Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A:Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A:Reference number: A93818; MUID:78158406; PMID:417344
A:Accession: A93818
A:Molecule type: protein
A:Residues: 1-113 <VRA>
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
|||||:|||||:|||||
Db 50 EIRLKSHNYATHYAESVKG 68

RESULT 6
AVMS61
IG heavy chain V-III region (U61) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: B93818; A02072
R:Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A:Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A:Reference number: A93818; MUID:78158406; PMID:417344
A:Accession: B93818
A:Molecule type: protein
A:Residues: 1-113 <VRA>
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
|||||:|||||:|||||
Db 50 EIRLKSHNYATHYAESVKG 68

RESULT 7
AVMS09
IG heavy chain V-III region (E109) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: C93818; A02072
R:Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A:Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A:Reference number: A93818; MUID:78158406; PMID:417344
A:Accession: C93818
A:Molecule type: protein
A:Residues: 1-113 <VRA>
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
|||||:|||||:|||||
Db 50 EIRLKSHNYATHYAESVKG 68

RESULT 8
AVMSB7
IG heavy chain V-III region (ABE-47N) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: A90406; A02072

```

R;Vrana, M.; Rudikoff, S.; Potter, M.
Biochemistry 16, 1170-1175, 1977

A;Title: Heavy-chain variable-region sequence from an inulin-binding myeloma protein.
A;Reference number: A90400; MUID:77134726; PMID:402936

A;Accession: A90400

A;Molecule type: protein

A;Residues: 1-113 <VRA>

C;Comment: This chain was isolated from a myeloma protein that binds inulin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;

Best Local Similarity 94.7%; Pred. No. 1.7e-07;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19

Db 50 EIRKSHNYATHYAESVKG 68

RESULT 9

AVMS82

Ig heavy chain V-III region (W3082) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996

C;Accession: D92811; A02072

R;Johnson, N.; Slankard, J.; Paul, L.; Hood, L.

J. Immunol. 128, 302-307, 1982

A;Title: The complete V domain amino acid sequences of two myeloma inulin-binding proteins

A;Reference number: A92811; MUID:8209361; PMID:679811

A;Accession: D92811

A;Molecule type: protein

A;Residues: 1-115 <JOH>

C;Comment: This chain was isolated from a myeloma protein that binds inulin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 115;

Best Local Similarity 94.7%; Pred. No. 1.7e-07;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19

Db 50 EIRKSHNYATHYAESVKG 68

RESULT 10

A25803

Ig heavy chain V region (2S1.3) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996

C;Accession: A25803

R;Herbst, H.; Grutter, T.; Aebersold, R.; Braun, D.G.

Biol. Chem. Hoppe-Seyler 367, 843-851, 1986

A;Title: The complete amino-acid sequence of the variable domain of a monoclonal anti-s

A;Reference number: A25803; MUID:87076047; PMID:3539142

A;Accession: A25803

A;Molecule type: protein

A;Residues: 1-115 <HER>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 90.8%; Score 89; DB 2; Length 115;

Best Local Similarity 89.5%; Pred. No. 3.6e-07;

Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19

Db 50 EIRKSHNYATHYAESVKG 68

Db 50 QIRLASDNYATHYAESVKG 68

RESULT 11

AVMS57

Ig heavy chain V-III region (T957) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996

C;Accession: A92810; A02072

R;Rudikoff, S.; Potter, M.

J. Immunol. 127, 191-194, 1981

A;Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a n

A;Reference number: A92810; MUID:81216632; PMID:6787122

A;Accession: A92810

A;Molecule type: protein

A;Residues: 1-113 <RUD>

C;Comment: This chain was isolated from a myeloma protein that binds inulin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match 87.8%; Score 86; DB 1; Length 113;

Best Local Similarity 89.5%; Pred. No. 1.1e-06;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19

Db 50 EIRKSHNYATHYAESVKG 68

RESULT 12

HVMSAM

Ig heavy chain V region (AMPC1) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 31-Mar-1997

C;Accession: A02073

R;Rudikoff, S.; Potter, M.

J. Immunol. 127, 191-194, 1981

A;Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a n

A;Reference number: A92810; MUID:81216632; PMID:6787122

A;Accession: A02073

A;Molecule type: protein

A;Residues: 1-113 <RUD>

C;Comment: This chain was isolated from a myeloma protein that binds inulin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match 86.7%; Score 85; DB 1; Length 113;

Best Local Similarity 89.5%; Pred. No. 1.6e-06;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19

Db 50 EIRKSHNYATHYAESVKG 68

RESULT 13

HMMS76

Ig heavy chain V-III region (HPC76) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1980 #sequence_revision 30-Sep-1980 #text_change 31-Mar-1997

C;Accession: A02074

R;Bernard, O.; Gough, N.M.

Proc. Natl. Acad. Sci. U.S.A. 77, 3630-3634, 1980

A;Title: Nucleotide sequence of immunoglobulin heavy chain joining segments between trans

A;Reference number: A02074; MUID:81013937; PMID:6251474

A;Accession: A02074

A;Molecule type: mRNA

A;Residues: 1-111 <BER>

A;Note: the sequence was also determined from the differentiated gene

A:Note: the sequence of the first 197 residues of the C region was also determined and d
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-94/Domain: immunoglobulin homology <IMM>
F:17-92/Disulfide bonds: #status predicted

Query Match 77.0%; Score 75.5; DB 1; Length 111;
Best Local Similarity 89.5%; Pred. No. 5.3e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 EIRLKSDNYATHYAESVKG 19
DB 45 EIRLKS-GYATHYAESVKG 62

RESULT 14

PC1213
Ig heavy chain precursor V region (mAb H8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Jul-1999
C:Accession: PC1213
R:Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim,
Gene 121, 331-335, 1992
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m
A:Reference number: PC1213; MUID:93077049; PMID:1446832
A:Accession: PC1213
A:Molecule type: mRNA
A:Residues: 1-139 <HON>
A:Cross-references: GB:M98041; NID:G195092; PIDN:AAA38159.1; PID:G195093
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Product: Ig heavy chain V region #status predicted <MAT>
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 73; DB 2; Length 139;
Best Local Similarity 73.7%; Pred. No. 0.00017;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
DB 69 EIRSKANNHATYAESVKG 87

RESULT 15

I77394
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C:Accession: I77394
R:Owens, J.D.
Mol. Cell. Biol. 11, 5660-5670, 1991
A:Title: Non-homologous recombination/deletion at sites within the mouse JH-Cdelta locus
A:Reference number: I57520; MUID:92017847; PMID:1922069
A:Accession: I77394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-64 <RES>
A:Cross-references: GB:M64568; NID:G198472; PIDN:AAA39341.1; PID:G198473
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 69.4%; Score 68; DB 2; Length 64;
Best Local Similarity 72.2%; Pred. No. 0.00047;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVKG 19
DB 9 ITVKSDNYANYAESVKG 26

Search completed: September 30, 2004, 06:00:37
Job time : 20.6102 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 11.5932 Seconds
(without alignments)
85.337 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98
Sequence: 1 BIRLSDNYATHYAESVKG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 93 | 94.9 | 115 | 1 HV32 MOUSE | P01801 mus musculus |
| 2 | 91 | 92.9 | 113 | 1 HV27 MOUSE | P01796 mus musculus |
| 3 | 91 | 92.9 | 113 | 1 HV28 MOUSE | P01797 mus musculus |
| 4 | 91 | 92.9 | 113 | 1 HV29 MOUSE | P01798 mus musculus |
| 5 | 91 | 92.9 | 113 | 1 HV30 MOUSE | P01799 mus musculus |
| 6 | 91 | 92.9 | 115 | 1 HV31 MOUSE | P01802 mus musculus |
| 7 | 86 | 87.8 | 113 | 1 HV34 MOUSE | P01803 mus musculus |
| 8 | 85 | 86.7 | 113 | 1 HV35 MOUSE | P01804 mus musculus |
| 9 | 75.5 | 77.0 | 111 | 1 HV01 RAT | P01805 rattus norv |
| 10 | 57 | 58.2 | 142 | 1 HV21 MOUSE | P01790 mus musculus |
| 11 | 48 | 49.0 | 122 | 1 HV18 MOUSE | P01787 mus musculus |
| 12 | 48 | 49.0 | 123 | 1 HV19 MOUSE | P01788 mus musculus |
| 13 | 48 | 49.0 | 123 | 1 HV20 MOUSE | P01791 mus musculus |
| 14 | 48 | 49.0 | 123 | 1 HV22 MOUSE | P01794 mus musculus |
| 15 | 48 | 49.0 | 123 | 1 HV25 MOUSE | P01789 mus musculus |
| 16 | 46 | 46.9 | 122 | 1 HV26 MOUSE | P01795 mus musculus |
| 17 | 46 | 46.9 | 144 | 1 HUNE CLOAL | O96785 clegmia alb |
| 18 | 45 | 45.9 | 485 | 1 HV23 MOUSE | P01792 mus musculus |
| 19 | 44 | 44.9 | 123 | 1 YS76 ANASP | O96785 clegmia alb |
| 20 | 43 | 43.9 | 280 | 1 YS76 ANASP | O96785 clegmia alb |
| 21 | 42 | 42.9 | 250 | 1 Y186 MYCGE | O96785 clegmia alb |
| 22 | 42 | 42.9 | 595 | 1 VPI_BPCHP | O96785 clegmia alb |
| 23 | 42 | 42.9 | 734 | 1 GLGE NITEU | O96785 clegmia alb |
| 24 | 42 | 42.9 | 822 | 1 BPBA_PSEAE | O96785 clegmia alb |
| 25 | 41.5 | 42.3 | 117 | 1 HV17 MOUSE | P01786 mus musculus |
| 26 | 41 | 41.8 | 123 | 1 HV24 MOUSE | P01793 mus musculus |
| 27 | 41 | 41.8 | 126 | 1 HV3K_HUMAN | P01772 homo sapien |
| 28 | 41 | 41.8 | 318 | 1 RLPA_TREPA | O83958 treponema p |
| 29 | 41 | 41.8 | 385 | 1 HUNE_BOMMO | O18326 bombyx mori |
| 30 | 41 | 41.8 | 664 | 1 DHSK_HUMAN | P31040 homo sapien |
| 31 | 41 | 41.8 | 665 | 1 DHSK_BOVIN | P31039 bos taurus |
| 32 | 41 | 41.8 | 705 | 1 CATS_RHIME | O9X576 rhizobium m |
| 33 | 41 | 41.8 | 868 | 1 N180_YEAST | P33420 saccharomyc |

34 40.5 41.3 627 1 GLGB_BACSU
35 40 40.8 116 1 HV05_CARAU
36 40 40.8 136 1 HV16_MOUSE
37 40 40.8 216 1 CAT_VIBAN
38 40 40.8 381 1 GRK2_ECOLI
39 40 40.8 430 1 YUCP_ECOLI
40 40 40.8 439 1 SYE2_HELPJ
41 40 40.8 439 1 SYE2_HELPY
42 40 40.8 500 1 MOO_EACHD
43 40 40.8 555 1 VGLF_P11HC
44 40 40.8 564 1 YC62_AQUAE
45 40 40.8 647 1 ACSA_XANCP

P39118 bacillus su
P19181 carassius a
P01783 mus musculu
P49417 vibrio angu
P3524 escherichia
P32704 escherichia
Q921J1 helicobacte
Q25360 helicobacte
Q829G7 bacillus ha
P12605 human parai
O87301 aquifex aeo
Q87311 xanthomonas

ALIGNMENTS

RESULT 1
HV32_MOUSE
ID HV32_MOUSE STANDARD; PRT; 115 AA.
AC P01801;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=8209361; PubMed=6798111;
RA Johnson N., Sliankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 114
FT DISULFID 22 98
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;
Query Match 94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 2e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 BIRLSDNYATHYAESVKG 19
Dd 50 BIRLSDNYATHYAESVKG 68

RESULT 2
HV27_MOUSE
ID HV27_MOUSE STANDARD; PRT; 113 AA.
AC P01796;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region A4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;

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RN      SEQUENCE.
RX      MEDLINE=78158406; PubMed=417344;
RA      Vrana M., Rudikoff S., Potter M.;
RT      "Sequence variation among heavy chains from inulin-binding myeloma
RL      proteins.";
RL      Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC      -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC      BINDS INULIN.
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR      PIR; A93818; AVMSAB.
DR      HSSP; P01810; 2FBJ.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; IG; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS00835; IG-LIKE; 1.
DR      Immunoglobulin V region.
FT      DOMAIN 1 >113
FT      DISULFID 22 98
FT      NON_TER 113 113
FT      SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;
SQ      QUERY MATCH 92.9%; Score 91; DB 1; Length 113;
      Best Local Similarity 94.7%; Pred. No. 4.2e-08;
      Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EIRLSDNYATHYAESVKG 19
      ||||| ||||| ||||| ||||| |||||
DB      50 EIRLSDNYATHYAESVKG 68

RESULT 3
HV28 MOUSE
ID HV28 MOUSE STANDARD; PRT; 113 AA.
AC P01797;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RL proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; B93818; AVMS61.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 >113
FT DISULFID 22 98
FT NON_TER 113 113
FT SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;
SQ QUERY MATCH 92.9%; Score 91; DB 1; Length 113;
      Best Local Similarity 94.7%; Pred. No. 4.2e-08;
      Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EIRLSDNYATHYAESVKG 19
      ||||| ||||| ||||| ||||| |||||
DB      50 EIRLSDNYATHYAESVKG 19

RESULT 5
HV30 MOUSE
ID HV30 MOUSE STANDARD; PRT; 113 AA.
AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region ABE-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=77134726; PubMed=402936;
RA Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
RL protein.";
RL Biochemistry 16:1170-1175(1977).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A30400; AVMSB7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.

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DB      50 EIRLSDNYATHYAESVKG 68

RESULT 4
HV29 MOUSE
ID HV29 MOUSE STANDARD; PRT; 113 AA.
AC P01798;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region E109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RL proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; C93818; AVMS09.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 >113
FT DISULFID 22 98
FT NON_TER 113 113
FT SEQUENCE 113 AA; 12647 MW; EE50F2F20EDB129B CRC64;
SQ QUERY MATCH 92.9%; Score 91; DB 1; Length 113;
      Best Local Similarity 94.7%; Pred. No. 4.2e-08;
      Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EIRLSDNYATHYAESVKG 19
      ||||| ||||| ||||| ||||| |||||
DB      50 EIRLSDNYATHYAESVKG 68

RESULT 5
HV30 MOUSE
ID HV30 MOUSE STANDARD; PRT; 113 AA.
AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region ABE-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=77134726; PubMed=402936;
RA Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
RL protein.";
RL Biochemistry 16:1170-1175(1977).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A30400; AVMSB7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.

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DR PFAM: PF00047; Ig; 1.
DR SMART: SMO0406; IGV; 1.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76659C16C779845E CRC64;

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
DB 50 EIRKSHNYATHYAESVKG 68

RESULT 5
HV33_MOUSE
ID HV33_MOUSE STANDARD; PRT; 115 AA.
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
EX MEDLINE=8209361; PubMed=6798111;
PA Johnson N., Slack J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: P92811; AVMS82.
DR HSSP: P01810; 2FEJ.
DR InterPro: IPR007110; IG-LIKE.
DR InterPro: IPR003596; IGV.
DR PFAM: PF00047; Ig; 1.
DR SMART: SMO0406; IGV; 1.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98 IG-LIKE.
FT NON TER 115 115 BY SIMILARITY.
SQ SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Query Match 92.9%; Score 91; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
DB 50 EIRKSHNYATHYAESVKG 68

RESULT 7
HV31_MOUSE
ID HV31_MOUSE STANDARD; PRT; 113 AA.
AC P01800;
DT 21-JUL-1986 (Rel. 01, Created)
DT 10-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region T957.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
EX MEDLINE=8209361; PubMed=6798111;
PA Johnson N., Slack J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: P92811; AVMS82.
DR HSSP: P01810; 2FEJ.
DR InterPro: IPR007110; IG-LIKE.
DR InterPro: IPR003596; IGV.
DR PFAM: PF00047; Ig; 1.
DR SMART: SMO0406; IGV; 1.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98 IG-LIKE.
FT NON TER 115 115 BY SIMILARITY.
SQ SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Query Match 92.9%; Score 91; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
DB 50 EIRKSHNYATHYAESVKG 68
```

```
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
EX MEDLINE=81216632; PubMed=6787122;
PA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment.";
RL J. Immunol. 127:191-194(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A92810; AVMS57.
DR HSSP: P01810; 2FEJ.
DR InterPro: IPR007110; IG-LIKE.
DR InterPro: IPR003596; IGV.
DR PFAM: PF00047; Ig; 1.
DR SMART: SMO0406; IGV; 1.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98 IG-LIKE.
FT NON TER 113 113 BY SIMILARITY.
SQ SEQUENCE 113 AA; 12732 MW; 26618F626B59859E CRC64;

Query Match 87.8%; Score 86; DB 1; Length 113;
Best Local Similarity 89.5%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
DB 50 EIRKSHNYATHYAESVKG 68

RESULT 8
HV34_MOUSE
ID HV34_MOUSE STANDARD; PRT; 113 AA.
AC P01803;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region AMPC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
EX MEDLINE=81216632; PubMed=6787122;
PA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment.";
RL J. Immunol. 127:191-194(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02073; HVMSAM.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; IG-LIKE.
DR InterPro: IPR003596; IGV.
DR PFAM: PF00047; Ig; 1.
DR SMART: SMO0406; IGV; 1.
DR PROSITE: PS0835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98 IG-LIKE.
FT NON TER 113 113 BY SIMILARITY.
SQ SEQUENCE 113 AA; 13691 MW; 7A6D906AAA965E9E CRC64;

Query Match 86.7%; Score 85; DB 1; Length 113;
Best Local Similarity 89.5%; Pred. No. 4.1e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
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Db      50 EIRLKSNNYATHYAESVKG 68
|||||
RESULT 9
HV35 MOUSE
ID HV35 MOUSE STANDARD; PRT; 111 AA.
AC P01804;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region HPC76 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81013937; PubMed=6251474;
RA Bernard O., Gough N.M.;
RT "Nucleotide sequence of immunoglobulin heavy chain joining segments
between translocated VH and mu constant regions genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C
CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.
CC REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
DR PIR; A02074; MHMS76.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 110 IG-LIKE.
FT NON TER 111
FT SEQUENCE 111 AA; 13304 MW; 0EDE98EC7348056A CRC64;

Query Match 77.0%; Score 75.5; DB 1; Length 111;
Best Local Similarity 89.5%; Pred. No. 1.5e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 EIRLKSNNYATHYAESVKG 19
|||||
Db      45 EIRLKS-GYATHYAESVKG 62
|||||
RESULT 10
HV01 RAT
ID HV01 RAT STANDARD; PRT; 142 AA.
AC P01805;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region IR2 precursor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83064537; PubMed=6292865;
RA Hellman L., Pettersson U., Engstrom A., Karlsson T., Bennich H.;
RT "Structure and evolution of the heavy chain from rat immunoglobulin
E.";
RL Nucleic Acids Res. 10:6041-6049(1982).
CC -!- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGE-SECRETING
IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RATS.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
DR PIR; A02075; EVRTE2.
DR HSSP; P01789; IMCP.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 142 IG HEAVY CHAIN V REGION IR2.
FT DOMAIN 20 133 IG-LIKE.
FT NON TER 142
SQ SEQUENCE 142 AA; 16024 MW; DE29E6CFE745DF3B CRC64;

Query Match 58.2%; Score 57; DB 1; Length 142;
Best Local Similarity 52.6%; Pred. NO. 0.023;
Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIRLKSNNYATHYAESVKG 19
|||||
Db      69 EIRKANNYVAYGKSLKG 87
|||||
RESULT 11
HV21 MOUSE
ID HV21 MOUSE STANDARD; PRT; 122 AA.
AC P01790;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MS11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054880; PubMed=6776528;
RA Robinson E.A., Appella E.;
RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain
(MOPC 511).";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORIC ACID.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 114 IG-LIKE.
FT NON TER 122
SQ SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;

Query Match 49.0%; Score 48; DB 1; Length 122;
Best Local Similarity 52.9%; Pred. No. 0.59;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVKG 19
|||||
Db      52 RNKANDYITEYSASVKG 68
|||||
RESULT 12
HV18 MOUSE
ID HV18 MOUSE STANDARD; PRT; 123 AA.
AC P01787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC      -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR      HSPs; P01789; IMCP.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG LIKE; 1.
DR      Immunoglobulin V region.
KW      DOMAIN 1
FT      DOMAIN 114
FT      NON_TER 123
FT      SEQUENCE 123 AA; 13805 MW; 9D581401912F7000 CRC64;
SQ
Query Match 49.0%; Score 48; DB 1; Length 123;
Best Local Similarity 52.9%; Pred. No. 0.59;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 RLKSDNYATHYASVKG 19
DB      52 RNKANDYTTYSASVKG 68
      |:::|::|::|::|
      |:::|::|::|::|

RESULT 14
HV22 MOUSE
ID HV22 MOUSE STANDARD; PRT; 123 AA.
AC P01791;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region HPGM6.
DE Ig heavy chain V region HPGM6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IGG antibodies to phosphorylcholine exhibit more diversity than
RT their IGM counterparts.";
RL Nature 291:28-34(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC FIR; D93256; AYMSH6.
DR      HSPs; P01789; IMCP.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG LIKE; 1.
DR      Immunoglobulin V region; Hybridoma.
KW      DOMAIN 1
FT      DOMAIN 114
FT      NON_TER 123
FT      SEQUENCE 123 AA; 13895 MW; 81361892ECBF7000 CRC64;
SQ
Query Match 49.0%; Score 48; DB 1; Length 123;
Best Local Similarity 52.9%; Pred. No. 0.59;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 RLKSDNYATHYASVKG 19
DB      52 RNKANDYTTYSASVKG 68
      |:::|::|::|::|
      |:::|::|::|::|

RESULT 15
HV25 MOUSE
ID HV25 MOUSE STANDARD; PRT; 123 AA.
AC P01794;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region HPGC14.
DE Ig heavy chain V region HPGC14.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81197602; PubMed=7231520;
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
 RT "IGG antibodies to phosphorylcholine exhibit more diversity than
 their IGM counterparts.";
 RL Nature 291:29-34(1981).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 BINDS PHOSPHORYLCHOLINE.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; G93256; AVMS14.
 DR HSP; P01789; 1MGP.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 114
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13807 MW; A7584FB098B7785D CRC64;
 Query Match 49.0%; Score 48; DB 1; Length 123;
 Best Local Similarity 52.9%; Pred. No. 0.59;
 Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 OY 3 RLKSDNYATHVAESVKG 19
 DB 52 RNKANDYTTTYSASVKG 68

Search completed: September 30, 2004, 06:01:21
 Job time : 12.5932 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 62.1525 Seconds
(without alignments)
96.454 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98
Sequence: 1 EIRKSDNYATHVAESVKG 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mmc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvrius.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 90 | 91.8 | 487 | 11 | Q80Z17 mus musculus |
| 2 | 68 | 69.4 | 64 | 11 | Q61750 mus musculus |
| 3 | 57 | 58.2 | 479 | 11 | Q7TWK4 |
| 4 | 51 | 52.0 | 469 | 11 | Q8R3V9 mus musculus |
| 5 | 51 | 52.0 | 480 | 11 | Q91XEL mus musculus |
| 6 | 49 | 50.0 | 361 | 2 | Q9RBZ2 pseudomonas |
| 7 | 47.5 | 48.5 | 754 | 11 | Q8CGQ1 mus musculus |
| 8 | 47 | 48.0 | 357 | 2 | Q9RBZ3 pseudomonas |
| 9 | 47 | 48.0 | 398 | 16 | Q88ZK4 lactobacill |
| 10 | 46 | 46.9 | 2910 | 10 | Q9FND5 |
| 11 | 45.5 | 46.4 | 703 | 11 | Q8COV3 |
| 12 | 45 | 45.9 | 121 | 4 | Q9UL71 homo sapien |
| 13 | 45 | 45.9 | 300 | 5 | Q8ID86 plasmodium |
| 14 | 45 | 45.9 | 422 | 5 | Q8WR61 lymantria d |
| 15 | 45 | 45.9 | 450 | 16 | Q8U651 agrobacteri |
| 16 | 44 | 44.9 | 253 | 16 | Q8E516 streptococc |

| | | | | | |
|----|------|------|------|----|--------------------|
| 17 | 44 | 44.9 | 253 | 16 | Q8DZT9 |
| 18 | 44 | 44.9 | 270 | 16 | Q7VLX9 |
| 19 | 44 | 44.9 | 362 | 2 | Q45962 clostridium |
| 20 | 44 | 44.9 | 432 | 16 | Q7VR52 candidatus |
| 21 | 43.5 | 44.4 | 115 | 16 | Q8CUX1 |
| 22 | 43 | 43.9 | 123 | 16 | Q8DWN2 |
| 23 | 43 | 43.9 | 145 | 2 | Q7WSG9 |
| 24 | 43 | 43.9 | 182 | 17 | Q35037 |
| 25 | 43 | 43.9 | 236 | 9 | Q85227 |
| 26 | 43 | 43.9 | 290 | 17 | Q8TZK5 |
| 27 | 43 | 43.9 | 310 | 16 | Q992F6 |
| 28 | 43 | 43.9 | 310 | 16 | Q8K7B9 |
| 29 | 43 | 43.9 | 314 | 16 | Q89D85 |
| 30 | 43 | 43.9 | 369 | 16 | Q89YD1 |
| 31 | 43 | 43.9 | 369 | 16 | Q877S5 |
| 32 | 43 | 43.9 | 474 | 16 | P73837 |
| 33 | 43 | 43.9 | 476 | 16 | Q8YCK5 |
| 34 | 43 | 43.9 | 476 | 16 | Q8FVQ7 |
| 35 | 43 | 43.9 | 499 | 5 | Q9XUT8 |
| 36 | 43 | 43.9 | 1127 | 16 | Q8AB59 |
| 37 | 42.5 | 43.4 | 405 | 2 | Q93NC6 |
| 38 | 42.5 | 43.4 | 766 | 4 | P82987 |
| 39 | 42 | 42.9 | 124 | 12 | Q9PZ19 |
| 40 | 42 | 42.9 | 147 | 10 | Q7XJG8 |
| 41 | 42 | 42.9 | 151 | 10 | Q7XJG9 |
| 42 | 42 | 42.9 | 263 | 16 | Q8A0Q5 |
| 43 | 42 | 42.9 | 264 | 10 | Q84R88 |
| 44 | 42 | 42.9 | 267 | 10 | Q84RB7 |
| 45 | 42 | 42.9 | 310 | 16 | Q8P0U7 |

ALIGNMENTS

RESULT 1

Q80Z17 PRELIMINARY; PRT; 487 AA.
AC Q80Z17;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVE/N; TISSUE=Colon;
RA Strausberg R;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049143; AAH49143.1;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_3.
DR SMART; SM00409; IG_3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 53019 MW; 31F2C893900A4D80 CRC64;

Query Match 91.8%; Score 90; DB 11; Length 487;

Best Local Similarity 89.5%; Pred.No. 2.4e-06;

Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EIRKSDNYATHVAESVKG 19

Db 69 EIRLSNNYATHVAESVKG 87

RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010798; AAH0798.1; -
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG MHC; 2.
 KW Hypothetical protein_1
 FT NON_TER
 SQ SEQUENCE 480 AA; 51936 MW; 20B9234E9F2B41ED CRC64;

Query Match 52.0%; Score 51; DB 11; Length 480;
 Best Local Similarity 50.0%; Pred. No. 6.8;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 LKSDNYATHYAESVK 19
 Db 69 ISNGYATHYPSMK 84

RESULT 6
 Q9RBZ2 PRELIMINARY; PRT; 361 AA.
 AC Q9RBZ2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE IS870-like transposase.
 OS Pseudomonas syringae (pv. glycinea).
 OG Plasmid p4180A.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=318;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PG4180;
 RX MEDLINE=20015131; PubMed=10545263;
 RA Alarcon-Chaidez F.J., Penaloza-Vazquez A., Ullrich M., Bender C.L.;
 RT "Characterization of plasmids encoding the phytotoxin coronatine in
 Pseudomonas syringae";
 RL Plasmid 42:210-220(1999).
 DR EMBL; AF170066; AAD50977.1; -
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 SQ SEQUENCE 361 AA; 41448 MW; 0416AA0203BESA27 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 361;
 Best Local Similarity 52.6%; Pred. No. 11;
 Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVK 19
 Db 247 QLHLVDNYATHKPKVK 265

RESULT 7
 Q8CGQ1 PRELIMINARY; PRT; 754 AA.
 AC Q8CGQ1;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE ADAM6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Testis;

RA Choi I., Cho C.;
 RT "Cloning and characterization of ADAM6";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY158689; AAN77878.1; -
 DR PIR; PT0706; PT0706.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR006586; ADAM_cysteine.
 DR InterPro; IPR001782; Disintegrin.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001590; Peptidase M12B.
 DR InterPro; IPR002870; Peptidase_M12B_N.
 DR Pfam; PF00200; disintegrin; 1.
 DR Pfam; PF01562; pep M12B propep; 1.
 DR Pfam; PF01421; RepZolysin; 1.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SM00608; ACR; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS50215; ADAM_MEPPO; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 SQ SEQUENCE 754 AA; 85089 MW; AP97643DBF05F648 CRC64;

Query Match 48.5%; Score 47.5; DB 11; Length 754;
 Best Local Similarity 64.7%; Pred. No. 43;
 Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 3 RLKSDNYATHYAESVK 19
 Db 204 RLSSKNYATHPA-AIKG 219

RESULT 8
 Q9RBZ3 PRELIMINARY; PRT; 357 AA.
 AC Q9RBZ3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Transposase.
 OS Pseudomonas syringae (pv. glycinea).
 OG Plasmid p4180A.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=318;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20015131; PubMed=10545263;
 RA Alarcon-Chaidez F.J., Penaloza-Vazquez A., Ullrich M., Bender C.L.;
 RT "Characterization of plasmids encoding the phytotoxin coronatine in
 Pseudomonas syringae";
 RL Plasmid 42:210-220(1999).
 DR EMBL; AF169828; AAD50908.1; -
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR001584; Rve.
 DR Pfam; PF00665; rve; 1.
 KW Plasmid.
 SQ SEQUENCE 357 AA; 40339 MW; F21B4028AA5A9BD2 CRC64;

Query Match 48.0%; Score 47; DB 2; Length 357;
 Best Local Similarity 58.8%; Pred. No. 22;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 RLKSDNYATHYAESVK 18
 Db 254 IHLIMVDNYATHKNDKVK 270

RESULT 9
 Q88ZK4 PRELIMINARY; PRT; 398 AA.
 ID Q88ZK4

Q882K4;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Acetate kinase (BC 2.7.2.1).
 GN ACK2 OR LP 0310.
 OS Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 8826 / WCFS1;
 RX MEDLINE=22480296; PubMed=12566566;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 RA Hofier S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
 RA De Vos W.M., Sijzen R.J.;
 RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 DR EMBL: AL935252; CAB62963.1; -;
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0008776; F:acetate kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR GO: GO:0016310; P:phosphorylation; IEA.
 DR InterPro: IPR000890; Acetate kin.
 DR Pfam: PF00871; Acetate kinase, 1.
 DR PRINTS: PR00471; ACETATEKINASE.
 DR PROSITE: PS01075; ACETATE KINASE 1; 1.
 DR PROSITE: PS01076; ACETATE KINASE 2; 1.
 KW Kinase; Transferase; Complete proteome.
 SQ SEQUENCE 398 AA; 43848 MW; 93EE9243DD71C94A CRC64;

Query Match 48.08; Score 47; DB 16; Length 398;
 Best Local Similarity 69.28; Pred. No. 25;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAE 15
 |||||
 DB 71 RLKSDNIVTHLSE 83

RESULT 10
 Q9FND5
 ID Q9FND5 PRELIMINARY; PRT; 2910 AA.
 AC Q9FND5
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Similarity to heat shock protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=98069011; PubMed=9405937;
 RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
 RT Sequence features of the regions of 1,044,062 bp covered by thirteen
 RT physically assigned P1 clones."
 RL DNA Res. 4:291-300(1997).
 DR EMBL: AB006702; BAB11602.1; -;
 DR EMBL: AB017062; BAB11602.1; JOINED.
 DR GO: GO:0003773; F:heat shock protein activity; IEA.
 KW Heat shock.
 SQ SEQUENCE 2910 AA; 325351 MW; A847EC3FE1427DF7 CRC64;

Query Match 46.9%; Score 46; DB 10; Length 2910;
 Best Local Similarity 60.0%; Pred. No. 3.5e+02;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LKSDNYATHYAESVK 18
 |||||
 DB 297 LKSDNYATHYAESVK 311

RESULT 11
 Q8COV3
 ID Q8COV3 PRELIMINARY; PRT; 703 AA.
 AC Q8COV3
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Similar to TMDC IV protein (Fragment).
 GN 4930523C11RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL: AK029742; BAC26593.1; -;
 DR MGI: 2444636; 4930523C11RIK.
 DR GO: GO:0004222; P:metalloendopeptidase activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR005886; ADAM_cysteine.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001590; Peptidase M12B.
 DR InterPro: IPR002870; Peptidase_M12B_N.
 DR Pfam: PF00200; disintegrin; 1.
 DR Pfam: PF01562; Pep_M12B_propep; 1.
 DR Pfam: PF01421; Reprolysin; 1.
 DR ProDom: PD000664; Disintegrin; 1.
 DR SMART: SMO0608; ACR; 1.
 DR SMART: SMO0050; DISTRIN; 1.
 DR PROSITE: PS02015; ADAM MEPRO; 1.
 DR PROSITE: PS02014; DISINTEGRIN_2; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 FT NON-TER 703
 SQ SEQUENCE 703 AA; 79325 MW; 1D80313DAECF2F3E CRC64;

Query Match 46.4%; Score 45.5; DB 11; Length 703;
 Best Local Similarity 58.8%; Pred. No. 85;
 Matches 10; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 3 RLKSDNYATHYAESVK 19
 |||||
 DB 204 RLKSDNYATHYAE-AIKG 219

RESULT 12
 Q9UL71
 ID Q9UL71 PRELIMINARY; PRT; 121 AA.
 AC Q9UL71
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 28045CCFA5D50736 CRC64;

Query Match 45.9%; Score 45; DB 4; Length 121;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 LKSDNYATHYAEVKG 19
DB 51 ISGDSGSGTYADSVKG 66

RESULT 13
Q8ID86 PRELIMINARY; PRT; 300 AA.
AC Q8ID86;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN MAL13P1.309
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrall B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844509; CAD52741.1; -.
DR GO; GO:0019904; F:protein domain specific binding; IEA.
DR InterPro; IPR00308; 14-3-3.
DR Pfam; PF00244; 14-3-3; 1.
DR PRINTS; PR00305; 1433ZETA.
DR ProDom; PD000600; 14-3-3; 1.
KW Hypothetical protein.
SQ SEQUENCE 300 AA; 35090 MW; B1B678EC606D2B63 CRC64;

Query Match 45.9%; Score 45; DB 5; Length 300;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAEVKG 18
DB 181 EKSMSKSYVALHYANKMK 198

RESULT 14
Q8WR61 PRELIMINARY; PRT; 422 AA.
AC Q8WR61;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hemolisin.

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OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE FROM N.A.
RA Denlinger D.L., Lee K.-Y., Horodyski F.M., Valaitis A.P.;
RT "Molecular characterization of the insect immune protein hemolin and
RT the high induction during embryonic diapause in the gypsy moth,
RT Lymantria dispar.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF453868; AAL49765.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR Immunoglobulin domain.
KW SEQUENCE 422 AA; 47234 MW; 0DC52EC4BF142617 CRC64;

Query Match 45.9%; Score 45; DB 5; Length 422;
Best Local Similarity 53.3%; Pred. No. 58;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAE 15
DB 42 EVRFKADNYSTALLE 56

RESULT 15
Q8U651 PRELIMINARY; PRT; 450 AA.
AC Q8U651;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nitrotriacetate monooxygenase, component A.
GN ATU6084 OR AGR_PTI_161.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.P. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Gordon D.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liac L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294.2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294.2323-2328(2001).
DR EMBL; AE009427; AAL46320.1; -.

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DR EMBL; AE007935; AAK91044.1; --
DR PIR; AB3238; AB3238.
DR GO; GO:004821; C:extrachromosomal DNA; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR002103; Bac luciferase.
DR InterPro; IPR001865; Ribosomal S2.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Monooxygenase; Plasmid; Complete proteome.
SQ SEQUENCE 450 AA; 50163 MW; D3ADB8261D68C026 CRC64;
Query Match 45.9%; Score 45; DB 16; Length 450;
Best Local Similarity 58.3%; Pred. No. 62;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 7 DNYATHYAESVK 18
Db ||| |::||
57 DNYGQHFDTVK 68

Search completed: September 30, 2004, 05:59:36
Job time : 65.3192 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 92.7458 Seconds
(without alignments)
57.883 Million cell updates/sec.

Title: US-09-674-716B-11

Perfect score: 98
Sequence: 1 EIRLKSDNYATHAESVKG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_29Jan04.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|-------------|
| 1 | 98 | 100.0 | 19 | 3 AAY32258 | Light cha |
| 2 | 98 | 100.0 | 123 | 6 ABO10742 | Variable |
| 3 | 98 | 100.0 | 123 | 6 ABR44686 | Murine Mu |
| 4 | 98 | 100.0 | 137 | 3 AAY32260 | Mouse ant |
| 5 | 98 | 100.0 | 286 | 4 AAB50426 | Antibody |
| 6 | 98 | 100.0 | 444 | 3 AAY32263 | Humanised |
| 7 | 95 | 96.9 | 100 | 4 AAE06973 | Mouse ger |
| 8 | 95 | 95.9 | 299 | 4 AAB50425 | Mouse ant |
| 9 | 93 | 94.9 | 115 | 2 AAR34018 | SM3 heavy |
| 10 | 93 | 94.9 | 116 | 2 AAY03869 | Amino aci |
| 11 | 93 | 94.9 | 119 | 2 AAW43958 | Hybridoma |
| 12 | 93 | 94.9 | 119 | 7 ABR82775 | Hybridoma |
| 13 | 93 | 94.9 | 119 | 7 ABR82885 | Hybridoma |
| 14 | 93 | 94.9 | 120 | 2 AAW01589 | Lead bind |
| 15 | 93 | 94.9 | 122 | 3 AAY90812 | 2G3 hybri |
| 16 | 93 | 94.9 | 142 | 2 AAW06212 | MAB Br-3 |
| 17 | 93 | 94.9 | 142 | 2 AAW85059 | Mouse Br- |
| 18 | 93 | 94.9 | 142 | 6 AAB50893 | Mouse ant |
| 19 | 93 | 94.9 | 143 | 2 AAR09423 | Br-3 heav |
| 20 | 93 | 94.9 | 255 | 5 AAU072870 | P5-23 sin |
| 21 | 93 | 94.9 | 256 | 5 AAU072866 | P5-3 sing |
| 22 | 93 | 94.9 | 503 | 5 AAU072874 | 3B10xP5-2 |
| 23 | 93 | 94.9 | 570 | 2 AAY39451 | Antibody |
| 24 | 91 | 92.9 | 19 | 4 AAB35297 | Murine PS |
| 25 | 91 | 92.9 | 151 | 4 AAU076696 | Mouse hea |

| | | | | | |
|----|------|------|-----|------------|---------------------|
| 26 | 91 | 92.9 | 151 | 4 AAB35292 | Aab35292 Murine PS |
| 27 | 90 | 91.8 | 123 | 6 ABO10743 | Abol0743 Consensus |
| 28 | 90 | 91.8 | 123 | 6 ABR44687 | Abra44687 Murine J4 |
| 29 | 88 | 89.8 | 160 | 2 AAR70829 | Aar70829 MAB 4197X |
| 30 | 88 | 89.8 | 554 | 2 AAR70827 | Aar70827 Anti-cata |
| 31 | 85 | 86.7 | 114 | 2 AAR25410 | Aar25410 Heavy cha |
| 32 | 85 | 86.7 | 114 | 2 AAR28748 | Aar28748 Heavy cha |
| 33 | 85 | 86.7 | 114 | 3 AAY90816 | Aay90816 113F1 hyb |
| 34 | 80.5 | 82.1 | 119 | 3 AAW01588 | Aaw01588 Lead bind |
| 35 | 80 | 81.6 | 17 | 3 AAB30033 | Abol30033 Scaffold |
| 36 | 79 | 80.6 | 19 | 6 ABO10709 | Abol10709 Murine J4 |
| 37 | 79 | 80.6 | 19 | 6 ABR44653 | Abra44653 Murine J4 |
| 38 | 79 | 80.6 | 116 | 6 ABO10728 | Abol10728 Variable |
| 39 | 79 | 80.6 | 116 | 6 ABO10734 | Abol10734 Consensus |
| 40 | 79 | 80.6 | 116 | 6 ABO10726 | Abol10726 Variable |
| 41 | 79 | 80.6 | 116 | 6 ABO10733 | Abol10733 Variable |
| 42 | 79 | 80.6 | 116 | 6 ABR44672 | Abra44672 Murine J4 |
| 43 | 79 | 80.6 | 116 | 6 ABR44670 | Abra44670 Murine J4 |
| 44 | 79 | 80.6 | 116 | 6 ABR44678 | Abra44678 Murine J4 |
| 45 | 79 | 80.6 | 116 | 6 ABR44677 | Abra44677 Murine J4 |

ALIGNMENTS

RESULT 1
AAY32258
ID AAY32258 standard; peptide; 19 AA.

XX AC AAY32258;
XX AC
DT 15-FEB-2000 (first entry)
XX

DE Light chain CDR H2 of mouse anti-CD23 MAB C11.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW Hashimoto's thyroiditis; lupus erythematosus; multiple sclerosis;
KW urticaria; nephrotic syndrome; diabetes; uveitis; dermatitis; psoriasis;
KW inflammatory bowel disease; glomerulonephritis;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
KW therapy.

XX Mus musculus.

XX WO9558679-A1.

PD 18-NOV-1999.

PF 07-MAY-1999; 99WO-GE001434.

XX 09-MAY-1998; 98GB-00009839.

(GLAX) GLAXO GROUP LTD.

PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

DR N-PSDB; AA234743.

PT Cell receptor specific antibodies useful for treating e.g. arthritis,

XX diabetes, multiple sclerosis and psoriasis.

PS Claim 1; Page 40; 81pp; English.

XX This sequence represents complementarity determining region 2 (CDR H2)
CC of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11
CC (see also AAY32263). The invention provides altered antibodies, such as
CC chimeric or humanised antibodies, which comprise sufficient of the amino
CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble CD23
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
 CC are also useful for studying interactions between CD23 and various
 CC ligands and determining the binding agents

XX Sequence 19 AA;
 SQ Query Match 100.0%; Score 98; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. NO. 2.5e-09; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0;

QY 1 EIRLKSNDYATHYAESVKG 19
 |||||
 Db 1 EIRLKSNDYATHYAESVKG 19

RESULT 2
 ABO10742
 ID ABO10742 standard; protein; 123 AA.

XX AC ABO10742;

XX DT 20-AUG-2003 (first entry)

XX DE Variable region of murine antibody MuVHIIC.

XX Modified antibody; deimmunised antibody; anti-PSMA antibody;
 KW prostate specific membrane antigen; immunogenic; CDR; murine;
 KW complementarity determining region; J591; J415; J533; E99; mouse;
 KW prostatic disorder; cancerous disorder; genitourinary inflammation;
 KW prostatitis; benign enlargement; prostatic cancer; testicular cancer;
 KW solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;
 KW antiinflammatory; cytostatic; framework region; variable heavy chain;
 KW variable light chain; VH; VL; variable region.

XX OS Mus musculus.

XX PN WO200298897-A2.

XX PD 12-DEC-2002.

XX PF 30-MAY-2002; 2002WO-US017068.

XX PR 01-JUN-2001; 2001US-0295214P.

XX PR 20-SEP-2001; 2001US-0323585P.

XX PR 08-MAR-2002; 2002US-0362810P.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Bander N, Carr FU, Hamilton A;

XX DR WPI; 2003-156839/15.

XX New modified anti-prostate specific membrane antigen (PSMA)
 PT immunoglobulins, useful for treating or preventing a prostatic or
 PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or
 PT prostatic or testicular cancer.

XX PS Disclosure; Fig 7C; 254pp; English.

XX The present invention relates to modified (e.g. deimmunised) antibodies
 CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA
 CC antibodies are less immunogenic compared to the unmodified anti-PSMA
 CC antibodies. The modified antibodies comprise complementarity determining
 CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415,

CC J533 or E99), and framework sequences that are less immunogenic in humans
 CC (e.g. less antigenic than the murine frameworks in which a murine CDR
 CC naturally occurs). The modified antibodies bind with PSMA, preferably
 CC human PSMA, with high affinity and specificity. The anti-PSMA antibodies
 CC are useful for treating or preventing a prostatic or cancerous disorder,
 CC e.g. genitourinary inflammation, prostatitis, benign enlargement,
 CC prostatic cancer or testicular cancer, or solid tumours, soft tissue
 CC tumours or metastatic lesions, and its associated pain. The present
 CC sequence represents a variable region from a murine antibody

XX Sequence 123 AA;

XX Query Match 100.0%; Score 98; DB 6; Length 123;

XX Best Local Similarity 100.0%; Pred. NO. 2.3e-08;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDYATHYAESVKG 19
 |||||
 Db 50 EIRLKSNDYATHYAESVKG 68

RESULT 3

ID ABR44686

XX ABR44686 standard; protein; 123 AA.

XX AC ABR44686;

XX DT 25-JUL-2003 (first entry)

XX DE Murine MuVHIIC amino acid sequence SEQ ID NO:69.

XX Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;
 KW prostate specific membrane antigen; antipsoriatic; antiarthritic;
 KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
 KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
 KW neoplastic disorder.

XX OS Mus musculus.

XX PN WO2003024388-A2.

XX PD 27-MAR-2003.

XX PF 30-MAY-2002; 2002WO-US017204.

XX PR 20-SEP-2001; 2001US-0324100P.

XX PR 08-MAR-2002; 2002US-0362612P.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Bander N;

XX DR WPI; 2003-313319/30.

XX Ablating/killing aberrant prostate specific membrane antigen-expressing
 PT cells for treating skin disorders, by contacting the cell with an
 PT antibody that binds to the extracellular domain of prostate specific
 PT membrane antigen.

XX PS Disclosure; Page 37; 225pp; English.

XX The present invention describes a method (M1) for ablating or killing an
 CC aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g.
 CC an epidermal and a dermal cell). M1 comprises contacting the cell, or a
 CC vascular endothelial cell proximate to the cell, with an antibody (or its
 CC antigen-binding fragment), which binds specifically to the extracellular
 CC domain of PSMA in an amount sufficient to ablate or kill the cell. The
 CC antibodies have antipsoriatic, antiarthritic, dermatological, cytostatic,
 CC antiinflammatory and antiallergic activities, and can be used in
 CC vaccines. M1 is useful for treating a skin disorder in a subject, by
 CC administering to the subject, an amount of an antibody which binds
 CC specifically to the extracellular domain of PSMA (the subject is a
 CC mammal, preferably human and is having, or at risk of, a skin disorder).

CC The skin disorder is a dermal or an epidermal disorder, and is selected
 CC from psoriasis (preferably chronic stationary psoriasis, psoriasis
 CC vulgaris, eruptive (glutinate) psoriasis, psoriatic erythroderma,
 CC generalised pustular psoriasis (Von Zumbusch), annular pustular
 CC psoriasis, and localised pustular psoriasis), psoriatic arthritis,
 CC exfoliative dermatitis, pityriasis rubra pilaris, pityriasis roseacea,
 CC parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus,
 CC ichthyosiform dermatosis, keratoderms, dermatosis, and prokeratosis,
 CC preferably psoriasis. MI is useful for treating a skin disorder such as
 CC an inflammatory or neoplastic disorder of the epidermis or dermis,
 CC preferably an epidermal precancerous or cancerous lesion. MI is also
 CC useful to treat or prevent disorders involving aberrant activity of PSMA-
 CC expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837
 CC and ABR44613 to ABR44733 represent sequences used in the exemplification
 CC of the present invention

SQ Sequence 123 AA;

Query Match 100.0%; Score 98; DB 6; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2.3e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
 |||||
 DB 50 EIRLKSNDNYATHYAESVKG 68

RESULT 4

AAI32260
 ID AAY32260 standard; protein; 137 AA.

XX AC AAY322260;

XX DT 15-FEB-2000 (first entry)

DE Mouse anti-CD23 Mab C11 heavy chain variable region.

XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
 XX monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulin;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.

XX OS Mus musculus.

XX FH Key Location/Qualifiers
 FT Region 59..63 /note= "CDR H1"
 FT Region 78..96 /note= "CDR H2"
 FT Region 129..131 /note= "CDR H3"

XX PN WO9958679-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001434.

XX PR 09-MAY-1998; 98GB-00009839.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX DR WPI; 2000-053101/04.

XX DR N-PSDB; AAZ34745.

XX

PT Cell receptor specific antibodies useful for treating e.g. arthritis,
 XX diabetes, multiple sclerosis and psoriasis.

PS Claim 8; Fig 1; 81pp; English.

XX This sequence represents the heavy chain variable region (VH) of murine
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies (see
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid
 CC sequences of the C11 light and heavy chain complementarity determining
 CC regions (see AAY32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies are
 CC used to block soluble CD23 formation in human therapy, for the treatment
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents

XX SQ Sequence 137 AA;

Query Match 100.0%; Score 98; DB 3; Length 137;
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
 |||||
 DB 78 EIRLKSNDNYATHYAESVKG 96

RESULT 5

AAI50426
 ID AAB50426 standard; protein; 286 AA.

XX AC AAB50426;

XX DT 13-MAR-2001 (first entry)

XX DE Antibody 33F12 catalytic fragment.

XX Antibody 33F12; ketone compound; antitumour; cytotoxic;
 KW targeted drug delivery.

XX OS Unidentified.

XX PN WO200071556-A1.

XX PD 30-NOV-2000.

XX PF 24-MAY-2000; 2000WO-US014366.

XX PR 25-MAY-1999; 99US-00318661.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Shabat D, Rader C, List B, Lerner RA;

XX DR WPI; 2001-061339/07.

XX DR N-PSDB; AAC90472.

XX PT New ketone compounds containing active agents useful as carriers for e.g.
 FT antitumor agents, antibiotics or fluorescent molecules.

XX PS Disclosure; Fig 10; 45pp; English.

XX The present sequence may be used in the activation of new ketone prodrug
 CC compounds containing active agents. The ketone derivatives are useful as
 CC carriers for antitumor agents such as cytotoxic agents, where the
 CC antitumor agent is a microtubule stabilising agent such as paclitaxel,

CC epothilone or its therapeutically active analogue or an anthracycline
 CC antibiotic such as doxorubicin or its therapeutically active analogue.
 CC The ketone derivatives are useful for targeted drug delivery. The
 CC inactive molecules in the ketone compounds are converted to active
 CC molecules by retro-Michael reaction. The antibody has bifunctional
 CC activity and specifically immunoreacts with cell surface antigen of a
 CC target cell. The active ingredients can be mixed effectively with
 CC excipients as per desired amount along with the buffering agent to
 CC enhance the effectiveness and activity of the compound
 XX
 XX

SQ Sequence 286 AA;

Query Match 100.0%; Score 98; DB 4; Length 286;
 Best Local Similarity 100.0%; Pred. No. 6.2e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIRLKSNDYATHYAESVKG 19
 DB 203 EIRLKSNDYATHYAESVKG 221
 |||||

RESULT 6
 AAY32263
 ID AAY32263 standard; protein; 444 AA.

AC AAY32263;

XX 15-FEB-2000 (first entry)

XX Humanised anti-CD23 Mab C11 heavy chain.

XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.

XX Homo sapiens.
 OS Synthetic.

| Key | Location/Qualifiers |
|-----------|-------------------------------------|
| FT Region | 1..30 /note="framework region 1" |
| FT Region | 31..35 /note="CDR 1" |
| FT Region | 36..49 /note="framework region 2" |
| FT Region | 50..68 /note="CDR 2" |
| FT Region | 69..100 /note="framework region 3" |
| FT Region | 101..103 /note="CDR 3" |
| FT Region | 104..111 /note="framework region 4" |
| FT Region | 112..444 /note="constant region" |

XX W0958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX) GLAXO GROUP LTD.

PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

XX N-PSDB; AAZ34748.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis.

XX Claim 9; Fig 4; 81pp; English.

XX This amino acid sequence represents the heavy chain of humanised anti-
 CC CD23 (FCERII) monoclonal antibody C11, composed of a human framework
 CC (HSGKVI) and the heavy chain complementarity determining regions (see
 CC AAY32257-59) of murine antibody C11. The DNA was constructed by splice
 CC overlap PCR. The invention provides altered antibodies, such as chimeric
 CC or humanised antibodies, which comprise sufficient of the amino acid
 CC sequences of the C11 light and heavy chain complementarity determining
 CC regions to render them capable of binding to the CD23 type II molecule
 CC expressed on haematopoietic cells. The antibodies are used to block
 CC soluble CD23 formation in human therapy, for the treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,
 CC glomerulonephritis, inflammatory bowel disease, ulcerative colitis,
 CC Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX

SQ Sequence 444 AA;

Query Match 100.0%; Score 98; DB 3; Length 444;

Best Local Similarity 100.0%; Pred. No. 1e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIRLKSNDYATHYAESVKG 19

DB 50 EIRLKSNDYATHYAESVKG 68
 |||||

RESULT 7

AAE06973

ID AAE06973 standard; protein; 100 AA.

XX AAE06973;

XX 16-OCT-2001 (first entry)

XX Mouse germline heavy chain variable (VH) region, V(H)22.1.

XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
 KW inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; VH; heavy chain variable region.

XX Mus sp.

XX W0200157226-A1.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US003537.

XX 03-FEB-2000; 2000US-00497625.

XX (MILL-) MILLENNIUM PHARM INC.

PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
 DR WPI; 2001-489888/53.
 XX
 XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
 PT disorder in a patient, comprises a binding specificity for CCR2, and a
 PT non-human antigen binding region and human immunoglobulin.
 XX
 XX Disclosure; Page 152-153; 183pp; English.
 CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
 CC comprising an antigen binding region of non-human origin and at least a
 CC portion of an immunoglobulin of human origin. The humanised antibodies
 CC are useful for inhibiting the interaction of a cell expressing CCR2. They
 CC are useful for inhibiting or treating HIV infection. The proteins of the
 CC invention are useful for inhibiting leukocyte trafficking. For treating
 CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
 CC disorders such as rheumatoid arthritis and multiple sclerosis,
 CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
 CC are useful in therapy or diagnosis, and in the manufacture of a
 CC medicament for treating CCR-2 mediated disease. They are also useful for
 CC treating allergy, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and IgE-mediated allergic reaction, shock,
 CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
 CC associated with vascular intervention, including angioplasty and/or stent
 CC placement in a mammal. Humanised antibodies are also useful for
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated
 CC with vascular intervention. The present sequence is mouse germline heavy
 CC chain variable (VH) region, V(H)22.1
 XX
 XX Sequence 100 AA;
 SQ
 Query Match 96.9%; Score 95; DB 4; Length 100;
 Best Local Similarity 94.7%; Pred. No. 5.6e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRKSDNYATHYAESVKG 19
 |||||
 DB 50 QIRKSDNYATHYAESVKG 68
 |||||
 RESULT 8
 ID AAB50425 standard; protein; 299 AA.
 AC AAB50425;
 XX
 XX 13-MAR-2001 (first entry)
 DE Mouse antibody 38C2 catalytic fragment.
 KW Mouse; antibody 38C2; ketone compound; antitumour; cytotoxic;
 KW targeted drug delivery.
 XX Mus sp.
 XX WO200071556-A1.
 PN 30-NOV-2000.
 XX
 XX 24-MAY-2000; 2000WO-US014366.
 PF 25-MAY-1999; 99US-00318661.
 XX (SCRI) SCRIPPS RES INST.
 PA Barbas CF, Shabat D, Rader C, List B, Lerner RA;
 PI WPI; 2001-061339/07.
 DR N-PSDB; AAC90471.
 CC

XX New ketone compounds containing active agents useful as carriers for e.g.
 PT antitumor agents, antibiotics or fluorescent molecules.
 XX
 XX Disclosure; Fig 9; 45pp; English.
 XX
 XX The present sequence may be used in the activation of new ketone prodrug
 CC compounds containing active agents. The ketone derivatives are useful as
 CC carriers for antitumour agents such as cytotoxic agents, where the
 CC antitumour agent is a microtubule stabilising agent such as paclitaxel,
 CC epothilone or its therapeutically active analogue or an anthracycline
 CC antibiotic such as doxorubicin or its therapeutically active analogue.
 CC The ketone derivatives are useful for targeted drug delivery. The
 CC inactive molecules in the ketone compounds are converted to active
 CC molecules by retro-Michael reaction. The antibody has bifunctional
 CC activity and specifically immunoreacts with cell surface antigen of a
 CC target cell. The active ingredients can be mixed effectively with
 CC excipients as per desired amount along with the buffering agent to
 CC enhance the effectiveness and activity of the compound
 XX
 XX Sequence 299 AA;
 SQ
 Query Match 96.9%; Score 95; DB 4; Length 299;
 Best Local Similarity 94.7%; Pred. No. 2.1e-07;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRKSDNYATHYAESVKG 19
 |||||
 DB 205 EIRKSDNYATHYAESVKG 223
 |||||
 RESULT 9
 AAR34018
 ID AAR34018 standard; protein; 115 AA.
 XX
 XX AAR34018;
 AC
 XX 25-MAR-2003 (revised)
 DT 02-AUG-1993 (first entry)
 XX
 XX BW 835 VH.
 DE
 XX Monoclonal antibody; MAB; hybridoma; lung; adenocarcinoma; mammary;
 KW ovary; prostate; polymorphic epithelial mucin; PEM.
 XX Synthetic.
 OS
 XX DE4133791-A1.
 PN
 XX 15-APR-1993.
 PD
 XX 11-OCT-1991; 91DE-04133791.
 PF
 XX 11-OCT-1991; 91DE-04133791.
 PR (BEHW) BEHRINGERWERKE AG.
 PA
 XX Bosslet K, Pfeleiderer P, Seemann G;
 PI WPI; 1993-127068/16.
 DR N-PSDB; AAQ40046.
 XX
 XX New monoclonal antibody BW835 specific for tumour antigens - useful for
 PT diagnosis and treatment of tumours affecting the breasts, ovaries,
 PT prostate and lungs.
 XX
 XX Disclosure; Fig 1a; 24pp; German.
 PS
 XX Monoclonal antibody BW 835 is produced by hybridoma cell line BW 835. The
 CC antibody strongly reacts with lung adenocarcinomas and human mammary;
 CC ovary- and prostate carcinomas. It additionally reacts with polymorphic
 CC epithelial mucin (PEM) but does not react with normal human tissue.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC

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XX SQ Sequence 115 AA;
Query Match 94.9%; Score 93; DB 2; Length 115;
Best Local Similarity 94.7%; Pred. No. 1.4e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
Db 46 EIRLKSNVATHYAESVKG 64

RESULT 10
AAV03869
ID AAY03869 standard; protein; 116 AA.
XX AC AAY03869;
XX DT 16-JUN-1999 (first entry)
XX DE SM3 heavy chain variable region.
XX KW SM3 antibody; epitope; mimic; crystal; tumour; MUC1 epitope; allergy;
XX KW immune response; arthritis; multiple sclerosis; asthma; diabetes;
XX KW inflammatory disorder; transplant rejection; graft versus host disease.
XX OS Unidentified.
XX PN WO9910379-A1.
XX PD 04-MAR-1999.
XX PF 24-AUG-1998; 98WO-GB002542.
XX PR 22-AUG-1997; 97GB-00017946.
XX PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX PI Freemont PS, Snary D, Sternberg MJE, Bates PA, Dokurno P;
XX DR WPI; 1999-204650/17.
XX DR N-PSDB; AAX31971.
XX PT New SM3 antibody crystal structures - used to develop agents for treating
XX PT e.g. tumors, autoimmune disorders, allergies, inflammatory disorders or
XX PT transplant rejection.
XX PS Disclosure; Page 279-280; 316pp; English.
XX CC The invention relates to a process for preparing a crystal using cadmium.
XX CC Structure factors or structural coordinates obtained from the crystal of
XX CC SM3 antibody bound to an epitope can be used to design mimics of the
XX CC antibody or the epitope. The crystals comprise at least an epitope
XX CC binding fragment of the SM3 antibody bound to a peptide recognised by the
XX CC epitope binding site of SM3. The products and methods can be used to
XX CC develop agents for the detection of tumour cells and for therapy against
XX CC tumours. MUC1 epitope mimics can also be used to prevent or decrease an
XX CC immune response, e.g. in the therapy of diseases caused by autoimmune
XX CC responses (such as arthritis, multiple sclerosis, asthma or diabetes),
XX CC allergies, inflammatory disorders or transplant rejections such as graft
XX CC versus host disease. The present sequence represents the amino acid
XX CC sequence of a heavy chain variable region of SM3 antibody
XX OS Homo sapiens.
XX PN WO2003072036-A2.
XX PD 04-SEP-2003.
XX PF 20-FEB-2003; 2003WO-US005323.
XX PR 21-FEB-2002; 2002US-0359419P.
XX PR 21-OCT-2002; 2002US-0420472P.

QY 1 EIRLKSDNYATHYAESVKG 19
Db 50 EIRLKSNVATHYAESVKG 68

RESULT 11
AAW46958
ID AAW46958 standard; protein; 119 AA.
XX AC AAW46958;
XX DT 06-JUL-1998 (first entry)
XX DE Amino acid sequence of a synthetic branched mucin type glycolipid.
XX KW Branched mucin type glycolipid; V region; heavy chain; antibody;
XX KW cancer treatment; diagnosis.
XX OS Synthetic.
XX PN JPI0084963-A.
XX PD 07-APR-1998.
XX PF 12-SEP-1996; 96JP-00241725.
XX PR 12-SEP-1996; 96JP-00241725.
XX PA (TOYJ ) TOSOH CORP.
XX DR WPI; 1998-264850/24.
XX DR N-PSDB; AAV22331.
XX PT Recognising branched mucin type synthetic glycolipid - using gene
XX PT fragment of an antibody, useful in cancer treatment and diagnosis.
XX PS Disclosure; Page 4-5; 6pp; Japanese.
XX CC The present sequence represents a branched mucin type synthetic
XX CC glycolipid. A gene fragment encoding the V region of the heavy chain of
XX CC an antibody recognising the present protein is claimed. The antibody gene
XX CC fragment is useful for the development of cancer treatments and
XX CC diagnosing agents
XX SQ Sequence 119 AA;
Query Match 94.9%; Score 93; DB 2; Length 119;
Best Local Similarity 94.7%; Pred. No. 1.5e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
Db 50 EIRLKSNVATHYAESVKG 68

RESULT 12
ABR82775
ID ABR82775 standard; protein; 119 AA.
XX AC ABR82775;
XX DT 18-DEC-2003 (first entry)
XX DE Hybridoma HB22-23 anti-CD22 MAB heavy chain Vh-D-Jh junction sequence.
XX KW CD22; B-cell malignancy; anti-CD22 antibody; cytostatic; human; HB22-23.
XX OS Homo sapiens.
XX PN WO2003072036-A2.
XX PD 04-SEP-2003.
XX PF 20-FEB-2003; 2003WO-US005323.
XX PR 21-FEB-2002; 2002US-0359419P.
XX PR 21-OCT-2002; 2002US-0420472P.

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XX (UYDU-) UNIV DUKE
PA (REGC) UNIV CALIFORNIA.
XX
PI Tedder T, Tuscano J;
XX
DR WPI; 2003-712652/67.
DR N-PSDB; ACF36425.
XX
XX Treating a human patient diagnosed with a B-cell malignancy by
PT administering a blocking anti-CD22 monoclonal antibody binding to the
PT first two Ig-like domains of native human CD22 (hCD22).
XX
XX Claim 31; Fig 14; 72pp; English.
XX
XX The invention relates to treating a human patient diagnosed with a B-cell
CC malignancy. The method involves (a) administering to the human patient a
CC blocking anti-CD22 monoclonal antibody binding to the first two Ig-like
CC domains, or to an epitope within the first two Ig-like domains of native
CC human CD22 (hCD22) (ABR82771) and (b) monitoring the response of the
CC malignancy to the treatment. The method is useful for treating a human
CC patient diagnosed with a B-cell malignancy comprising Hodgkin's lymphoma,
CC Burkitt's lymphoma, multiple myeloma, chronic lymphocytic leukemia, hairy
CC cell leukemia or polymphocytic leukemia. The present sequence represents
CC the amino acid sequence for heavy chain Vh-D-Jh junction for anti-CD22
CC antibody from hybridoma HB22-23
XX
XX Sequence 119 AA;
CC
CC Query Match 94.9%; Score 93; DB 7; Length 119;
CC Best Local Similarity 94.7%; Pred. No. 1.5e-07;
CC Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EIRLKSNDVATHYAESVKG 19
XX |||||:|||||
XX Db 50 EIRLKSNNYATHYAESVKG 68
XX
XX RESULT 13
XX ABR82885
XX ID ABR82885 standard; protein; 119 AA.
XX AC ABR82885;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Hybridoma HB22-23 anti-CD22 MAb heavy chain (VH) fragment.
XX
XX CD22; autoimmune disease; anti-CD22 antibody; immunosuppressive;
XX cytostatic; nephrotropic; dermatological; antiinflammatory; anti-ulcer;
XX antirheumatic; antiarthritic; antipsoriatic; thyromimetic; antianemic;
XX antidiabetic; antiallergic; gene therapy; HB22-23.
XX
XX OS Homo sapiens.
XX
XX PN WO2003072736-A2.
XX
XX PD 04-SEP-2003.
XX
XX PF 21-FEB-2003; 2003WO-US005549.
XX
XX PR 21-FEB-2002; 2002US-0359419P.
XX PR 21-OCT-2002; 2002US-0420472P.
XX
XX PA (UYDU-) UNIV DUKE.
XX
XX PI Tedder TF;
XX
XX DR WPI; 2003-721765/68.
XX DR N-PSDB; ACF36493.
XX
XX PT Treating an autoimmune disease or a B-cell malignancy in a human patient
PT comprises administering an amount of an anti-CD22 monoclonal antibody to

PT the patient and monitoring the response of the disease to the treatment.
XX
XX Claim 1; Fig 14; 59pp; English.
XX
XX The invention relates to treating a human patient diagnosed with an
CC autoimmune disease. The method involves administering to the patient an
CC amount of a blocking anti-CD22 monoclonal antibody and monitoring the
CC response of the autoimmune disease to the treatment. The method is useful
CC in treating autoimmune diseases (e.g. glomerulonephritis, systemic lupus
CC erythematosus, rheumatoid arthritis, psoriasis, ulcerative colitis,
CC Hashimoto's thyroiditis, autoimmune haemolytic anemias, diabetes or
CC allergies) or B-cell malignancies (e.g. lymphomas or leukemias). The
CC present sequence represents the amino acid sequence for heavy chain Vh-D-
CC Jh junction for anti-CD22 antibody from hybridoma HB22-23
XX
XX SQ Sequence 119 AA;
CC
CC Query Match 94.9%; Score 93; DB 7; Length 119;
CC Best Local Similarity 94.7%; Pred. No. 1.5e-07;
CC Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EIRLKSNDVATHYAESVKG 19
XX |||||:|||||
XX Db 50 EIRLKSNNYATHYAESVKG 68
XX
XX RESULT 14
XX AAW01589
XX ID AAW01589 standard; protein; 120 AA.
XX AC AAW01589;
XX
XX DT 22-AUG-1997 (first entry)
XX
XX DE Lead binding MAb 4E8 heavy chain variable region.
XX
XX KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
XX pharmaceutical; health care; skin treatment; pesticide; herbicide;
XX heavy metal.
XX
XX OS Mus musculus.
XX
XX PN WO9639518-A1.
XX
XX PD 12-DEC-1996.
XX
XX PF 05-JUN-1996; 96WO-US009258.
XX
XX PR 05-JUN-1995; 95US-00462798.
XX PR 10-OCT-1995; 95US-00541373.
XX
XX PA (BION-) BIONEERASKA INC.
XX
XX PI Wylie DE, Lopez O, Murray PJ;
XX
XX DR WPI; 1997-043140/04.
XX DR N-PSDB; AAT58263.
XX
XX PT DNA encoding heavy metal binding polypeptide sequences - used for
XX detecting, removing, adding or neutralising heavy metals, such as lead
XX cations.
XX
XX PS Claim 12; Page 81; 125pp; English.
XX
XX CC The present sequence represents the heavy chain variable region for
XX monoclonal antibody (MAb) 4E8, which immunoreacts with a lead cation. The
XX sequence was derived from RNA isolated from mouse hybridoma cells. The
XX protein can be used for binding heavy metals, such as lead cations. It
XX can be used for detecting, removing, adding or neutralising the heavy
XX metals in biological and inanimate systems. It can be used in e.g.
XX aqueous liquid systems, in biological or environmental systems or in such
XX compositions as perfumes, cosmetics, pharmaceuticals, health care
XX products, skin treatment products, pesticides, herbicides, solvents used

CC in the production of semi-conductor and integrated circuit components and
CC production materials for electronic components. The products can provide
CC for applications involving minute amounts of specific heavy metals
XX
SQ Sequence 120 AA;

Query Match 94.9%; Score 93; DB 2; Length 120;
Best Local Similarity 94.7%; Pred. No. 1.5e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNNYATHYAESVKG 19
DB 50 EIRLKSNNYATHYAESVKG 68

RESULT 15

AAAY0812
ID AAY0812 standard; protein; 122 AA.

XX AC AAY0812;

XX DT 29-AUG-2000 (first entry)

XX DE 2G3 hybridoma VH domain SEQ ID NO:2.

XX KW Antigen binding site; immunoglobulin; cancer antigen; immunological;
KW antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;
KW specific binding assay; affinity purification; drug targeting;
KW toxin targeting; imaging; genetic; therapeutic.

XX OS Homo sapiens.

XX PN US6054561-A.

XX PD 25-APR-2000.

XX PE 07-JUN-1995; 95US-00483749.

XX PR 08-FEB-1984; 84US-00577976.

XX PR 11-JAN-1985; 85US-00690750.

XX PR 21-MAR-1986; 86US-00842476.

XX PR 08-MAY-1988; 88US-00190778.

XX PR 11-AUG-1994; 94US-00288981.

XX PA (CHIR) CHIRON CORP.

XX PI Ring DB;

XX DR WPI; 2000-338508/29.

XX DR N-PSDB; AAA38896.

XX PT Monoclonal antibody capable of binding to human breast cancer antigen
PT useful for affinity purification, drug or toxin targeting, imaging, and
PT treating cancer.

XX PS Disclosure; Fig 1; 57pp; English.

XX CC The present invention describes a monoclonal antibody (Mab) (I) that
CC binds to a human breast cancer antigen that is also bound by Mab 454C11
CC and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also
CC described is a hybridoma that produces (I). (I) is useful in specific
CC binding assays, affinity purification, drug or toxin targeting, imaging,
CC and genetic or immunological therapeutics for various cancers. The
CC present sequence represents a VH domain derived from a 2G3 hybridoma,
CC which is used in the exemplification of the present invention

XX SQ Sequence 122 AA;

Query Match 94.9%; Score 93; DB 3; Length 122;
Best Local Similarity 94.7%; Pred. No. 1.5e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNNYATHYAESVKG 19

Db 50 EIRLKSNNYATHYAESVKG 68
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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:01:30 ; Search time 318.814 Seconds
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Title: US-09-674-716B-11

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Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 1351062

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Listing first 45 summaries

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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 98 | 100.0 | 123 | 14 | US-10-160-506-69 |
| 2 | 98 | 100.0 | 123 | 16 | US-10-449-379-69 |
| 3 | 98 | 100.0 | 123 | 15 | US-10-688-015-69 |
| 4 | 98 | 100.0 | 285 | 9 | US-09-883-758-4 |
| 5 | 95 | 96.9 | 100 | 9 | US-09-840-459-36 |
| 6 | 95 | 96.9 | 100 | 16 | US-10-766-773-36 |
| 7 | 95 | 96.9 | 100 | 16 | US-10-766-610-36 |
| 8 | 95 | 96.9 | 100 | 16 | US-10-733-563-36 |
| 9 | 95 | 96.9 | 298 | 9 | US-09-883-758-2 |
| 10 | 93 | 94.9 | 119 | 12 | US-10-372-481-15 |
| 11 | 93 | 94.9 | 119 | 15 | US-10-371-797-15 |
| 12 | 93 | 94.9 | 255 | 12 | US-10-239-656-69 |
| 13 | 93 | 94.9 | 256 | 12 | US-10-239-656-61 |
| 14 | 93 | 94.9 | 503 | 12 | US-10-239-656-77 |
| 15 | 91 | 92.9 | 151 | 9 | US-09-564-329A-15 |

| | | | | | | |
|----|----|------|-----|----|------------------|-------------------|
| 16 | 91 | 92.9 | 151 | 9 | US-09-855-153-15 | Sequence 15, Appl |
| 17 | 91 | 92.9 | 151 | 9 | US-09-854-811-15 | Sequence 15, Appl |
| 18 | 91 | 92.9 | 151 | 9 | US-09-934-773-15 | Sequence 15, Appl |
| 19 | 91 | 92.9 | 151 | 9 | US-09-963-620-15 | Sequence 15, Appl |
| 20 | 91 | 92.9 | 151 | 10 | US-09-855-632-15 | Sequence 15, Appl |
| 21 | 91 | 92.9 | 151 | 14 | US-10-225-784-15 | Sequence 15, Appl |
| 22 | 91 | 92.9 | 151 | 14 | US-10-224-720-15 | Sequence 15, Appl |
| 23 | 91 | 92.9 | 151 | 14 | US-10-225-779-15 | Sequence 15, Appl |
| 24 | 91 | 92.9 | 151 | 15 | US-10-374-381-15 | Sequence 15, Appl |
| 25 | 91 | 92.9 | 151 | 15 | US-10-446-542-15 | Sequence 15, Appl |
| 26 | 90 | 91.8 | 123 | 14 | US-10-160-506-70 | Sequence 70, Appl |
| 27 | 90 | 91.8 | 123 | 16 | US-10-449-379-70 | Sequence 70, Appl |
| 28 | 90 | 91.8 | 123 | 16 | US-10-688-015-70 | Sequence 70, Appl |
| 29 | 85 | 86.7 | 114 | 14 | US-10-422-049-11 | Sequence 11, Appl |
| 30 | 85 | 86.7 | 114 | 14 | US-10-422-049-12 | Sequence 12, Appl |
| 31 | 82 | 83.7 | 117 | 14 | US-10-277-471A-7 | Sequence 7, Appl |
| 32 | 82 | 83.7 | 262 | 14 | US-10-160-506-30 | Sequence 30, Appl |
| 33 | 79 | 80.6 | 19 | 14 | US-10-160-506-30 | Sequence 30, Appl |
| 34 | 79 | 80.6 | 19 | 16 | US-10-449-379-30 | Sequence 30, Appl |
| 35 | 79 | 80.6 | 19 | 16 | US-10-688-015-30 | Sequence 30, Appl |
| 36 | 79 | 80.6 | 116 | 14 | US-10-160-506-47 | Sequence 47, Appl |
| 37 | 79 | 80.6 | 116 | 14 | US-10-160-506-49 | Sequence 49, Appl |
| 38 | 79 | 80.6 | 116 | 14 | US-10-160-506-60 | Sequence 60, Appl |
| 39 | 79 | 80.6 | 116 | 14 | US-10-160-506-61 | Sequence 61, Appl |
| 40 | 79 | 80.6 | 116 | 16 | US-10-449-379-47 | Sequence 47, Appl |
| 41 | 79 | 80.6 | 116 | 16 | US-10-449-379-49 | Sequence 49, Appl |
| 42 | 79 | 80.6 | 116 | 16 | US-10-449-379-60 | Sequence 60, Appl |
| 43 | 79 | 80.6 | 116 | 16 | US-10-449-379-61 | Sequence 61, Appl |
| 44 | 79 | 80.6 | 116 | 16 | US-10-688-015-47 | Sequence 47, Appl |
| 45 | 79 | 80.6 | 116 | 16 | US-10-688-015-49 | Sequence 49, Appl |

ALIGNMENTS

RESULT 1
US-10-160-506-69
; Sequence 69, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR PROSTATE SPECIFIC MEMBRANE ANTIGEN
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
; FILE REFERENCE: 10448-162001
; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-160-506-69

Query Match 100.0%; Score 98; DB 14; Length 123;
Best Local Similarity 100.0%; Pred No. 9,3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLKSDNYATHAESVKG 19
|||||
Db 50 EIRLKSDNYATHAESVKG 68

RESULT 2
US-10-449-379-69
; Sequence 69, Application US/10449379
; Publication No. US20040120958A1
; GENERAL INFORMATION:

; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 10448-163002
; CURRENT APPLICATION NUMBER: US/10/449,379
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 10/160,505
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/323,585
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,810
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/295,214
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-449-379-69

Query Match 100.0%; Score 98; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 9.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLXSDNYATHYAESVKG 19
Db 50 EIRLXSDNYATHYAESVKG 69

RESULT 3
US-10-688-015-69
; Sequence 69, Application US/10688015
; Publication No. US20040136998A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; FILE REFERENCE: 10448-196001
; CURRENT APPLICATION NUMBER: US/10/688,015
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/422,396
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-688-015-69

Query Match 100.0%; Score 98; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 9.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLXSDNYATHYAESVKG 19
Db 50 EIRLXSDNYATHYAESVKG 69

RESULT 4
US-09-893-758-4
; Sequence 4, Application US/09893758
; Patent No. US20020058804A1
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Leiner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES

; FILE REFERENCE: PLF0011S
; CURRENT APPLICATION NUMBER: US/09/893,758
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 10448-163002
; CURRENT APPLICATION NUMBER: US/10/449,379
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 10/160,505
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/323,585
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,810
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/295,214
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-449-379-69

Query Match 100.0%; Score 98; DB 9; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLXSDNYATHYAESVKG 19
Db 203 EIRLXSDNYATHYAESVKG 221

RESULT 5
US-09-840-459-36
; Sequence 36, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-36

Query Match 96.9%; Score 95; DB 9; Length 100;
Best Local Similarity 94.7%; Pred. No. 2.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLXSDNYATHYAESVKG 19
Db 50 EIRLXSDNYATHYAESVKG 68

RESULT 6
US-10-766-773-36
; Sequence 36, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher

APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-028
CURRENT APPLICATION NUMBER: US/10/766,773
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-10-766-773-36

Query Match 96.9%; Score 95; DB 16; Length 100;
Best Local Similarity 94.7%; Pred. No. 2.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
:|||||
Db 50 QIRLKSDNYATHYAESVKG 68

RESULT 7
US-10-766-610-36
Sequence 36, Application US/10766610
Publication No. US20040132980A1
GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-029
CURRENT APPLICATION NUMBER: US/10/766,610
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: 09/840,459
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-10-766-610-36

Query Match 96.9%; Score 95; DB 16; Length 100;
Best Local Similarity 94.7%; Pred. No. 2.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
:|||||
Db 50 QIRLKSDNYATHYAESVKG 68

RESULT 8
US-10-733-563-36
Sequence 36, Application US/10733563
Publication No. US20040151721A1
GENERAL INFORMATION:
APPLICANT: O'Keefe, Theresa
APPLICANT: Ponath, Paul
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 10448-213001
CURRENT APPLICATION NUMBER: US/10/733,563
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US 10/272,899
PRIOR FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 60/392,364
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/350,166
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-10-733-563-36

Query Match 96.9%; Score 95; DB 16; Length 100;
Best Local Similarity 94.7%; Pred. No. 2.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
:|||||
Db 50 QIRLKSDNYATHYAESVKG 68

RESULT 9
US-09-883-758-2
Sequence 2, Application US/09883758
Patent No. US20020058804A1
GENERAL INFORMATION:
APPLICANT: Barbas III, Carlos F.
APPLICANT: Shabat, Doron
APPLICANT: Rader, Christoph
APPLICANT: List, Benjamin
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
FILE REFERENCE: PLF00115
CURRENT APPLICATION NUMBER: US/09/883,758
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US/09/318,661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 298
TYPE: PRT
ORGANISM: Mus musculus
US-09-883-758-2

Query Match 96.9%; Score 95; DB 9; Length 298;
Best Local Similarity 94.7%; Pred. No. 7.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
:|||||
Db 205 EIRLKSDNYATHYAESVKG 223

RESULT 10
US-10-372-481-15
Sequence 15, Application US/10372481

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; Publication No. US20030202975A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 5405.306
; CURRENT APPLICATION NUMBER: US/10/372,481
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05549
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-481-15

Query Match          94.9%; Score 93; DB 12; Length 119;
Best Local Similarity 94.7%; Pred. No. 5.6e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19
    |||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 11
US-10-371-797-15
; Sequence 15, Application US/10371797
; Publication No. US20040001828A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TUSCANO, Joseph
; APPLICANT: TEDDER, Thomas
; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 39754-0951
; CURRENT APPLICATION NUMBER: US/10/371,797
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 119
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-371-797-15

Query Match          94.9%; Score 93; DB 15; Length 119;
Best Local Similarity 94.7%; Pred. No. 5.6e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19
    |||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 12
US-10-239-656-69
; Sequence 69, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-2 single
; OTHER INFORMATION: chain Fv
US-10-239-656-61

Query Match          94.9%; Score 93; DB 12; Length 256;
Best Local Similarity 94.7%; Pred. No. 1.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19
    |||||:|||||
Db 51 EIRLKSNNYATHYAESVKG 69

RESULT 13
US-10-239-656-61
; Sequence 61, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-2 single
; OTHER INFORMATION: chain Fv
US-10-239-656-61

Query Match          94.9%; Score 93; DB 12; Length 256;
Best Local Similarity 94.7%; Pred. No. 1.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19
    |||||:|||||
Db 51 EIRLKSNNYATHYAESVKG 69

US-10-239-656-69
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-11 single
; OTHER INFORMATION: chain Fv
US-10-239-656-69

Query Match          94.9%; Score 93; DB 12; Length 255;
Best Local Similarity 94.7%; Pred. No. 1.3e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19
    |||||:|||||
Db 51 EIRLKSNNYATHYAESVKG 69
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RESULT 14
US-10-239-656-77
; Sequence 77, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFWEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; TITLE OF INVENTION: TO AN EPIOTOPE OF THE NKG2D RECEPTOR COMPLEX
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 3B10XP5-
; OTHER INFORMATION: 2 Dispecific single chain Fv
US-10-239-656-77

Query Match 94.9%; Score 93; DB 12; Length 503;
Best Local Similarity 94.7%; Pred. No. 2.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
|||:|||||
DB 298 EIRLKSDNYATHYAESVKG 316

RESULT 15
US-09-564-329A-15
; Sequence 15, Application US/09564329A
; Patent No. US20010055751A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-15
Query Match 92.9%; Score 91; DB 9; Length 151;
Best Local Similarity 89.5%; Pred. No. 1.5e-06;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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|||:|||||
DB 69 EIRLKSDNYATHYAESVKG 87
Search completed: September 30, 2004, 06:54:53
Job time : 319.814 secs

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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:00:45 ; Search time 32.2034 Seconds
(without alignments)
30.459 Million cell updates/sec

Title: US-09-674-716B-11
Perfect score: 98
Sequence: 1 EIRKSDNVATHYAESVKG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 98 | 100.0 | 285 | 3 | US-09-318-661-4 |
| 2 | 98 | 100.0 | 285 | 4 | US-09-883-758-4 |
| 3 | 95 | 96.9 | 298 | 3 | US-09-318-661-2 |
| 4 | 95 | 96.9 | 298 | 4 | US-09-883-758-2 |
| 5 | 93 | 94.9 | 115 | 1 | US-08-468-661-1 |
| 6 | 93 | 94.9 | 115 | 1 | US-08-468-272A-1 |
| 7 | 93 | 94.9 | 115 | 1 | US-08-478-857-1 |
| 8 | 93 | 94.9 | 115 | 2 | US-08-471-771-1 |
| 9 | 93 | 94.9 | 115 | 3 | US-09-130-783-1 |
| 10 | 93 | 94.9 | 120 | 3 | US-08-767-128-28 |
| 11 | 93 | 94.9 | 122 | 3 | US-08-483-749A-2 |
| 12 | 91 | 92.9 | 151 | 4 | US-09-564-329A-15 |
| 13 | 85 | 86.7 | 114 | 3 | US-08-483-749A-10 |
| 14 | 80.5 | 82.1 | 119 | 3 | US-08-767-128-26 |
| 15 | 74 | 75.5 | 119 | 1 | US-08-192-102-5 |
| 16 | 74 | 75.5 | 119 | 2 | US-08-324-799-5 |
| 17 | 74 | 75.5 | 119 | 1 | US-08-192-861A-5 |
| 18 | 74 | 75.5 | 119 | 3 | US-09-133-119-5 |
| 19 | 74 | 75.5 | 119 | 3 | US-08-192-093A-5 |
| 20 | 72 | 73.5 | 119 | 1 | US-08-442-542-45 |
| 21 | 72 | 73.5 | 119 | 3 | US-08-765-469-45 |
| 22 | 71 | 72.4 | 227 | 1 | US-08-681-432-2 |
| 23 | 68 | 69.4 | 19 | 3 | US-08-737-085A-4 |
| 24 | 68 | 69.4 | 19 | 3 | US-09-246-258-4 |
| 25 | 68 | 69.4 | 19 | 3 | US-09-532-106-4 |
| 26 | 68 | 69.4 | 19 | 4 | US-09-839-666-4 |
| 27 | 68 | 69.4 | 27 | 2 | US-08-737-085A-21 |

28 68 69.4 27 3 US-09-246-258-21 Sequence 21, Appl
29 68 69.4 27 3 US-09-532-106-21 Sequence 21, Appl
30 68 69.4 27 4 US-09-839-666-21 Sequence 21, Appl
31 67 68.4 110 3 US-08-767-128-24 Sequence 24, Appl
32 67 68.4 115 3 US-08-767-128-36 Sequence 36, Appl
33 66 67.3 19 1 US-07-977-696C-78 Sequence 78, Appl
34 66 67.3 19 1 US-08-129-930B-78 Sequence 78, Appl
35 66 67.3 19 4 US-08-978-288A-78 Sequence 13, Appl
36 66 67.3 134 1 US-07-977-696C-13 Sequence 13, Appl
37 66 67.3 134 1 US-08-129-930B-13 Sequence 13, Appl
38 66 67.3 134 4 US-08-976-288A-13 Sequence 12, Appl
39 65 66.3 117 4 US-09-809-739-12 Sequence 20, Appl
40 65 66.3 117 4 US-09-809-739-20 Sequence 21, Appl
41 65 66.3 117 4 US-09-809-739-21 Sequence 22, Appl
42 65 66.3 117 4 US-09-809-739-22 Sequence 23, Appl
43 65 66.3 117 4 US-09-809-739-23 Sequence 23, Appl
44 64 65.3 119 1 US-08-442-542-14 Sequence 14, Appl
45 64 65.3 119 3 US-08-765-469-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-318-661-4
; Sequence 4, Application US/09318661
; Patent No. 6286488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment
US-09-318-661-4
Query Match 100.0%; Score 98; DB 3; Length 285;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNVATHYAESVKG 19
Db 203 EIRKSDNVATHYAESVKG 221
RESULT 2
US-09-883-758-4
; Sequence 4, Application US/09883758
; Patent No. 6677435
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 285

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

OTHER INFORMATION: residue sequence of catalytic fragment

US-09-883-758-4

Query Match 100.0%; Score 98; DB 4; Length 285;

Best Local Similarity 100.0%; Pred. No. 3.7e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHAESVKG 19

Db 203 EIRKSDNYATHAESVKG 221

RESULT 3

US-09-318-661-2

Sequence 2, Application US/09318661

Patent No. 6268488

GENERAL INFORMATION:

APPLICANT: Barbas III, Carlos F.

APPLICANT: Shabat, Doron

APPLICANT: Rader, Christoph

APPLICANT: List, Benjamin

APPLICANT: Lerner, Richard A.

TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES

FILE REFERENCE: PLF00115

CURRENT APPLICATION NUMBER: US/09/318,661

CURRENT FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 298

TYPE: PRT

ORGANISM: Mus musculus

US-09-318-661-2

Query Match

Best Local Similarity 96.9%; Score 95; DB 3; Length 298;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHAESVKG 19

Db 205 EIRKSDNYATHAESVKG 223

RESULT 4

US-09-883-758-2

Sequence 2, Application US/09883758

Patent No. 6677435

GENERAL INFORMATION:

APPLICANT: Barbas III, Carlos F.

APPLICANT: Shabat, Doron

APPLICANT: Rader, Christoph

APPLICANT: List, Benjamin

APPLICANT: Lerner, Richard A.

TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES

FILE REFERENCE: PLF00115

CURRENT APPLICATION NUMBER: US/09/883,758

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: US/09/318,661

PRIOR FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 298

TYPE: PRT

ORGANISM: Mus musculus

US-09-883-758-2

Query Match

Best Local Similarity 96.9%; Score 95; DB 4; Length 298;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHAESVKG 19

Db 205 EIRKSDNYATHAESVKG 223

RESULT 5

US-08-468-661-1

Sequence 1, Application US/08468661

Patent No. 5639621

GENERAL INFORMATION:

APPLICANT: Boslet, Klaus

APPLICANT: Pfeleiderer, Peter

APPLICANT: Seeman, Gerhard

TITLE OF INVENTION: Monoclonal Antibodies Against

TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the

TITLE OF INVENTION: Preparation Thereof and the Use Thereof

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,661

FILING DATE: 06-JUNE-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/957,827

FILING DATE: 08-OCT-1992

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Forman, David S.

REGISTRATION NUMBER: 35,694

REFERENCE/DOCKET NUMBER: 05552-1227-02000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 115 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-468-661-1

Query Match

Best Local Similarity 94.9%; Score 93; DB 1; Length 115;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHAESVKG 19

Db 46 EIRKSDNYATHAESVKG 64

RESULT 6

US-08-466-272A-1

Sequence 1, Application US/08466272A

Patent No. 5674994

GENERAL INFORMATION:

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/ APPLICANT: Bosslet, Klaus
/ APPLICANT: Pfeleiderer, Peter
/ APPLICANT: Seeman, Gerhard
/ TITLE OF INVENTION: Monoclonal Antibodies Against
/ TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the Preparation
/ TITLE OF INVENTION: Thereof and the Use Thereof
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESS: Dunner
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/466,272A
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/957,827
/ FILING DATE: 08-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 02481-1227-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 115 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: Peptide
/ US-08-466-272A-1

Query Match 94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 8.7e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAEVKG 19
| | | | | : | | | | |
Db 46 EIRKSNNYATHYAEVKG 64

RESULT 7
US-08-478-857-1
/ Sequence 1, Application US/08478857
/ Patent No. 5695758
/ GENERAL INFORMATION:
/ APPLICANT: Bosslet, Klaus
/ APPLICANT: Pfeleiderer, Peter
/ APPLICANT: Seeman, Gerhard
/ TITLE OF INVENTION: Monoclonal Antibodies Against
/ TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the Preparation
/ TITLE OF INVENTION: Thereof and the Use Thereof
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESS: Dunner
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM: disk
/ MEDIUM TYPE: Floppy disk
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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/478,857
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/957,827
/ FILING DATE: 08-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 02481-1227-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 115 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-478-857-1

Query Match 94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 8.7e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAEVKG 19
| | | | | : | | | | |
Db 46 EIRKSNNYATHYAEVKG 64

RESULT 8
US-08-471-771-1
/ Sequence 1, Application US/08471771
/ Patent No. 5837824
/ GENERAL INFORMATION:
/ APPLICANT: Bosslet, Klaus
/ APPLICANT: Pfeleiderer, Peter
/ APPLICANT: Seeman, Gerhard
/ TITLE OF INVENTION: Monoclonal Antibodies Against
/ TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
/ TITLE OF INVENTION: Preparation Thereof and the Use Thereof
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESS: Dunner
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/471,771
/ FILING DATE: 06-JUNE-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/957,827
/ FILING DATE: 08-OCT-1992
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Forman, David S.
/ REGISTRATION NUMBER: 33,694
/ REFERENCE/DOCKET NUMBER: 05552-1227-01000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
```

TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 115 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-471-771-1

Query Match 94.9%; Score 93; DB 2; Length 115;
 Best Local Similarity 94.7%; Pred. No. 8.7e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
 |||||:|||||
 Db 46 EIRLKSNNYATHYAESVKG 64

RESULT 9

US-09-130-783-1
 Sequence 1, Application US/09130783
 Patent No. 6030797

GENERAL INFORMATION:
 APPLICANT: Bosslet, Klaus
 APPLICANT: Pfeleider, Peter
 APPLICANT: Seeman, Gerhard
 TITLE OF INVENTION: Monoclonal Antibodies Against
 Tumor-Associated Antigens, Processes for the
 TITLE OF INVENTION: Preparation Thereof and the Use Thereof
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ADDRESSEE: Dunner
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/130,783
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/471,771
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Forman, David S.
 REGISTRATION NUMBER: 33,694
 REFERENCE/DOCKET NUMBER: 05552-1227-01000
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 115 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-130-783-1

Query Match 94.9%; Score 93; DB 3; Length 115;
 Best Local Similarity 94.7%; Pred. No. 8.7e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
 |||||:|||||
 Db 46 EIRLKSNNYATHYAESVKG 64

RESULT 10
 US-08-767-128-28
 Sequence 28, Application US/08767128
 Patent No. 611079
 GENERAL INFORMATION:
 APPLICANT: WYLIE, DWANE E.
 APPLICANT: LOPEZ, OSVALDO
 APPLICANT: MURRAY, PETER JOSEPH
 APPLICANT: GOEBEL, PETER
 TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
 TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
 STREET: 3100 No. 611079west Center, 90 South Seventh St
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/767,128
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE: 04-DEC-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/09258
 FILING DATE: 05-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/541,373
 FILING DATE: 10-OCT-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/462,798
 FILING DATE: 05-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Carter, Charles G.
 REGISTRATION NUMBER: 35,093
 REFERENCE/DOCKET NUMBER: 8648.49USF1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612/371-5278
 TELEFAX: 612/332-9081
 TELEX:
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 US-08-767-128-28

Query Match 94.9%; Score 93; DB 3; Length 120;
 Best Local Similarity 94.7%; Pred. No. 9.1e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
 |||||:|||||
 Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 11
US-08-483-749A-2
; Sequence 2, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-749A-2
Query Match 94.9%; Score 93; DB 3; Length 122;
Best Local Similarity 94.7%; Pred. No. 9.2e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKSNDNYATHYAESVKG 19
Db 50 EIRLKSNNYATHYAESVKG 68
RESULT 12
US-09-564-329A-15
; Sequence 15, Application US/09564329A
; Patent No. 6541212
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-15
Query Match 92.9%; Score 91; DB 4; Length 151;
Best Local Similarity 89.5%; Pred. No. 2.5e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKSNDNYATHYAESVKG 19
Db 69 EIRLRSNVATHYAESVKG 87
RESULT 13
US-08-483-749A-10
; Sequence 10, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-749A-10
Query Match 86.7%; Score 85; DB 3; Length 114;
Best Local Similarity 84.2%; Pred. No. 1.7e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIRLKSNDNYATHYAESVKG 19
Db 114 EIRLKSNDNYATHYAESVKG 114

Db 50 EIKLKNYPHYAESVKG 68

RESULT 14

US-08-767-128-26
; Sequence 26, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 611079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-3081
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-26

Query Match 82.1%; Score 80.5; DB 3; Length 119;
Best Local Similarity 89.5%; Pred. No. 9.4e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Db 50 EIKLKNYPHYAESVKG 68

RESULT 15

US-08-192-102-5
; Sequence 5, Application US/08192102
; Patent No. 5656272
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter E.
; APPLICANT: Chrayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott A.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND ASSAYS EMPLOYING
; NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,102
; FILING DATE: 04-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,093
; FILING DATE: 04-FEB-1994
; APPLICATION NUMBER: US/08/013,413
; FILING DATE: 02-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/010,406
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/943,852
; FILING DATE: 11-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/853,606
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/670,827
; FILING DATE: 18-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: NYU93-01M3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-192-102-5

Query Match 75.5%; Score 74; DB 1; Length 119;
Best Local Similarity 84.2%; Pred. No. 0.00011;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 50 EIKLKNYPHYAESVKG 68

us-09-674-716b-11.open.ra1

Thu Sep 30 13:18:30 2004

Job time : 34.2034 secs

Blank sheet

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 3.25424 Seconds
(without alignments)
88.677 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 28366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 16 | 100.0 | 18 | 2 S43834 | DNA topoisomerase |
| 2 | 16 | 100.0 | 21 | 2 D48518 | PEB1 5'-region hyp |
| 3 | 16 | 100.0 | 23 | 1 S20453 | pyrroloquinoline q |
| 4 | 16 | 100.0 | 25 | 2 F84056 | hypothetical prote |
| 5 | 16 | 100.0 | 30 | 2 A26188 | lipocortin I - pig |
| 6 | 16 | 100.0 | 30 | 2 A46892 | nitrobenzene nitro |
| 7 | 16 | 100.0 | 31 | 2 H82818 | hypothetical prote |
| 8 | 16 | 100.0 | 32 | 2 PQ0413 | nonstructural prot |
| 9 | 16 | 100.0 | 33 | 2 PQ0416 | RNA-directed RNA p |
| 10 | 16 | 100.0 | 33 | 2 A95119 | hypothetical prote |
| 11 | 16 | 100.0 | 33 | 2 H32096 | hypothetical prote |
| 12 | 16 | 100.0 | 33 | 2 S33646 | hypothetical prote |
| 13 | 16 | 100.0 | 35 | 2 PS0363 | protein-tyrosine-p |
| 14 | 16 | 100.0 | 35 | 2 P80364 | protein-tyrosine-p |
| 15 | 16 | 100.0 | 36 | 2 D87544 | hypothetical prote |
| 16 | 16 | 100.0 | 37 | 2 C70186 | hypothetical prote |
| 17 | 16 | 100.0 | 37 | 2 G95919 | probable transposa |
| 18 | 16 | 100.0 | 38 | 2 S33402 | Ig heavy chain v r |
| 19 | 16 | 100.0 | 38 | 2 B39803 | proline-rich phosph |
| 20 | 16 | 100.0 | 39 | 2 D82085 | hypothetical prote |
| 21 | 16 | 100.0 | 39 | 2 A96026 | probable transposa |
| 22 | 16 | 100.0 | 40 | 2 A23098 | larvicidal toxin - |
| 23 | 16 | 100.0 | 43 | 1 ZBPT9 | gene 55.4 protein |
| 24 | 16 | 100.0 | 43 | 2 B37505 | hypothetical prote |
| 25 | 16 | 100.0 | 45 | 2 C34669 | calmodulin-related |
| 26 | 16 | 100.0 | 45 | 2 H83816 | hypothetical prote |
| 27 | 16 | 100.0 | 46 | 2 B82461 | hypothetical prote |
| 28 | 16 | 100.0 | 47 | 2 PC4133 | hypothetical 47 pr |
| 29 | 16 | 100.0 | 48 | 2 C95060 | hypothetical prote |

| | | | | | |
|----|----|-------|----|----------|--------------------|
| 30 | 16 | 100.0 | 48 | 2 T07316 | hypothetical prote |
| 31 | 16 | 100.0 | 50 | 2 AB0367 | hypothetical prote |
| 32 | 16 | 100.0 | 51 | 2 S00576 | hypothetical prote |
| 33 | 16 | 100.0 | 52 | 2 A71002 | hypothetical prote |
| 34 | 16 | 100.0 | 52 | 2 PNO481 | cell division cycl |
| 35 | 16 | 100.0 | 52 | 2 S15922 | hypothetical prote |
| 36 | 16 | 100.0 | 52 | 2 C82621 | hypothetical prote |
| 37 | 16 | 100.0 | 52 | 2 AF0293 | hypothetical prote |
| 38 | 16 | 100.0 | 53 | 2 A82862 | hypothetical prote |
| 39 | 16 | 100.0 | 53 | 2 H98094 | hypothetical prote |
| 40 | 16 | 100.0 | 54 | 2 S22937 | sex-determining pr |
| 41 | 16 | 100.0 | 54 | 2 S22946 | SOX-11 protein - A |
| 42 | 16 | 100.0 | 54 | 2 I50028 | Sry-related sequen |
| 43 | 16 | 100.0 | 54 | 2 I50029 | Sry-related sequen |
| 44 | 16 | 100.0 | 54 | 2 I50190 | Sry-related sequen |
| 45 | 16 | 100.0 | 54 | 2 I50191 | Sry-related sequen |

ALIGNMENTS

RESULT 1

S43834 DNA topoisomerase (EC 5.99.1.2) - Klebsiella sp. (ATCC 15380) (fragment)
C/Species: Klebsiella sp.
A/Variety: ATCC 15380
C/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 07-May-1999
C/Accession: S43834
R/Lynch, A.S.; Tyrrell, R.; Smerdon, S.J.; Briggs, G.S.; Wilkinson, A.J.
Biochem. J. 299, 129-136, 1994
A/Title: Characterization of the CysB protein of Klebsiella aerogenes: direct evidence t
A/Reference number: S43834; MUID:94220019; PMID:8166630
A/Accession: S43834
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-18 <LYN>
A/Experimental source: ATCC 15380
C/Genetics:
A/Gene: topI
C/Function:
A/Description: catalyzes ATP-independent transient breakage of DNA phosphodiester bonds
rejoining; this reaction will lead to the conversion of one topological isomer of DNA to
C/Superfamily: bacterial type I DNA topoisomerase
C/Keywords: DNA binding; DNA replication; isomerase; zinc finger

Query Match 100.0%; Score 16; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FID 3
Db 8 FID 10

RESULT 2

D48518 PEB1 5'-region hypothetical protein A - Campylobacter jejuni (fragment)
C/Species: Campylobacter jejuni
C/Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 19-May-1995
C/Accession: D48518
R/Pei, Z.; Blaser, M.J.
J. Biol. Chem. 268, 18717-18725, 1993
A/Title: PEB1, the major cell-binding factor of Campylobacter jejuni, is a homolog of the
A/Reference number: A48518; MUID:93366784; PMID:8360165
A/Accession: D48518
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-21 <PEI>
A/Cross-references: GB:I13662

Query Match 100.0%; Score 16; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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C/Date: 19-Nov-1998 #sequence_revision 19-Nov-1998 #text_change 23-Feb-1997
C/Accession: A26188
R/De, B.K.; Misono, K.S.; Lukas, T.J.; Mroczkowski, B.; Cohen, S.
J. Biol. Chem. 261, 13784-13792, 1986
A/Title: A calcium-dependent 35-kilodalton substrate for epidermal growth factor receptor:
A/Reference number: A26188; MUID:87008618; PMID:3020049
A/Accession: A26188
A/Molecule type: protein
A/Residues: 1-30 <DEB>
C/Superfamily: annexin I; annexin repeat homology
C/Keywords: phosphoprotein

Query Match 100.0%; Score 16; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 1 FID 3

RESULT 6
A44682
nitrobenzene nitroreductase (BC 1.-.-.-) - Pseudomonas pseudoalcaligenes (fragment)
C/Species: Pseudomonas pseudoalcaligenes
C/Date: 28-Feb-1995 #sequence_revision 03-Mar-1995 #text_change 21-Mar-1996
C/Accession: A44682
R/Somerville, C.C.
submitted to the Protein Sequence Database, February 1995
A/Description: Purification and characterization of nitrobenzene nitroreductase from Pse
A/Reference number: A44682
A/Accession: A44682
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-30 <SOM>
A/Experimental source: strain JS45
C/Keywords: oxidoreductase

Query Match 100.0%; Score 16; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 5 FID 7

RESULT 7
H82818
hypothetical protein XF0341 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: H82818
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: H82818
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-31 <SIM>
A/Cross-references: GB:AE003896; GB:AE003849; NID:g9105157; PIDN:AAF03151.1; GSPDB:GN001;
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmieri, D.A.

```

```

QY 1 FID 3
Db 17 FID 19

RESULT 3
S20453
pyrroloquinoline quinone precursor pqGA - Klebsiella pneumoniae
C/Species: Klebsiella pneumoniae
C/Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C/Accession: S20453; S21838
R/Neuendorf, J.J.M.; Sellink, E.; Riegman, N.H.; Postma, P.W.
Mol. Gen. Genet. 232, 284-294, 1992
A/Title: Nucleotide sequence and structure of the Klebsiella pneumoniae pqg operon.
A/Reference number: S20452; MUID:92212293; PMID:1313537
A/Accession: S20453
A/Molecule type: DNA
A/Residues: 1-23 <MEU>
A/Cross-references: EMBL:X58778; NID:G43903; PIDN:CAA41579.1; PID:G43905
R/Velterop, J.S.; Sellink, E.; Meulenbergh, J.J.; David, I.; Postma, P.W.
J. Bacteriol. 177, 5088-5098, 1995
A/Title: Synthesis of pyrroloquinoline quinone in vivo and in vitro and detection of an
A/Reference number: A69181; MUID:95394815; PMID:7665488
A/Contents: annotation
C/Genetics:
A/Gene: pqGA
C/Superfamily: pyrroloquinoline quinone precursor pqGA
C/Keywords: quinoprotein
F15-19/Product: pyrroloquinoline quinone #status predicted <MAT>
F15-19/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 100.0%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 7 FID 9

RESULT 4
F84066
hypothetical protein BH3334 [imported] - Bacillus halodurans (strain C-125)
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C/Accession: F84066
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: F84066
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-25 <STO>
A/Cross-references: GB:AP001518; GB:BA000004; NID:g1017592; PIDN:BA07053.1; GSPDB:GN00
A/Experimental source: strain C-125
C/Genetics:
A/Gene: BH3334

Query Match 100.0%; Score 16; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 13 FID 15

RESULT 5
A26188
lipocortin I - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)

```

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0341

Query Match 100.0%; Score 16; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 16 FID 18

RESULT 8
PQ0413
nonstructural protein NS1 - influenza A virus (strain A/Hebei/24/89 [H1N2]) (fragment)
C;Species: influenza A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0413
R;Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Nerom
J. Gen. Virol. 73, 1329-1337, 1992
A;Title: Origin and evolutionary characteristics of antigenic reassortant influenza A (H
A;Reference number: PQ0408; MUID:92300326; PMID:1607856
A;Accession: PQ0413
A;Molecule type: Genomic RNA
A;Residues: 1-32 <LIA>
C;Genetics:
A;Map position: segment 8
C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: nonstructural protein

Query Match 100.0%; Score 16; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 10 FID 12

RESULT 9
PQ0416
RNA-directed RNA polymerase (EC 2.7.7.48) 3 - influenza A virus (strain A/Yamagata/120/8
N;Alternate names: P2 protein; PA protein
C;Species: influenza A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PQ0416
R;Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Nerom
J. Gen. Virol. 73, 1329-1337, 1992
A;Title: Origin and evolutionary characteristics of antigenic reassortant influenza A (H
A;Reference number: PQ0408; MUID:92300326; PMID:1607856
A;Accession: PQ0416
A;Molecule type: Genomic RNA
A;Residues: 1-33 <LIA>
C;Genetics:
A;Map position: segment 3
C;Superfamily: influenza virus RNA-directed RNA polymerase 3
C;Keywords: nucleotidyltransferase

Query Match 100.0%; Score 16; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 11 FID 13

RESULT 10

A95119
hypothetical protein SP1031 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: A95119
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Kang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Kang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: A95119
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-33 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75146.1; PID:gi4972505; GSPDB:GN00164; TIGR:SP48
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1031

Query Match 100.0%; Score 16; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 22 FID 24

RESULT 11
H82096
hypothetical protein VC2284 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: H82096
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: H82096
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-33 <HEI>
A;Cross-references: GB:AE003852; GB:AE004299; GB:AE03852; NID:g9656835; PIDN:AAF95428.1; GSPDB:GN001;
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2284
A;Map position: 1

Query Match 100.0%; Score 16; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 19 FID 21

RESULT 12
S33646
Hypothetical protein 2 - pin mould (Absidia glauca) plasmid PSSP15 (fragment)
C;Species: Absidia glauca
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C;Accession: S33646
R;Haefliger, J.; Woestemeyer, J.; Weigel, C.T.
submitted to the EMBL Data Library, June 1992
A;Description: Complete nucleotide sequence of the papD9 extrachromosomal DNA element of
A;Reference number: S33645
A;Accession: S33646
A;Molecule type: DNA

A;Residues: 1-33 <HAE>
 A;Cross-references: EMBL:M94861
 C;Genetics:
 A;Genome: plasmid

Query Match 100.0%; Score 16; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 |||
 Db 22 FID 24

RESULT 13

PS0363
 protein-tyrosine-phosphatase (EC 3.1.3.48) (clone PTP5) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 20-Mar-1998
 C;Accession: PS0363
 R;den Hertog, J.; Fals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.
 Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992
 A;Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase
 A;Reference number: JH0609; MUID:92272714; PMID:1590786
 A;Accession: PS0363
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-35 <DEN>
 A;Experimental source: embryonal carcinoma cell, P19 cell
 C;Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repeat
 -tyrosine-phosphatase homology
 C;Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 100.0%; Score 16; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 |||
 Db 6 FID 8

RESULT 14

PS0364
 protein-tyrosine-phosphatase (EC 3.1.3.48) (clone PTP31) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 20-Mar-1998
 C;Accession: PS0364
 R;den Hertog, J.; Fals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.
 Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992
 A;Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase
 A;Reference number: JH0609; MUID:92272714; PMID:1590786
 A;Accession: PS0364
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-35 <DEN>
 A;Experimental source: embryonal carcinoma cell, P19 cell
 C;Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repeat
 -tyrosine-phosphatase homology
 C;Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 100.0%; Score 16; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 |||
 Db 6 FID 8

RESULT 15

DB87544
 hypothetical protein CC2381 [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C;Accession: D87544
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.H.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: D87544
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-36 <STO>
 A;Cross-references: GB:AE005673; NID:gl3423914; PIDN:AAK24352.1; GSPDB:GN00148
 C;Genetics:
 A;Gene: CC2381

Query Match 100.0%; Score 16; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 |||
 Db 28 FID 30

Search completed: September 30, 2004, 06:00:39
 Job time : 5.25424 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 1.83051 Seconds
(without alignments)
85.337 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Match | Length | ID | Description |
|------------|-------|---------|-------|--------|-------------|--------------------|
| 1 | 16 | 100.0 | 16 | 1 | FIBA_RABIT | P14461 oryctolagus |
| 2 | 16 | 100.0 | 18 | 1 | TOPI_KLEAE | P46155 klebsiella |
| 3 | 16 | 100.0 | 23 | 1 | PQA_ENTIT | P59726 enterobacte |
| 4 | 16 | 100.0 | 23 | 1 | PQA_KLEPN | P27503 klebsiella |
| 5 | 16 | 100.0 | 24 | 1 | HMT_LINRE | P23543 lingula ree |
| 6 | 16 | 100.0 | 32 | 1 | RS19_YEREN | Q56847 yersinia en |
| 7 | 16 | 100.0 | 36 | 1 | SKK2_CENLM | P59848 centruloide |
| 8 | 16 | 100.0 | 37 | 1 | Y692_BOREU | O51635 borrelia bu |
| 9 | 16 | 100.0 | 43 | 1 | Y04D_BPT4 | P07080 bacterioph |
| 10 | 16 | 100.0 | 52 | 1 | YORV_FT11 | P19306 thermoprote |
| 11 | 16 | 100.0 | 54 | 1 | AWA2_ALLMT | P40642 alligator m |
| 12 | 16 | 100.0 | 54 | 1 | AWA3_ALLMT | P40643 alligator m |
| 13 | 16 | 100.0 | 54 | 1 | CH01_CHICK | P40665 gallus gall |
| 14 | 16 | 100.0 | 54 | 1 | CH02_CHICK | P40666 gallus gall |
| 15 | 16 | 100.0 | 54 | 1 | CH03_CHICK | P40667 gallus gall |
| 16 | 16 | 100.0 | 54 | 1 | CH04_CHICK | P40668 gallus gall |
| 17 | 16 | 100.0 | 54 | 1 | CH07_CHICK | P40669 gallus gall |
| 18 | 16 | 100.0 | 54 | 1 | CH31_CHICK | P40670 gallus gall |
| 19 | 16 | 100.0 | 54 | 1 | DM10_DROME | P40658 drosophila |
| 20 | 16 | 100.0 | 54 | 1 | DM23_DROME | P40660 drosophila |
| 21 | 16 | 100.0 | 54 | 1 | DM36_DROME | P40662 drosophila |
| 22 | 16 | 100.0 | 54 | 1 | DM63_DROME | P40663 drosophila |
| 23 | 16 | 100.0 | 54 | 1 | DM64_DROME | P40664 drosophila |
| 24 | 16 | 100.0 | 56 | 1 | SOX1_PLEWA | P37839 pleurodeles |
| 25 | 16 | 100.0 | 57 | 1 | ANDE_DROME | O16825 drosophila |
| 26 | 16 | 100.0 | 57 | 1 | ANDE_DROME | P21663 drosophila |
| 27 | 16 | 100.0 | 57 | 1 | ANDE_DROSE | Q8wsv2 drosophila |
| 28 | 16 | 100.0 | 58 | 1 | Y016_METUA | Q60322 methanococ |
| 29 | 16 | 100.0 | 60 | 1 | ANDE_DROSL | Q8wsv4 drosophila |
| 30 | 16 | 100.0 | 60 | 1 | Y02B_BPT4 | P39232 bacterioph |
| 31 | 16 | 100.0 | 62 | 1 | Y12D_BPT4 | P39496 bacterioph |
| 32 | 16 | 100.0 | 63 | 1 | YEBW_ECOLI | P76275 escherichia |
| 33 | 16 | 100.0 | 66 | 1 | COPP_HELPFU | Q9zm70 helicobacte |

| | | | | | | |
|----|----|-------|----|---|-------------|--------------------|
| 34 | 16 | 100.0 | 66 | 1 | COPP_HELPFY | Q48271 helicobacte |
| 35 | 16 | 100.0 | 66 | 1 | SM64_HUMAN | Q9nrt5 homo sapien |
| 36 | 16 | 100.0 | 67 | 1 | VG10_SPVIR | P15901 spiroplasma |
| 37 | 16 | 100.0 | 67 | 1 | Y023_RICCN | Q92jp4 rickettsia |
| 38 | 16 | 100.0 | 69 | 1 | ACP_RHOSH | P12784 rhodobacter |
| 39 | 16 | 100.0 | 70 | 1 | Y06C_BPT4 | P13308 bacterioph |
| 40 | 16 | 100.0 | 71 | 1 | RECA_STRGC | P49986 streptococ |
| 41 | 16 | 100.0 | 72 | 1 | YA94_ARCFU | O29171 archaeoglob |
| 42 | 16 | 100.0 | 72 | 1 | YVGB_VACCC | P20566 vaccinia vi |
| 43 | 16 | 100.0 | 73 | 1 | RR18_GUITH | O78488 guillardia |
| 44 | 16 | 100.0 | 73 | 1 | RS19_YERPS | P11256 yersinia ps |
| 45 | 16 | 100.0 | 73 | 1 | YPO4_NPVLD | P30326 lymantria d |

ALIGNMENTS

RESULT 1
FIBA_RABIT STANDARD; PRT; 16 AA.
AC P14461;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965)
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1651 MW; DB623279EA55EB6 CRC64;
Query Match 100.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FID 3
DB 8 FID 10
RESULT 2
TOPI_KLEAE STANDARD; PRT; 18 AA.
AC P46155;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA topoisomerase I (BC 5.99.1.2) (Omega-protein) (Relaxing enzyme) (Untwisting enzyme) (Swivelase) (Fragment).
GN TOPA.
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=28451;
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 418 / ATCC 15380;
RX MEDLINE=9420019; PubMed=8166630;
RA Lynch A.S., Tyrell R., Smerdon S.J., Briggs G.S., Wilkinson A.J.;
RT "Characterization of the CysB protein of Klebsiella aerogenes: direct
RT evidence that N-acetylserine rather than O-acetylserine serves as the
RT inducer of the cysteine regulon.";
RL Biochem. J. 299:129-136(1994).
CC -!- FUNCTION: The reaction catalyzed by topoisomerases leads to the
CC conversion of one topological isomer of DNA to another.
CC -!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
CC DNA, followed by passage and rejoining.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- MISCELLANEOUS: When a topoisomerase transiently breaks a DNA
CC backbone bond, it simultaneously forms a protein-DNA link, in
CC which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus
CC at one end of the enzyme-severed DNA strand.
CC -!- SIMILARITY: Belongs to the prokaryotic type I/III topoisomerase
CC family.
CC
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CC
CC EMBL; X78729; -; NOT_ANNOTATED_CDS.
CC HSSP; P06612; LYU.
CC InterPro; IPR000380; DNA topoisomerase.
CC PROSITE; PS00396; TOPOISOMERASE_I_PROK; PARTIAL.
CC Isomerase; Topoisomerase; DNA-binding.
CC NON_TER 1
CC SEQUENCE 18 AA; 2043 MW; 8C1C81238FF0EFA4 CRC64;
CC
CC Query Match 100.0%; Score 16; DB 1; Length 18;
CC Best Local Similarity 100.0%; Pred. No. 1.9e+02;
CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 FID 3
CC Db 8 FID 10
CC
CC RESULT 3
CC PQQA_ENTIT STANDARD; PRT; 23 AA.
CC ID PQQA_ENTIT
CC AC P59726;
CC DT 10-OCT-2003 (Rel. 42, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Coenzyme PQQ synthetase protein A (Pyrroloquinoline quinone
CC biosynthesis protein A).
CC GN PQQA.
CC OS Enterobacter intermedius.
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC OC Enterobacteriaceae; Enterobacter.
CC NCBI_TaxID=61648;
CC [1]
CC SEQUENCE FROM N.A.
CC Kim C.H., Han S.H., Kim K.Y., Cho B.H., Kim Y.H., Gu B.S., Kim Y.C.;
CC "Cloning and expression of pyrroloquinoline (PQQ) genes from a
CC phosphate-solubilizing bacterium Enterobacter intermedius.";
CC Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ)
CC biosynthesis. Probably provides the glutamate and tyrosine
CC residues that are cross-linked and modified to form the coenzyme
CC (By similarity).
CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
CC -!- SIMILARITY: Belongs to the pqqa family.
CC [1]
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AY216883; AAP34378.1; -
CC HAMAP; MF_00656; -; 1.
CC PQQ biosynthesis; PQQ.
CC CROSSLINK 15 19 Pyrroloquinoline quinone (Glu-Tyr)
CC (Probable).
CC SQ SEQUENCE 23 AA; 2764 MW; ACCB321460871C5D CRC64;
CC
CC Query Match 100.0%; Score 16; DB 1; Length 23;
CC Best Local Similarity 100.0%; Pred. No. 2.4e+02;
CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 FID 3
CC Db 7 FID 9
CC
CC RESULT 4
CC PQQA_KLEPN STANDARD; PRT; 23 AA.
CC ID PQQA_KLEPN
CC AC P27503;
CC DT 01-AUG-1992 (Rel. 23, Created)
CC DT 01-AUG-1992 (Rel. 23, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Coenzyme PQQ synthetase protein A (Pyrroloquinoline quinone
CC biosynthesis protein A).
CC GN PQQA.
CC OS Klebsiella pneumoniae.
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC OC Enterobacteriaceae; Klebsiella.
CC NCBI_TaxID=573;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=NCTC 418;
CC MEDLINE=95394815; PubMed=7655488;
CC Vetterop J.S., Sellink E., Meulenber J.J., David S., Bulder I.,
CC Postma P.W.;
CC "Synthesis of pyrroloquinoline quinone in vivo and in vitro and
CC detection of an intermediate in the biosynthetic pathway.";
CC J. Bacteriol. 177:5088-5098(1995).
CC -!- FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ)
CC biosynthesis. Probably provides the glutamate and tyrosine
CC residues that are cross-linked and modified to form the coenzyme.
CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
CC -!- SIMILARITY: Belongs to the pqqa family.
CC [1]
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CC
CC EMBL; X58778; CAA41579.1; -
CC PIR; S20453; S20453.
CC HAMAP; MF_00656; -; 1.
CC PQQ biosynthesis; PQQ.
CC CROSSLINK 15 19 Pyrroloquinoline quinone (Glu-Tyr)

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FT SEQUENCE 23 AA; 2764 MW; ACCB321460871C5D CRC64;
SQ SEQUENCE 23 AA; 2764 MW; ACCB321460871C5D CRC64;

Query Match 100.0%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 7 FID 9

RESULT 5
HEMT LINE
ID HEMT LINE STANDARD; PRT; 24 AA.
AC P23543;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hemerythrin alpha chain (Fragment).
OS Lingula reevii.
OC Eukaryota; Metazoa; Brachiopoda; Linguliformea; Lingulata; Lingulida;
OC Linguloidae; Lingulidae; Lingula.
OX NCBI_TaxID=7575;
RN [1]
RP SEQUENCE.
RX MEDLINE=91369922; PubMed=1892823;
RA Zhang J.-H., Kurtz D.M. Jr.;
RT "Two distinct subunits of hemerythrin from the brachiopod Lingula
RL Biochemistry 30:9121-9124(1991).
CC reevii; an apparent requirement for cooperativity in O2 binding.";
CC -!- FUNCTION: Hemerythrin is a respiratory protein in blood cells of
CC certain marine worms. The oxygen-binding site in each chain
CC contains two iron atoms.
CC -!- SUBUNIT: Octamer composed of two types of chains: alpha and beta.
CC -!- SIMILARITY: Belongs to the hemerythrin family.
DR InterPro: IPR002053; Hemerythrin.
DR Pfam: PF01814; Hemerythrin; 1.
DR PROSITE; PS00550; HEMERYTHRINS; PARTIAL.
KW Oxygen transport; Metal-binding; Iron.
FT METAL 24 24 IRON 1 (BY SIMILARITY).
FT NON TER 24 24
SQ SEQUENCE 24 AA; 2825 MW; 28675F45462C44BB CRC64;

Query Match 100.0%; Score 16; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 19 FID 21

RESULT 6
RS19 YEREN
ID RS19 YEREN STANDARD; PRT; 32 AA.
AC Q56847;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPSS.
OS Versinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=6471/76 / Serotype O:3;
RX MEDLINE=96382736; PubMed=8790600;
RA Mertz A.K.H., Daser A., Skurnik M., Wiesmuller K., Braun J., Appel H.,
RA Batsford S., Wu P., Distler A., Sieper J.;
RT "The evolutionarily conserved ribosomal protein L23 and the cationic

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RT urease beta-subunit of Versinia enterocolitica O:3 belong to the
RT immunodominant antigens in Versinia-triggered reactive arthritis;
RL Mol. Med. 1:44-55(1994).
CC -!- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
CC to the 16S ribosomal RNA (By similarity).
CC -!- SIMILARITY: Belongs to the S19P family of ribosomal proteins.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: U11251; AAC43514.1; -
DR HAMAP; MF_00531; -; 1
DR InterPro: IPR002222; Ribosomal S19.
DR Pfam: PF00203; Ribosomal S19; 1.
DR ProDom; PD001012; Ribosomal S19; 1.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON TER 32 32
SQ SEQUENCE 32 AA; 3659 MW; E534F701330F0338 CRC64;

Query Match 100.0%; Score 16; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 10 FID 12

RESULT 7
SCK2_CENLM
ID _SCK2_CENLM STANDARD; PRT; 36 AA.
AC P59848;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hongotoxin 2 (HGTX2) (Fragment).
OS Centruroides limbatus (Scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Centruroides.
OX NCBI_TaxID=244936;
RN [1]
RP SEQUENCE.
RX MEDLINE=98112806; PubMed=9446567;
RA Koschak A., Bugianesi R.M., Mitterdorfer J., Kaczorowski G.J.,
RA Garcia M.L., Knaus H.-G.;
RT "Subunit composition of brain voltage-gated potassium channels
RT determined by hongotoxin-1, a novel peptide derived from Centruroides
RT limbatus venom.";
RT J. Biol. Chem. 273:2639-2644(1998).
CC -!- FUNCTION: Potent selective inhibitor of Kv1 voltage-gated
CC potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the short scorpion toxin family. Potassium
CC channel inhibitor subfamily.
DR PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
KW Toxin; Neurotoxin; Ionic channel inhibitor;
KW Potassium channel inhibitor.
FT NON TER 36 36
SQ SEQUENCE 36 AA; 3946 MW; A9D585FC06312E16 CRC64;

Query Match 100.0%; Score 16; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3

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Db      |||
        2 FID 4
RESULT 8
Y692 BORBU
ID Y692 BORBU STANDARD; PRT; 37 AA.
AC Q51635;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein BB0692.
GN BB0692.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kervlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586 (1997).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y00122; CAA68317.1; -.
CC EMBL; AF158101; AAD42495.1; -.
CC PIR; C30292; ZDBPT9.
CC KW Hypothetical protein.
CC SQ SEQUENCE 37 AA; 4589 MW; 5FA1F9470EDB51E2 CRC64;
Query Match 100.0%; Score 16; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FID 3
Db |||
20 FID 22
RESULT 9
Y04D BPT4
ID Y04D BPT4 STANDARD; PRT; 43 AA.
AC P07080;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 5.1 kDa protein in Gp55-nrdG intergenic region.
GN Y04D OR 55.4.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10665;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C;
RX MEDLINE=87203398; PubMed=3575111;
Tomaschewski J., Rueger W.;

```

```

RT "Nucleotide sequence and primary structures of gene products coded
RT for by the T4 genome between map positions 48.266 kb and 39.166 kb.";
RL Nucleic Acids Res. 15:3632-3633 (1987).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=22514363; PubMed=12626685;
RT Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
RT "Bacteriophage T4 genome.";
RL Microbiol. Mol. Biol. Rev. 67:86-156 (2003).
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CC -----
CC EMBL; Y00122; CAA68317.1; -.
CC EMBL; AF158101; AAD42495.1; -.
CC PIR; C30292; ZDBPT9.
CC KW Hypothetical protein.
CC SQ SEQUENCE 43 AA; 5146 MW; 9549CB24D73F8D0C CRC64;
Query Match 100.0%; Score 16; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FID 3
Db |||
34 FID 36
RESULT 10
YORV TTV1
ID YORV TTV1 STANDARD; PRT; 52 AA.
AC P19306;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hypothetical 5.9 kDa protein.
OS Thermoproteus tenax virus 1 (strain KRA1) (TTV1).
OC Viruses; dsDNA viruses, no RNA stage; Lipothirixviridae;
OC Lipothirixvirus.
OX NCBI_TaxID=10480;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=90245666; PubMed=2336394;
RA Neumann H., Zillig W.;
RT "Nucleotide sequence of the viral protein TPX of the TTV1 variant
RT VT3.";
RL Nucleic Acids Res. 18:2171-2171 (1990).
CC -----
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CC -----
CC EMBL; X14855; CAA33003.1; -.
CC EMBL; X14717; CAA32839.1; -.
CC PIR; S15922; S15922.
CC KW Hypothetical protein.
CC SQ SEQUENCE 52 AA; 5903 MW; 6293C63C4CCEDE2B CRC64;
Query Match 100.0%; Score 16; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FID 3
Db |||

```



```

KW DNA-binding; Nuclear protein.
FT NON_TER 1 1
FT DNA_BIND <1 >54 HMG BOX.
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 6574 MW; A5B915076E95957D CRC64;

Query Match 100.0%; Score 16; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 32 FID 34

RESULT 14
CH02-CHICK STANDARD; PRT; 54 AA.
AC P40666;

DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE SRY-related protein CH2 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93184703; PubMed=8443573;
RA Coriat A.M., Mueller U., Harry J.L., Uwanogho D., Sharpe P.T.;
RT "PCR amplification of SRY-related gene sequences reveals evolutionary
conservation of the SRY-box motif.";
RL PCR Methods Appl. 2:218-222(1993).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: Contains 1 HMG box domain.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; M86322; AAA48681.1; -.
CC HSSP; Q05066; IHRV.
CC InterPro; IPR000910; HMG_12_box.
CC Pfam; PF00505; HMG_box; 1.
CC SMART; SM00398; HMG; 1.
CC PROSITE; PS50118; HMG_BOX_2; 1.
CC DNA-binding; Nuclear protein.
FT NON_TER 1 >54 HMG BOX.
FT DNA_BIND <1 >54
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 6489 MW; 1677E4B8EE59FD54 CRC64;

Query Match 100.0%; Score 16; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 32 FID 34

Search completed: September 30, 2004, 06:01:23
Job time : 3.83051 secs

KW DNA-binding; Nuclear protein.
FT NON_TER 1 1
FT DNA_BIND <1 >54 HMG BOX.
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 6574 MW; A5B915076E95957D CRC64;

Query Match 100.0%; Score 16; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 32 FID 34

RESULT 15
CH03-CHICK STANDARD; PRT; 54 AA.
AC P40667;

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 9.81356 Seconds
(without alignments)
96.454 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 16 | 100.0 | 15 | 2 Q9KIV5 | Q9kiv5 anabaena sp |
| 2 | 16 | 100.0 | 15 | 2 Q9R4K0 | Q9r4k0 nocardia. n |
| 3 | 16 | 100.0 | 20 | 15 Q95485 | Q95485 avian leuko |
| 4 | 16 | 100.0 | 24 | 2 Q92630 | Q92630 streptococc |
| 5 | 16 | 100.0 | 24 | 2 Q9R2R0 | Q9r2r0 streptococc |
| 6 | 16 | 100.0 | 24 | 11 Q8CGM9 | Q8cgm9 mus musculu |
| 7 | 16 | 100.0 | 25 | 16 Q9K7M7 | Q9k7m7 bacillus ha |
| 8 | 16 | 100.0 | 28 | 2 Q8KS87 | Q8ks87 escherichia |
| 9 | 16 | 100.0 | 29 | 16 Q8CLJ9 | Q8clj9 versinia pe |
| 10 | 16 | 100.0 | 29 | 16 Q87L17 | Q87l17 vibrio para |
| 11 | 16 | 100.0 | 30 | 4 Q9NRCS | Q9nrcs homo sapien |
| 12 | 16 | 100.0 | 30 | 16 Q8INQ6 | Q8inq6 bacillus an |
| 13 | 16 | 100.0 | 31 | 2 Q9S0E6 | Q9s0e6 borrelia bu |
| 14 | 16 | 100.0 | 31 | 16 Q9PGG1 | Q9pgg1 xylella fas |
| 15 | 16 | 100.0 | 31 | 16 Q8KGF6 | Q8kgf6 chlorobium |
| 16 | 16 | 100.0 | 31 | 16 Q8EIW8 | Q8eiw8 shewanella |

| | | | | | |
|----|----|-------|----|-----------|---------------------|
| 17 | 16 | 100.0 | 32 | 2 Q50110 | Q50110 mycobacteri |
| 18 | 16 | 100.0 | 32 | 16 Q87IR8 | Q87ir8 vibrio para |
| 19 | 16 | 100.0 | 33 | 10 Q987Y3 | Q987y3 picea abies |
| 20 | 16 | 100.0 | 33 | 16 Q9KPS8 | Q9kps8 vibrio chol |
| 21 | 16 | 100.0 | 33 | 16 Q97R10 | Q97r10 streptococc |
| 22 | 16 | 100.0 | 34 | 3 Q00062 | Q00062 absidia gla |
| 23 | 16 | 100.0 | 34 | 16 Q8FXD9 | Q8fxd9 brucella su |
| 24 | 16 | 100.0 | 34 | 16 Q8FA7 | Q8fa7 leptospira |
| 25 | 16 | 100.0 | 34 | 16 Q8EFC4 | Q8efc4 shewanella |
| 26 | 16 | 100.0 | 35 | 2 Q939H2 | Q939h2 pseudomonas |
| 27 | 16 | 100.0 | 35 | 2 P95513 | P95513 pasteurellia |
| 28 | 16 | 100.0 | 35 | 16 Q98NE6 | Q98ne6 rhizobium l |
| 29 | 16 | 100.0 | 35 | 16 Q8FOE7 | Q8foe7 leptospira |
| 30 | 16 | 100.0 | 36 | 16 Q9ASR6 | Q9asr6 caulobacter |
| 31 | 16 | 100.0 | 37 | 10 Q9SMC9 | Q9smc9 lycopersico |
| 32 | 16 | 100.0 | 37 | 16 Q9ZVS6 | Q9zvs6 rhizobium m |
| 33 | 16 | 100.0 | 37 | 16 Q8F3C0 | Q8f3c0 leptospira |
| 34 | 16 | 100.0 | 37 | 16 Q8EZA2 | Q8eza2 leptospira |
| 35 | 16 | 100.0 | 38 | 5 Q7Z149 | Q7z149 caenorhabdi |
| 36 | 16 | 100.0 | 38 | 11 Q9ES99 | Q9es99 rattus norv |
| 37 | 16 | 100.0 | 38 | 16 Q8DYH6 | Q8dyh6 streptococc |
| 38 | 16 | 100.0 | 38 | 16 Q87LD2 | Q87ld2 vibrio para |
| 39 | 16 | 100.0 | 39 | 2 Q7WTL7 | Q7wtl7 bacillus ce |
| 40 | 16 | 100.0 | 39 | 16 Q9KPJ5 | Q9kps5 vibrio chol |
| 41 | 16 | 100.0 | 39 | 16 Q92TN5 | Q92tn5 rhizobium m |
| 42 | 16 | 100.0 | 40 | 2 Q8KSF6 | Q8ksf6 mycobacteri |
| 43 | 16 | 100.0 | 40 | 5 Q8MN47 | Q8mn47 dictyosteli |
| 44 | 16 | 100.0 | 40 | 8 Q8HBM1 | Q8hbm1 arabidopsis |
| 45 | 16 | 100.0 | 40 | 8 Q8HBM0 | Q8hbm0 arabidopsis |

ALIGNMENTS

RESULT 1

| | | | |
|--------|---|------|--------|
| Q9KIV5 | PRELIMINARY; | PRT; | 15 AA. |
| ID | Q9KIV5 | | |
| AC | Q9KIV5; | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Created) | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) | | |
| DE | Putative deoxyribose-phosphate aldolase (Fragment). | | |
| OS | Anabaena sp. (strain FCC 7120). | | |
| OC | Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc. | | |
| NC | NCBI_TaxID=103690; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=PC7120; | | |
| RA | Matveyev A.V., Young K.T., Elhai J.; | | |
| RT | "DNA methyltransferases with unusual structural properties from the cyanobacterium Anabaena PCC7120." | | |
| RL | Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; AF220508; AAF75233.1; - | | |
| FT | NON TER | | |
| SQ | SEQUENCE 15 AA; 1608 MW; 1B1307FDA6850099 CRC64; | | |

Query Match 100.0%; Score 16; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3

Db 13 FID 15

RESULT 2

| | | | |
|--------|---|------|--------|
| Q9R4K0 | PRELIMINARY; | PRT; | 15 AA. |
| ID | Q9R4K0 | | |
| AC | Q9R4K0; | | |
| DT | 01-MAY-2000 (TrEMBLrel. 13, Created) | | |
| DT | 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) | | |
| DT | 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) | | |
| DE | Nitric oxide synthase (EC 4.14.23.-) (Fragment). | | |

OS Nocardia.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Nocardiae.
 OX NCBI_TaxID=1817;
 RN [1]
 RN SEQUENCE.
 RX MEDLINE=95394819; PubMed=7545152;
 RA Chen Y., Rosazza J.P.;
 RT "Purification and characterization of nitric oxide synthase (NOSVoc)
 from a Nocardia species.";
 RL J. Bacteriol. 177:5122-5128(1995).
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1818 MW; 2BD5B859DE288B77 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 Db 13 FID 15

RESULT 3
 Q85485
 ID Q85485 PRELIMINARY; PRT; 20 AA.
 AC Q85485;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gag-erbB fusion protein (Fragment).
 OS Avian leukosis virus.
 OC Viruses; Retroviridae; Retroviridae; Alpharetrovirus.
 OX NCBI_TaxID=11864;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=RAV1;
 RX MEDLINE=88230605; PubMed=2897475;
 RA Raines M.A., Mailhe N.J., Moscovici C., Crittenden L., Kung H.-J.;
 RT "Mechanism of c-erbB transduction: Newly released transducing viruses
 retain poly(A) tracts of erbB transcripts and encode C-terminally
 intact erbB proteins";
 RL J. Virol. 62:2437-2443(1988).
 DR EMBL; M19970; AAA42586.1; -;
 DR InterPro; IPR009030; Grow_fac_recep.
 FT NON_TER 1 1
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2167 MW; 2A4EFD2E3A709011 CRC64;

Query Match 100.0%; Score 16; DB 15; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 Db 11 FID 13

RESULT 4
 Q92630
 ID Q92630 PRELIMINARY; PRT; 24 AA.
 AC Q92630;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Capsular polysaccharide B (Fragment).
 GN CPBB.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=99287847; PubMed=10348877;
 RA Morona J.K., Morona R., Paton J.C.;
 RT "Analysis of the 5' portion of the type 19A capsule locus identifies
 two classes of cpsC, cpsD, and cpsE genes in Streptococcus
 pneumoniae.";
 RL J. Bacteriol. 181:3599-3605(1999).
 DR EMBL; AF106135; AAD17981.1; -;
 FT NON_TER 1 1
 SQ SEQUENCE 24 AA; 2834 MW; ED047715CF82D83B CRC64;

Query Match 100.0%; Score 16; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 Db 11 FID 13

RESULT 5
 Q9R2R0
 ID Q9R2R0 PRELIMINARY; PRT; 24 AA.
 AC Q9R2R0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Capsular polysaccharide B (Fragment).
 GN CPBB.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99287847; PubMed=10348877;
 RA Morona J.K., Morona R., Paton J.C.;
 RT "Analysis of the 5' portion of the type 19A capsule locus identifies
 two classes of cpsC, cpsD, and cpsE genes in Streptococcus
 pneumoniae.";
 RL J. Bacteriol. 181:3599-3605(1999).
 DR EMBL; AF106134; AAD17979.1; -;
 DR EMBL; AF106132; AAD17975.1; -;
 DR EMBL; AF106133; AAD17977.1; -;
 FT NON_TER 1 1
 FT NON_TER 24 AA; 2820 MW; ED047715CF90483B CRC64;

Query Match 100.0%; Score 16; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 Db 11 FID 13

RESULT 6
 Q8CGM9
 ID Q8CGM9 PRELIMINARY; PRT; 24 AA.
 AC Q8CGM9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Retinoblastoma-binding protein 1 (Fragment).
 GN RBPL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=129X1/SVD;
 RA Binda O., Branton P.E.;

RT "Mus musculus 129x1/SvJ Partial RBSP1 Genomic Sequence."
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY163235; AAN84616.1; -
 FT NON_TER 1
 FT NON_TER 24 24
 SQ SEQUENCE 24 AA; 2685 MW; BF6991AC3D52BC4E CRC64;

Query Match 100.0%; Score 16; DB 11; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 ||||
 Db 20 FID 22

RESULT 7
 Q9K7M7 PRELIMINARY; PRT; 25 AA.

AC Q9K7M7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein BH3334.

OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=86665;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11059132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis."
 RL Nucleic Acids Res. 28:4317-4331(2000).

DR EMBL; AP001518; BAB07053.1; -
 DR PIR; F84066; F84066.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 25 AA; 2986 MW; OC31EA93BE976875 CRC64;

Query Match 100.0%; Score 16; DB 16; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 ||||
 Db 13 FID 15

RESULT 8
 Q8KS87 PRELIMINARY; PRT; 28 AA.

AC Q8KS87;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Putative oxidoreductase Fe-S subunit (Fragment).

GN B1589.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=ECOR-9;
 RX MEDLINE=22053230; PubMed=12057959;
 RA Sandt C.H., Hopper J.E., Hill C.W.;
 RT "Activation of Prophage eib Genes for Immunoglobulin-Binding Proteins
 RT by Genes from the IbrAB Genetic Island of Escherichia coli ECOR-9";
 RL J. Bacteriol. 184:3640-3648(2002).

DR EMBL; AF520223; AAM53254.1; -
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3185 MW; A2F42416487ED57B CRC64;

Query Match 100.0%; Score 16; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 ||||
 Db 8 FID 10

RESULT 9
 Q8CLJ9 PRELIMINARY; PRT; 29 AA.

AC Q8CLJ9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical.

GN Y1162.
 OS Versinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Versinia.
 OC NCBI_TaxID=632;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIMS / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;

RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;

RT "Genome sequence of Versinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL; AE013720; AAM84740.1; -
 KW Hypothetical protein.

SQ SEQUENCE 29 AA; 3489 MW; A300F9DE223524E CRC64;

Query Match 100.0%; Score 16; DB 16; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 ||||
 Db 11 FID 13

RESULT 10
 Q87L17 PRELIMINARY; PRT; 29 AA.

AC Q87L17;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.

GN VP2800.
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.

OX NCBI_TaxID=670;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=RIMD 2210633 / Serotype O3:K6;
 RX MEDLINE=22508454; PubMed=12620739;
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Najiima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
 RT distinct from that of V. cholerae";
 RL Lancet 361:743-749(2003).

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DR EMBL; AF005082; BAC61063.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 29 AA; 3534 MW; B1263708FB2189DB CRC64;

Query Match 100.0%; Score 16; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 9 FID 11

RESULT 11
Q2NRCS
ID Q2NRCS PRELIMINARY; PRT; 30 AA.
AC Q2NRCS5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ATP7B (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu Z.Y., Wang N., Murong S.X.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF234621; AAF89169.1; -.
FT NON_TER 1
FT NON_TER 30
SQ SEQUENCE 30 AA; 3451 MW; 90ED003AF2D173FB CRC64;

Query Match 100.0%; Score 16; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 19 FID 21

RESULT 12
Q81NQ6
ID Q81NQ6 PRELIMINARY; PRT; 30 AA.
AC Q81NQ6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN B3122.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Remond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
DR EMBL; AE017033; AAP26932.1; -.

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DR TIGR; BA3122; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 30 AA; 3565 MW; 8614AD8904A34084 CRC64;

Query Match 100.0%; Score 16; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 11 FID 13

RESULT 13
Q9S0E6
ID Q9S0E6 PRELIMINARY; PRT; 31 AA.
AC Q9S0E6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN BBR30.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteriia; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RA Fraser C.M., Castjens S., Huang W.M., Sutton G.G., Lathigra R.,
RA White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-Vugt R.,
RA Palmer N., Haft D., Rosa P., Stevenson B.;
RT "A bacterial genome in flux: The twelve linear and nine circular
RT extrachromosomal DNAs in an infectious isolate of the Lyme disease
RT spirochete Borrelia burgdorferi."
RL Mol. Microbiol. 0:0-0(1999).
DR EMBL; AE001577; AAF07528.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 31 AA; 3761 MW; E9DF7A1F04A6FF3B CRC64;

Query Match 100.0%; Score 16; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 5 FID 7

RESULT 14
Q9PGG1
ID Q9PGG1 PRELIMINARY; PRT; 31 AA.
AC Q9PGG1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Xf0341.
GN XF0341.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5c;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvares M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.F., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

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Db 12 FID 14
Search completed: September 30, 2004, 05:59:39
Job time : 12.9802 secs

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hobeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuranai E.Z., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.B.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Feixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
RA "The genome sequence of the plant pathogen Xylella fastidiosa."
RL Nature 406:151-159(2000).
DR EMBL; AF003886; AAF83151.1; -.
DR PIR; H82818; H82818.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 31 AA; 3827 MW; E895F867670E7382 CRC64;

Query Match 100.0%; Score 16; DB 16; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FID 3
Db 16 FID 18

RESULT 15
Q8KGF6 PRELIMINARY; PRT; 31 AA.
AC Q8KGF6
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein CT0012.
GN CT0012.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; Pubmed=12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium."
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; AE012781; AAM71260.1; -.
DR TIGR; CT0012; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 31 AA; 3608 MW; 353F138B1A882EDF CRC64;

Query Match 100.0%; Score 16; DB 16; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FID 3
Db 16 FID 18

Blank Sheet

CC render them capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble CD23
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
 CC (particularly type I diabetes), and B-cell malignancies (claimed). They
 CC are also useful for studying interactions between CD23 and various
 CC ligands and determining the binding agents
 XX
 SQ Sequence 3 AA;

Query Match 100.0%; Score 16; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
 |||
 Db 1 FID 3

RESULT 2
 AAP94794
 ID AAP94794 standard; protein; 5 AA.

AC AAP94794;
 XX
 XX 25-MAR-2003 (revised)
 DT 09-JUL-1990 (first entry)
 XX
 XX Peripheral nervous system myelin protein, proteolipid protein, a PNS CNS
 DE myelin component and acetyl choline receptor epitope associated motif.
 XX
 XX Autoantigen; MBP; myelin basic protein; transplantation antigen;
 KW myasthenia gravis; myasthenics; Transplantation antigen.
 XX
 XX Synthetic.

XX
 XX EP304279-A.

XX 22-FEB-1989.

XX 17-AUG-1988; 88EP-00307608.

XX 17-AUG-1987; 87US-00086694.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Steinman L, Zamvil S;

XX WPI; 1989-055696/08.

XX Oligopeptide and polypeptide compns. - based on the amino acid sequence
 PT of an immunogen and used for modulating the immune system.

XX Disclosure; Page; 7pp; English.

XX Sequences will normally be part of 9 to 15 AA sequence, excluded as
 CC motifs for immunisation but useful in tolerisation. (Updated on 25-MAR-
 CC 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 16; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
 |||

Db 3 FID 5

RESULT 3
 AAW55773

ID AAW55773 standard; peptide; 5 AA.

XX AAW55773;

XX 25-MAR-2003 (revised)

DT 08-JUL-1998 (first entry)

XX Immunisation motif associated with AChR 4.

XX Myelin basic protein; immunity; immune response; neurological; T-cell;
 KW human; immunogen; B-cell; transplantation antigen; immunomodulator.

XX Unidentified.

XX EP805162-A1.

XX 05-NOV-1997.

XX 17-AUG-1988; 97EP-00106788.

XX 17-AUG-1987; 87US-00086694.

XX 17-AUG-1988; 88EP-00307608.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Steinman L, Zamvil S;

XX WPI; 1998-034664/04.

XX Polypeptide comprising human myelin basic protein fragment - useful as
 PT immuno modulator.

XX Disclosure; Page 8; 8pp; English.

XX The present sequence represents an immunisation motif normally excluded,
 CC but which may be used with advantage for tolerisation by itself or in
 CC conjunction with other epitope sequences from the present invention. The
 CC present invention describes a polypeptide comprising a human myelin basic
 CC protein (hMBP) fragment including P89-101 of hMBP, excluding native hMBP.
 CC The term P89-101 is not defined but may be intended to mean amino acids
 CC 89-101 of hMBP. The polypeptide can be used for tolerising a mammalian
 CC host immune system comprising B and T cells to an immunogen of interest,
 CC wherein said immunogen is restricted by a transplantation antigen of said
 CC host. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-
 CC 2003 to correct PR field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 16; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3

|||

Db 3 FID 5

RESULT 4

AAU86974

ID AAU86974 standard; peptide; 5 AA.

XX AAU86974;

XX 21-MAY-2002 (first entry)

XX Estradiol mimotope peptide #22.

XX Estradiol; mimotope; estrone-3-glucuronide; steroid detection;

immunosuppressive; neuroprotective.
Homo sapiens.
US2002076412-A1.
20-JUN-2002.
07-JUN-1995; 95US-00484409.
17-AUG-1987; 87US-00086694.
12-JUL-1989; 89US-00379500.
01-MAY-1990; 90US-00517245.
01-MAY-1991; 91WO-US0002991.
30-APR-1992; 92US-00877444.
21-MAY-1993; 93US-0006325.
22-SEP-1993; 93US-00125407.
(STEI/) STEINMAN L.
(ZAMV/) ZAMVIL S.
Steinman L, Zamvil S;
WPI; 2002-598709/64.
Modulating or tolerizing the immune system, useful for treating multiple sclerosis, by administering a peptide derived from human myelin binding protein.
Disclosure; Page 15; 21pp; English.
This invention describes a novel method for modulating or tolerizing the immune system, and for treating multiple sclerosis comprising administering a peptide derived from MBP (human myelin basic protein). The peptide induces an autoimmune response (T cell) to a self-antigen (or part of it), and binds to an MHC (major histocompatibility complex) antigen of a host susceptible to autoimmune diseases, i.e. competes with binding to MBP and inhibit proliferation of MBP-reactive cells. The peptide has immunosuppressive and neuroprotective activity. This sequence represents a peptide derived from the human MBP protein which can be used for tolerization
Sequence 5 AA;
Query Match 100.0%; Score 16; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FID 3
Db 3 FID 5
RESULT 6
AAR29321
ID AAR29321 standard; peptide; 6 AA.
XX AAR29321;
AC
XX 25-MAR-2003 (revised)
DT 13-APR-1993 (first entry)
XX Endothelin antagonist peptide.
DE Hypertension; myocardial infarction; congestive heart failure;
XX endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;
KW acute renal failure; pre-eclampsia; diabetes; metabolic; endocrinological;
KW neurological; disorders.
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Misc-difference 1
FT

immunosuppressive; phage display; immunogen.
Synthetic.
WO200212270-A1.
14-FEB-2002.
26-JUL-2001; 2001WO-BP008705.
03-AUG-2000; 2000EP-00306613.
(UNIL) UNILEVER PLC.
(UNIL) UNILEVER NV.
PA (UNIL) HINDUSTAN LEVER LTD.
XX Badley RA, Berry MJ, Williams SC;
XX WPI; 2002-241729/29.
XX Peptide mimotope capable of binding specifically to antibody specific to estradiol, useful for assaying presence and/or amount of estradiol, especially estrone-3-glucuronide in sample.
Claim 3; Page 22; 57pp; English.
The invention relates to a purified peptide mimotope capable of binding specifically to an antibody specific to estradiol. Also included are a solid support having immobilised (releasably or non-releasably) peptide mimotopes, an immunoassay test device for the detection of estradiol in the sample, comprising the mimotopes and an antibody capable of binding specifically to the mimotopes to generate a detectable signal and an isolated nucleic acid encoding the peptide mimotopes. The mimotope is useful for assaying the presence and/or amount of estradiol preferably estrone-3-glucuronide in a sample which is urine or serum sample to be tested and is also utilised in an immunoassay test device, and further can be used as immunogens. The mimotope be used to construct new, or improve the performance of old, immunoassay test formats and devices. They can, for example, be utilised essentially to tune the signal in conventional displacement assays for the detection of estradiol. The mimotope can be bound directly to certain assay surfaces which are otherwise non-compatible with estradiol on such surfaces needing to be bound to the surface by complexing with another - often proteinaceous - molecule. The mimotope is capable of being bound to the antigen-binding site of an antibody in a selective fashion in the presence of excess quantities of other undesired materials, and tightly enough (i.e. with high enough affinity) that when used in an immunoassay, it provides a useful result). The present sequence is a peptide mimotopes of the invention
Sequence 5 AA;
Query Match 100.0%; Score 16; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FID 3
Db 3 FID 5
RESULT 5
ABB84336
ID ABB84336 standard; peptide; 5 AA.
XX ABB84336;
AC
XX 17-OCT-2002 (first entry)
DT Human MBP protein derived peptide SEQ ID 36.
DE MBP; myelin basic protein; human; tolerance; immune system;
XX multiple sclerosis; autoimmune response; autoimmune disease;
KW

FT XX WO9220706-A1. /note= "Ac-D-Phe"

FN XX 26-NOV-1992.

PD XX 24-APR-1992; 92WO-US003408.

PF XX 16-MAY-1991; 91US-00701274.

PR XX 18-DEC-1991; 91US-00809746.

XX (WARN) WARNER LAMBERT CO.

XX Cody WL, Depue P, Doherty AM, Taylor MD;

XX WPI; 1992-415705/50.

XX New peptide(s) used as endothelin antagonists - for treating

PT hypertension, metabolic and endocrine disorders, heart failure, diabetes,

PT asthma, neurological disorders, etc.

XX Claim 5; Page 86; 116pp; English.

XX The peptide is an endothelin antagonist useful in controlling

CC hypertension, myocardial infarction, congestive heart failure, endotoxemic

CC shock, subarachnoid haemorrhage, asthma, arrhythmias, acute renal

CC failure, preeclampsia, diabetes and metabolic, endocrinological and

CC neurological disorders. Administration is oral parenteral or by

CC inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/ day. It may be

CC prepared by conventional peptide synthesis. (Updated on 25-MAR-2003 to

CC correct PN field.)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 16; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. NO. 1.4e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3

Db 1 FID 3

RESULT 7

AA69115

ID AAR69115 standard; peptide; 6 AA.

XX AAR69115;

XX 25-MAR-2003 (revised)

DT 05-MAR-1995 (first entry)

XX Endothelin C-terminal peptide analog, useful as antagonist.

DE Endothelin; ET-1; receptor; antagonist.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Ac-D-Phe"

FT WO9414843-A1.

XX 07-JUL-1994.

XX 17-DEC-1993; 93WO-US012377.

XX 21-DEC-1992; 92US-00995480.

XX (WARN) WARNER LAMBERT CO.

XX Cody WL, Depue P, Doherty AM, He JX, Taylor MD;

XX WPI; 1994-234617/28.

XX New hexa-peptide derivs. inhibiting endothelin - for treatment of e.g.

PT renal failure, hypertension, asthma, restenosis, angina, cancer etc.

XX Claim 5; Page 112; 146pp; English.

XX Novel antagonists of endothelin are claimed which are C-terminal

CC hexapeptides and analogs of ET-1. The first (N-terminal) amino acid of

CC the new peptides has D-configuration. The peptides are claimed

CC generically. The present peptide is a specifically claimed example of the

CC generic compounds. The peptides are useful for treating hypertension,

CC metabolic and endocrine disorders, congestive heart failure, myocardial

CC infarction, endotoxic shock, subarachnoid haemorrhage, arrhythmia,

CC asthma, acute and chronic renal failure, preeclampsia, diabetes,

CC neurological disorders, pulmonary hypertension, ischaemic disease,

CC ischaemic bowel disease, gastric mucosal damage, Raynaud's disease,

CC restenosis, percutaneous transluminal coronary angioplasty, angina and

CC cancer. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 16; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. NO. 1.4e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3

Db 1 FID 3

RESULT 8

AAW31469

ID AAW31469 standard; protein; 6 AA.

XX AAW31469;

XX 04-AUG-1998 (first entry)

DT Transcriptional activator peptide fragment LSI32.

XX Activating sequence; Gal4; transcriptional activator; RNA polymerase;

KW Protein-protein interaction; gene therapy; therapeutic; holoenzyme;

KW Gal4; DNA binding domain.

XX Synthetic.

XX WO9744447-A2.

XX 27-NOV-1997.

XX 02-MAY-1997; 97WO-US007338.

XX 03-MAY-1996; 96US-0017016P.

PR 01-MAY-1997; 97US-00017016.

XX (HARD) HARVARD COLLEGE.

XX Ptashne M, Lu X, Wu Y;

XX WPI; 1998-018502/02.

DR N-PSDB; AAV02567.

XX New transcriptional activator containing DNA binding domain bound to

PT peptide - useful for controlling gene expression, especially in gene

PT therapy, and in protein-protein interaction assays, does not inhibit

PT other transcription activators.

XX Example 1; Page 26; 55pp; English.

XX AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076 are

CC fragments used in an assay to determine novel transcriptional activators.

CC The method involves the production of transcriptional activators
CC comprising of a DNA-binding group and a 6-25 amino acid peptide that is
CC covalently bonded to the DNA binding group and does not represent a
CC fragment of a natural transcription activator. Protein-protein
CC interactions are identified in the assay by fusing a DNA-binding domain
CC to a library of DNA fragments and introducing this and a fusion of target
CC protein and a polypeptide containing a region of Gal4 which interacts
CC with Galp1p into a cell containing Galp1p and identifying members of the
CC library that interact with the target from activation of transcription.
CC Such constructs are used to activate transcription in a cell, e.g. for
CC controlling gene activity, particularly in gene therapy (e.g. recognizing
CC a site close to a selected therapeutic gene). Transcription can be
CC activated without blocking other transcriptional activators. They
CC probably act by interacting with a component of the RNA polymerase II
CC holoenzyme. Gall, the strongest known yeast activator, which provides a
CC more sensitive assay allowing detection of even weak protein-protein
CC interactions. Such activators do not create toxicity problems even when
CC overexpressed
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 16; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 1 FID 3

RESULT 9
AAB06774
ID AAB06774 standard; peptide; 7 AA.
AC AAB06774;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 345.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.

XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA001029.
XX
XX 03-NOV-1998; 98US-00185908.
XX 30-MAR-1999; 99US-00282029.
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin.

XX Claim 73; Page 103; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
XX are cadherins, which are membrane glycoproteins involved in cell
XX adhesion. In some situations, cell adhesion occurs at abnormal levels,
XX and these peptides can be used to modulate these levels, and thus treat
XX autoimmune diseases, inflammatory diseases and cancer, and aid wound

CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present sequence
CC has a cyclic conformation
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 16; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 5 FID 7

RESULT 10
AAB06594
ID AAB06594 standard; peptide; 7 AA.
XX
AC AAB06594;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 227.

XX
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.

XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA001029.

XX
XX 03-NOV-1998; 98US-00185908.
XX 30-MAR-1999; 99US-00282029.
XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin.

XX Claim 55; Page 99; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-3 group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and these peptides
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, they can also be used to facilitate drug delivery
XX to the desired target site. The present sequence has a cyclic
XX conformation

XX Sequence 7 AA;

Query Match 100.0%; Score 16; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 5 FID 7

XX New polymorphic variants of the gene encoding Cytochrome P450 polypeptide
PT 2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.
PT arachidonic acid metabolism, cancer or cardiovascular diseases.
XX
XX
PS Disclosure, Page 58; 178pp; English.
XX
XX The invention describes a new polynucleotide comprises a polynucleotide:
CC (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined
CC in the specification; (b) encoding any of seven polypeptides having 7
CC amino acids, or a polypeptide with 3 amino acids; (c) capable of
CC hybridizing to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)
CC encoding a molecular CYP2C8 variant polypeptide or its fragment. The
CC polynucleotide, gene, vector, polypeptide or antibody is useful for
CC diagnosing or treating a disease, for preparing a diagnostic composition
CC for diagnosing a disease, or for preparing a pharmaceutical composition
CC for treating a disease. This disease includes arachidonic acid
CC metabolism, cancer or cardiovascular diseases. This is the amino acid
CC sequence of a human cytochrome P450 polypeptide 2C8 (CYP2C8) wild type
XX peptide
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 16; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 3 FID 5

RESULT 14
AAB06597
ID AAB06597 standard; peptide; 8 AA.
XX
XX AAB06597;
AC
DT 28-SEP-2000 (first entry)
XX
XX Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 230.
DE
XX Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.

WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA001029.
XX
XX 03-NOV-1998; 98US-00185908.
XX
XX 30-MAR-1999; 99US-00282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI; 2000-365610/31.
XX

Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin.

Claim 55; Page 99; 121pp; English.

The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides

CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation

XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 16; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 6 FID 8

RESULT 15
AAB06777
ID AAB06777 standard; peptide; 8 AA.
XX
XX AAB06777;
AC
DT 28-SEP-2000 (first entry)
XX
XX Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 348.
DE
XX Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
XX Mammalia.

WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA001029.
XX
XX 03-NOV-1998; 98US-00185908.
XX
XX 30-MAR-1999; 99US-00282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI; 2000-365610/31.

Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin.

Claim 73; Page 103; 121pp; English.

The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present sequence
CC has a cyclic conformation

XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 16; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 6 FID 8

Thu Sep 30 13:18:33 2004

us-09-674-716b-13.open.rag

Page 8

Search completed: September 30, 2004, 06:06:24
Job time : 16.6441 secs

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OM protein - protein search, using sw model

Run on: September 30, 2004, 06:01:30 ; Search time 50.339 Seconds
(without alignments)
19.178 Million cell updates/sec

Title: US-09-674-716B-13
Perfect score: 16
Sequence: 1 FID 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799.91 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap.*
- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 3: /cgn2_6/prodata/1/pubpaa/US05_NEW_PUB.pap.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pap.*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pap.*
- 6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pap.*
- 7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pap.*
- 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap.*
- 9: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pap.*
- 10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pap.*
- 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pap.*
- 12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pap.*
- 13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pap.*
- 14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pap.*
- 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pap.*
- 16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pap.*
- 17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pap.*
- 18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 16 | 100.0 | 5 | 8 | US-08-484-409-36 |
| 2 | 16 | 100.0 | 5 | 12 | US-09-920-306-25 |
| 3 | 16 | 100.0 | 6 | 11 | US-09-943-944E-130 |
| 4 | 16 | 100.0 | 7 | 9 | US-09-185-908-174 |
| 5 | 16 | 100.0 | 7 | 9 | US-09-185-908-227 |
| 6 | 16 | 100.0 | 7 | 14 | US-10-190-082-567 |
| 7 | 16 | 100.0 | 8 | 9 | US-09-946-678-8 |
| 8 | 16 | 100.0 | 8 | 9 | US-09-791-378-511 |
| 9 | 16 | 100.0 | 8 | 9 | US-09-185-908-177 |
| 10 | 16 | 100.0 | 8 | 9 | US-09-185-908-230 |
| 11 | 16 | 100.0 | 8 | 10 | US-09-880-748-2842 |
| 12 | 16 | 100.0 | 8 | 12 | US-10-293-418-2842 |
| 13 | 16 | 100.0 | 8 | 12 | US-10-601-100-92 |
| 14 | 16 | 100.0 | 8 | 12 | US-10-601-100-108 |
| 15 | 16 | 100.0 | 8 | 12 | US-09-791-377-511 |

| | | | | | |
|----|-------|----|----|---------------------|--------------------|
| 16 | 100.0 | 8 | 14 | US-10-190-082-501 | Sequence 501, App |
| 17 | 100.0 | 8 | 16 | US-10-712-425-1352 | Sequence 1352, App |
| 18 | 100.0 | 9 | 9 | US-09-185-908-180 | Sequence 180, App |
| 19 | 100.0 | 9 | 9 | US-09-185-908-233 | Sequence 233, App |
| 20 | 100.0 | 9 | 10 | US-09-932-165-862 | Sequence 862, App |
| 21 | 100.0 | 9 | 10 | US-09-932-165-1235 | Sequence 1235, App |
| 22 | 100.0 | 9 | 12 | US-10-363-791-121 | Sequence 121, App |
| 23 | 100.0 | 10 | 9 | US-09-757-417-45 | Sequence 45, App1 |
| 24 | 100.0 | 10 | 10 | US-09-572-404B-644 | Sequence 644, App |
| 25 | 100.0 | 10 | 10 | US-09-572-404B-1464 | Sequence 1464, App |
| 26 | 100.0 | 10 | 10 | US-09-572-404B-2015 | Sequence 2015, App |
| 27 | 100.0 | 10 | 10 | US-09-572-404B-2017 | Sequence 2017, App |
| 28 | 100.0 | 10 | 10 | US-09-572-404B-3882 | Sequence 3882, App |
| 29 | 100.0 | 10 | 10 | US-09-572-404B-3883 | Sequence 3883, App |
| 30 | 100.0 | 10 | 10 | US-09-932-165-153 | Sequence 153, App |
| 31 | 100.0 | 10 | 10 | US-09-932-165-356 | Sequence 356, App |
| 32 | 100.0 | 10 | 10 | US-09-932-165-563 | Sequence 563, App |
| 33 | 100.0 | 10 | 10 | US-09-932-165-583 | Sequence 583, App |
| 34 | 100.0 | 10 | 10 | US-09-932-165-1361 | Sequence 1361, App |
| 35 | 100.0 | 10 | 10 | US-09-573-822C-8 | Sequence 8, App11 |
| 36 | 100.0 | 10 | 10 | US-09-573-822C-693 | Sequence 693, App |
| 37 | 100.0 | 10 | 14 | US-10-042-945-45 | Sequence 45, App1 |
| 38 | 100.0 | 10 | 16 | US-10-327-598-462 | Sequence 462, App |
| 39 | 100.0 | 11 | 9 | US-09-817-310-5 | Sequence 5, App11 |
| 40 | 100.0 | 11 | 12 | US-10-372-876-560 | Sequence 560, App |
| 41 | 100.0 | 11 | 14 | US-10-097-065-560 | Sequence 560, App |
| 42 | 100.0 | 12 | 9 | US-09-214-371-27 | Sequence 27, App1 |
| 43 | 100.0 | 12 | 9 | US-09-214-371-63 | Sequence 63, App1 |
| 44 | 100.0 | 12 | 12 | US-10-609-217-136 | Sequence 136, App |
| 45 | 100.0 | 12 | 12 | US-10-632-388-136 | Sequence 136, App |

ALIGNMENTS

RESULT 1
US-08-484-409-36
; Sequence 36, Application US/08484409
; Publication No. US20020076412A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Zamvil, Scott
; TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7032
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,409
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 690068.409C1
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

US-08-484-409-36

Query Match 100.0%; Score 16; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 3 FID 5

RESULT 2

US-09-920-306-25
; Sequence 25, Application US/09920305
; Publication No. US20040029808A1
; GENERAL INFORMATION:
; APPLICANT: Unilever PLC
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for
; FILE REFERENCE: Peptide Mimotopes
; CURRENT APPLICATION NUMBER: US/09/920.306
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: EP00306613.1
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-920-306-25

Query Match 100.0%; Score 16; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 3 FID 5

RESULT 3

US-09-943-944E-130
; Sequence 130, Application US/09943944E
; Publication No. US20040014036A1
; GENERAL INFORMATION:
; APPLICANT: Ptashne, et al.,
; TITLE OF INVENTION: Transcriptional Activation System, Activators, and Uses
; FILE REFERENCE: Therefor
; FILE REFERENCE: 0342941-0065
; CURRENT APPLICATION NUMBER: US/09/943.944E
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Random peptide
US-09-943-944E-130

Query Match 100.0%; Score 16; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||

Db 1 FID 3

RESULT 4

US-09-185-908-174
; Sequence 174, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185.908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; OTHER INFORMATION: sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-174

Query Match 100.0%; Score 16; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 5 FID 7

RESULT 5

US-09-185-908-227
; Sequence 227, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185.908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 227
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-227

Query Match 100.0%; Score 16; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 5 FID 7

RESULT 6

```

US-10-190-082-567
; Sequence 567, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Lasky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P190581
; CURRENT APPLICATION NUMBER: US/10/190.082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 567
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-567

Query Match      100.0%; Score 16; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      4 FID 6

RESULT 7
US-09-946-678-8
; Sequence 8, Application US/09946678
; Patent No. US20020106782A1
; GENERAL INFORMATION:
; APPLICANT: ITO, Kotaro
; APPLICANT: KOYAMA, Yasuji
; TITLE OF INVENTION: Protein Having Glutaminase Activity and Gene Encoding the Same
; FILE REFERENCE: 0283-0158P
; CURRENT APPLICATION NUMBER: US/09/946.678
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: JP 2000-270371
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Cryptococcus nodansensis
US-09-946-678-8

Query Match      100.0%; Score 16; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      2 FID 4

RESULT 8
US-09-791-378-511
; Sequence 511, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791.378
; CURRENT FILING DATE: 2001-02-23

US-10-190-082-567
; Sequence 567, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Lasky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P190581
; CURRENT APPLICATION NUMBER: US/10/190.082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 567
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-567

Query Match      100.0%; Score 16; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      4 FID 6

RESULT 7
US-09-946-678-8
; Sequence 8, Application US/09946678
; Patent No. US20020106782A1
; GENERAL INFORMATION:
; APPLICANT: ITO, Kotaro
; APPLICANT: KOYAMA, Yasuji
; TITLE OF INVENTION: Protein Having Glutaminase Activity and Gene Encoding the Same
; FILE REFERENCE: 0283-0158P
; CURRENT APPLICATION NUMBER: US/09/946.678
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: JP 2000-270371
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Cryptococcus nodansensis
US-09-946-678-8

Query Match      100.0%; Score 16; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      2 FID 4

RESULT 8
US-09-791-378-511
; Sequence 511, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791.378
; CURRENT FILING DATE: 2001-02-23

US-09-185-908-177
; Sequence 177, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185.908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 177
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; OTHER INFORMATION: sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-177

Query Match      100.0%; Score 16; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      6 FID 8

RESULT 9
US-09-185-908-177
; Sequence 177, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185.908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 177
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; OTHER INFORMATION: sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-177

Query Match      100.0%; Score 16; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      6 FID 8

RESULT 10
US-09-185-908-230
; Sequence 230, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185.908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 230
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

OTHER INFORMATION: Description of Artificial Sequence: Product of
 OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
 FEATURE:
 OTHER INFORMATION: Cyclic Peptide
 US-09-183-908-230

Query Match 100.0%; Score 16; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 |||
 Db 6 FID 8

RESULT 11
 US-09-880-748-2842
 ; Sequence 2842, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2842
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-2842

Query Match 100.0%; Score 16; DB 10; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 |||
 Db 5 FID 7

RESULT 12
 US-10-293-418-2842
 ; Sequence 2842, Application US/10293418
 ; Publication No. US20030223996A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF53P2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248

OTHER INFORMATION: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17
 PRIOR APPLICATION NUMBER: 60/212,210
 PRIOR FILING DATE: 2000-06-16
 NUMBER OF SEQ ID NOS: 3247
 SEQ ID NO 2842
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-293-418-2842

Query Match 100.0%; Score 16; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 |||
 Db 5 FID 7

RESULT 13
 US-10-601-100-92
 ; Sequence 92, Application US/10601100
 ; Publication No. US20040072261A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INNOGENETICS N.V.
 ; TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of
 ; FILE REFERENCE: 11362.0038.NFUS01
 ; CURRENT APPLICATION NUMBER: US/10/601,100
 ; CURRENT FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: EP 02447121.1
 ; PRIOR FILING DATE: 2002-06-21
 ; PRIOR APPLICATION NUMBER: US 60/396,437
 ; PRIOR FILING DATE: 2002-07-17
 ; NUMBER OF SEQ ID NOS: 113
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 92
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-601-100-92

Query Match 100.0%; Score 16; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 |||
 Db 2 FID 4

RESULT 14
 US-10-601-100-108
 ; Sequence 108, Application US/10601100
 ; Publication No. US20040072261A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INNOGENETICS N.V.
 ; TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of
 ; FILE REFERENCE: 11362.0038.NFUS01
 ; CURRENT APPLICATION NUMBER: US/10/601,100
 ; CURRENT FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: EP 02447121.1
 ; PRIOR FILING DATE: 2002-06-21
 ; PRIOR APPLICATION NUMBER: US 60/396,437
 ; PRIOR FILING DATE: 2002-07-17
 ; NUMBER OF SEQ ID NOS: 113
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 108
 ; LENGTH: 8
 ; TYPE: PRT

; ORGANISM: homo sapiens
US-10-601-100-108

Query Match 100.0%; Score 16; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
|||
Db 5 FID 7

RESULT 15

US-09-791-377-511
; Sequence 511, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parakh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 511
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-377-511

Query Match 100.0%; Score 16; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
|||
Db 2 FID 4

Search completed: September 30, 2004, 06:54:53
Job time : 50.339 secs

Blank Sheet

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:29:27; Search time 13.7964 Seconds
(without alignments)
4852.647 Million cell updates/sec

Title: US-09-674-716B-17
Perfect score: 619
Sequence: 1 Gattattgtgactcagtc.....agatcaaacgtacggtggct 348

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09674716@cgn_1152@runat_30092004_070259_25882 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 522 | 84.3 | 136 | 2 S40357 | Ig kappa chain V-J |
| 2 | 518 | 83.7 | 135 | 2 S40342 | Ig kappa chain - h |
| 3 | 517 | 83.5 | 125 | 2 S40356 | Ig kappa chain V-I |
| 4 | 506 | 81.7 | 113 | 1 K2HUTM | Ig light chain V r |
| 5 | 504 | 81.4 | 112 | 2 S58207 | Ig kappa chain - h |
| 6 | 502.5 | 81.2 | 130 | 2 S40321 | Ig kappa chain V r |
| 7 | 500 | 80.8 | 132 | 2 S26882 | Ig kappa chain - h |
| 8 | 497 | 80.3 | 121 | 2 S40371 | Ig kappa chain pre |
| 9 | 494 | 79.8 | 117 | 1 K2HUGM | Ig kappa chain V-I |
| 10 | 493.5 | 79.7 | 115 | 1 K2HUCM | Ig light chain V r |
| 11 | 492 | 79.5 | 112 | 2 S58206 | Ig kappa chain V r |
| 12 | 490 | 79.2 | 113 | 1 K2HUCM | Ig kappa chain - h |
| 13 | 489.5 | 79.1 | 126 | 2 S40339 | Ig kappa chain V-J |
| 14 | 484 | 78.2 | 131 | 2 S40372 | Ig kappa chain V-J |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 15 | 483 | 78.0 | 112 | 1 KVM516 | Ig kappa chain V r |
| 16 | 481 | 77.7 | 113 | 1 K2HUFH | Ig kappa chain V-I |
| 17 | 481 | 77.7 | 133 | 2 S40324 | Ig kappa chain V r |
| 18 | 476 | 76.9 | 124 | 2 S03876 | Ig kappa chain V-I |
| 19 | 475 | 76.7 | 133 | 2 S23230 | Ig kappa chain pre |
| 20 | 473.5 | 76.5 | 126 | 2 S40341 | Ig kappa chain - h |
| 21 | 473 | 76.4 | 133 | 1 K2HURP | Ig kappa chain pre |
| 22 | 472.5 | 76.3 | 114 | 2 S40340 | Ig kappa chain V-J |
| 23 | 472.5 | 76.3 | 127 | 2 S40323 | Ig kappa chain - h |
| 24 | 469.5 | 75.8 | 140 | 2 S22858 | Ig kappa chain pre |
| 25 | 468 | 75.6 | 122 | 2 S40338 | Ig kappa chain - h |
| 26 | 465 | 75.1 | 112 | 2 PL0275 | Ig kappa chain V r |
| 27 | 465 | 75.1 | 133 | 1 A24452 | Ig kappa chain pre |
| 28 | 465 | 75.1 | 142 | 2 S22902 | Ig kappa chain V r |
| 29 | 464.5 | 75.0 | 114 | 2 S49572 | Ig kappa chain pre |
| 30 | 463.5 | 74.9 | 112 | 1 K2HUML | Ig kappa chain V-I |
| 31 | 462 | 74.6 | 126 | 2 S40312 | HUNK protein prec |
| 32 | 462 | 74.6 | 133 | 2 S42611 | Ig kappa chain (WM |
| 33 | 461 | 74.5 | 197 | 2 S29593 | Ig kappa chain V r |
| 34 | 460.5 | 74.4 | 123 | 2 S40319 | Ig kappa chain V r |
| 35 | 460 | 74.3 | 112 | 2 I26317 | Ig kappa chain V r |
| 36 | 458 | 74.0 | 112 | 2 I26317 | Ig kappa chain V r |
| 37 | 458 | 74.0 | 112 | 2 F26317 | Ig kappa chain V r |
| 38 | 457 | 73.8 | 112 | 2 D26317 | Ig kappa chain V r |
| 39 | 455 | 73.5 | 112 | 2 B26317 | Ig kappa chain V r |
| 40 | 455 | 73.5 | 120 | 1 KVM567 | Ig kappa chain pre |
| 41 | 454 | 73.3 | 112 | 2 G26317 | Ig kappa chain V r |
| 42 | 453.5 | 73.3 | 114 | 2 B49002 | Ig kappa chain - h |
| 43 | 453 | 73.2 | 118 | 2 S40374 | Ig kappa chain pre |
| 44 | 453 | 73.2 | 131 | 2 B30577 | Ig kappa chain V r |
| 45 | 452 | 73.0 | 118 | 2 PT0359 | Ig kappa chain V r |

ALIGNMENTS

RESULT 1
S40357
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40357
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40357
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-136 <KLE>
A:Cross-references: EMBL:X72467
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

| | | | | |
|--|------------------------|---|---------------|-----|
| Alignment Scores: | | 1.2e-44 | Length: | 136 |
| Pred. No.: | Score: | 522.00 | Matches: | 101 |
| Percent Similarity: | Percent Similarity: | 93.10% | Conservative: | 7 |
| Best Local Similarity: | Best Local Similarity: | 87.07% | Mismatches: | 8 |
| Query Match: | Query Match: | 84.33% | Indels: | 0 |
| DB: | DB: | 2 | Gaps: | 0 |
| US-09-674-716B-17 (1-348) x S40357 (1-136) | | | | |
| QY | 1 | GATATTGTGATCACTCAGTCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGGCGCTCC | 60 | |
| Db | 21 | AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer | 40 | |
| QY | 61 | ATCTCTGTCGCTCAGTAAGAGTCTCTGTATAGGATGGAGACATCTTGATTTGG | 120 | |
| Db | 41 | IleSerCysArgSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTyr | 60 | |
| QY | 121 | TACCTGCAGAGCCAGGCGAGTCCTCCACAGCTCTGATGATTTGATTCACCCCGGCA | 180 | |

DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x K2HUCM (1-117)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCCCTGGAGAGCGGCTCC 60

Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24

QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTCTGTAAGAGTGGGAAGACATCTTGAATTGG 120

Db 25 IleSerCysArgSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTyr 44

QY 121 TACTGTCAGAGCAGGCGAGTCTCCAGCTCTCTGATCTATTGATGTCACCCGGGCA 180

Db 45 TyrLeuGlnLysProGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 64

QY 181 TCAGGGTCTCCACAGGTCAGTGGCAGTGGTACAGGACAGATTTTACACTGAAATC 240

Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 84

QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCACAGCTGGTAGAGTATCCA 300

Db 85 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyLeuGlnThrPro 104

QY 301 TTCACGTCGCGCAAGGACCAAGGTGGAGATCAAAAGT 339

Db 105 GlnThrPheGlyGlnGlyThrLysValGluLeuLysArg 117

RESULT 10

K2HUCM

Ig kappa chain V-II region (Cum) - human

C:Species: Homo sapiens (man)

C:Date: 24-Apr-1994 #sequence_revision 02-Jul-1998 #text_change 02-Jul-1998

C:Accession: B91639; MUID:68242259; S02576

R:Hiltschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967

A:Title: Die voltaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).

A:Reference number: A91639; MUID:68242259; PMID:5586923

A:Accession: B91639

A:Molecule type: protein

A:Residues: 1-49, 'Q', 'S', '53-95, 'QM', '98-115 <HIL>

A:Note: the sequence of the C region, which has the Inv (3) marker, is also given

R:Hiltschmann, N.

Naturwissenschaften 56, 195-205, 1969

A:Title: Die molekularen Grundlagen der Antikoeperbildung.

A:Reference number: A93409; MUID:70063440; PMID:4188189

A:Accession: A93409

A:Molecule type: protein

A:Residues: 1-115 <Hiz>

R:Steiner, V.; Chang, J.Y.

FEBS Lett. 222, 6-10, 1987

A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the

A:Reference number: S02572; MUID:89005152; PMID:3115831

A:Contents: annotation

C:Comment: This is a Bence Jones protein.

C:Genetics:

A:Gene: IGHV2

A:Cross-references: GDB:136265

A:Map position: 2p12-2p12

C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds; in some cases, such as Iga and IgM, the subunits associate into larger complexes.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:17-97/Domain: immunoglobulin homology <IMM>

F:24-95/Disulfide bonds: #status predicted

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 9,07e-42 | Length: | 115 |
| Score: | 493.50 | Matches: | 96 |
| Percent Similarity: | 91.23% | Conservative: | 8 |
| Best Local Similarity: | 84.21% | Mismatches: | 9 |
| Query Match: | 79.73% | Indels: | 1 |
| DB: | 1 | Gaps: | 1 |

US-09-674-716B-17 (1-348) x K2HUCM (1-115)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCCCTGGAGAGCGGCTCC 60

Db 2 AspIleValMetThrGlnThrProLeuSerLeuProValThrProGlyGluProAlaSer 21

QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTCTGTAAGAGTGGGAAGACATCTTGAATTGG 117

Db 22 IleSerCysArgSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAsn 41

QY 118 TGGTACCTGTCAGAGCCAGGCGAGTCTCCAGCTCTCTGATCTATTGATGTCACCCGG 177

Db 42 TrpTyrLeuGlnLysAlaGlyGlnSerProGlnLeuLeuLeuTyrThrLeuSerTyrArg 61

QY 178 GCATCAGGGTCTCCAGCTGAGTGGCAGTGGTACAGGACAGATTTTACACTGAAATC 237

Db 62 AlaSerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLys 81

QY 238 ATCAGCAGAGTGGAGTGGAGTGGTGGGTTTATTACTGTCACAGCTGGTAGAGTAT 297

Db 82 IleSerArgValGlnAlaGluAspValGlyValTyrCysMetGlnArgLeuGluLeu 101

QY 298 CCATTACGTTCCGCAAGGACCAAGGTGGAGATCAAAAGT 339

Db 102 ProTyrThrPheGlyGlnGlyThrLysLeuGluLeuArgArg 115

RESULT 11

S58206

Ig light chain V region anti-F(ab')2 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000

C:Accession: S58206

R:Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebl, S.; Breitling, I.

Submitted to the EMBL Data Library, July 1995

A:Description: Characterization of heavy and light chain immunoglobulin variable region

A:Reference number: S58206

A:Accession: S58206

A:Molecule type: mRNA

A:Residues: 1-112 <WEL>

A:Cross-references: EMBL:X89054; NID:G929640; PID:CAA61441.1; PID:G929641

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 1,29e-41 | Length: | 112 |
| Score: | 492.00 | Matches: | 95 |
| Percent Similarity: | 90.18% | Conservative: | 6 |
| Best Local Similarity: | 84.82% | Mismatches: | 11 |
| Query Match: | 79.48% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-09-674-716B-17 (1-348) x S58206 (1-112)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCCCTGGAGAGCGGCTCC 60

Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20

QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTCTGTAAGAGTGGGAAGACATCTTGAATTGG 120

Db 21 IleSerCysArgSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrPheAspTyr 40

QY 121 TACTGTCAGAGCCAGGCGAGTCTCCAGCTCTCTGATCTATTGATGTCACCCGGGCA 180

Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 60

QY 181 TCAGGGTCTCCAGAGTTCAGTGGCAGTGGTACAGCAGATTTTACACTGAAATC 240

Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80

QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCACAGCTGGTAGAGTATCCA 300

```

Db      81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 100
      |||
QY      301 TTCAGTTCGGCCCAAGGACCAAGTGGAGATCAAA 336
      |||
Db      101 LeuThrPheGlyGlyThrLysValGluLeuLys 112
      |||
RESULT 12
KWS51
Ig kappa chain V region (M511) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C:Accession: A01910
R:Appella, E.
Mol Immunol. 17, 711-718, 1980
A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine
A:Reference number: A01910; MUID:81052016; PMID:6776396
A:Accession: A01910
A:Molecule type: protein
A:Residues: 1-113 <App>
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 2,05e-41 Length: 113
Score: 490.00 Matches: 95
Percent Similarity: 90.27% Conservatve: 7
Best Local Similarity: 84.07% Mismatches: 11
Query Match: 79.16% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x KWS51 (1-113)

QY      1 GATATTGTGATCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGACCGGCTCC 60
      |||
Db      1 AspileValIleThrGlnAspGluLeuSerLysProValThrSerGlyGluSerValSer 20
      |||
QY      61 ATCTCTCTGCTCGCTGAGTACAGTCTCTCTATAGGATGGAGACATATCTGATTGG 120
      |||
Db      21 IleSerCysArgSerLysSerLeuLeuTyrLysAspGlyLysThrThrLeuAsnTrp 40
      |||
QY      121 TACCTGCAGAACCCAGGCGAGTCTCCACAGTCTCTGATCTATTGATGTCCACCCGGGCA 180
      |||
Db      41 PheLeuGlnGlyProGlnGlnSerProArgLeuLeuIleTyrLeuMetSerThrArgAla 60
      |||
QY      181 TCAGGGTCCCTGACAGTTCAGTGGCAGGATGATCAGGACACAGATTTCACCTGAAATC 240
      |||
Db      61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluIle 80
      |||
QY      241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTATTATTACGTCAACAGCTGGTAGAGTATCCA 300
      |||
Db      81 SerArgValLysAlaGluAspValGlyValTyrCysGlnGlnLeuValGluTyrPro 100
      |||
QY      301 TTCAGTTCGGCCCAAGGACCAAGTGGAGATCAAAAGT 339
      |||
Db      101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuLysArg 113
      |||
RESULT 13
S40339
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40339
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40339

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A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-126 <LE>
A:Cross-references: EMBL:X72449; NID:9441366; PIDN:CAA51117.1; PID:9441367
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-110/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2.3e-41 Length: 126
Score: 489.50 Matches: 96
Percent Similarity: 92.86% Conservatve: 8
Best Local Similarity: 85.71% Mismatches: 7
Query Match: 79.08% Indels: 1
DB: 2 Gaps: 1

US-09-674-716B-17 (1-348) x S40339 (1-126)

QY      1 GATATTGTGATCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGACCGGCTCC 60
      |||
Db      16 AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 35
      |||
QY      61 ATCTCTCTGCTCGCTGAGTACAGTCTCTCTATAGGATGGAGACATATCTGATTGG 120
      |||
Db      36 IleSerCysArgSerSerGlnSerLeuLeuHisIleAsnGlyTyrAsnTyrLeuAspTrp 55
      |||
QY      121 TACCTGCAGAACCCAGGCGAGTCTCCACAGTCTCTGATCTATTGATGTCCACCCGGGCA 180
      |||
Db      56 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 75
      |||
QY      181 TCAGGGTCCCTGACAGTTCAGTGGCAGTGGATGATCAGGACACAGATTTTACACTGAAATC 240
      |||
Db      76 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 95
      |||
QY      241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTATTATTACGTCAACAGCTGGTAGAGTATCCA 300
      |||
Db      96 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGln---Pro 114
      |||
      |||
QY      301 TTCAGTTCGGCCCAAGGACCAAGTGGAGATCAAA 336
      |||
Db      115 TrpThrPheGlyGlnGlyThrLysValGluLeuLys 126
      |||
RESULT 14
S40372
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40372
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40372
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <LE>
A:Cross-references: EMBL:X72482; NID:9441432; PIDN:CAA51150.1; PID:9441433
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 8.28e-41 Length: 131
Score: 484.00 Matches: 92
Percent Similarity: 91.89% Conservatve: 10
Best Local Similarity: 82.88% Mismatches: 9
Query Match: 78.19% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-17 (1-348) x S40372 (1-131)

QY      1 GATATTGTGATCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGACCGGCTCC 60
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Db 21 AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluSerAlaSer 40
Qy 61 ATCTCTGTCGTCGAGTAAAGTCTCCGTGTATAGGATGGGAAGACATCTGTAATTGG 120
Db 41 PheSerCysIysThrSerGlnSerLeuLeuHisSerAsnGlyHisAsnTyrLeuAspTrp 60
Qy 121 TACTCTCAGAACCCAGGAGCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerThrArgAla 80
Qy 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAAATC 240
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
Qy 241 AGCAGAGTGGAGGCTGAGGATGTGGGTTTATTCTGTCAACAGCTGGTAGAGTATCCA 300
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnProLeuGlnThrPro 120
Qy 301 TTCACGTTCCGCCCAAGGACCAAGGTGGAGATC 333
Db 121 TyrThrPheGlyGlnGlyThrLysLeuGluIle 131

RESULT 15
KVMS16
Ig kappa chain V region (M167) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
C:Accession: A01908
R:Rudikoff, S.; Potter, M.
Biochemistry 17, 2703-2707, 1978
A:Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma protein
A:Reference number: A01908; MUID:79000273; PMID:99160
A:Accession: A01908
A:Molecule type: protein
A:Residues: 1-112 <RUD>
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 1.04e-40 Length: 112
Score: 483.00 Matches: 94
Percent Similarity: 90.18% Conservative: 7
Best Local Similarity: 83.93% Mismatches: 11
Query Match: 78.03% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x KVMS16 (1-112)

Qy 1 CATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCAGCCCTGAGAGCGCGCTCC 60
Db 1 AspileValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
Qy 61 ATCTCTGTCGTCGAGTAAAGTCTCCGTGTATAGGATGGGAAGACATCTGTAATTGG 120
Db 21 IleSerCysArgSerSerLysSerLeuLysLysAspGlyLysThrTyrLeuAsnTrp 40
Qy 121 TACTCTCAGAACCCAGGAGCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180
Db 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleSerLeuMetSerThrArgAla 60
Qy 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAAATC 240
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80
Qy 241 AGCAGAGTGGAGGCTGAGGATGTGGGTTTATTCTGTCAACAGCTGGTAGAGTATCCA 300
Db 81 SerArgValLysAlaGluAspValGlyValTyrCysGlnGlnLeuValGluLysPro 100

Qy 301 TTCACGTTCCGCCCAAGGACCAAGGTGGAGATCAAA 336
Db 101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuLys 112

Search completed: September 30, 2004, 08:57:03
Job time : 15.7964 secs

Blank sheet

OM protein - protein search, using sw model

Run on: September 30, 2004, 06:00:45 ; Search time 5.08475 Seconds
(without alignments)
30.459 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
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3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----|--------------------|
| 1 | 16 | 100.0 | 7 | 1 | US-08-197-792-25 |
| 2 | 16 | 100.0 | 7 | 1 | US-08-459-850-25 |
| 3 | 16 | 100.0 | 7 | 1 | US-08-459-214-25 |
| 4 | 16 | 100.0 | 8 | 3 | US-09-042-071-52 |
| 5 | 16 | 100.0 | 8 | 4 | US-09-946-678-8 |
| 6 | 16 | 100.0 | 9 | 4 | US-09-359-304B-2 |
| 7 | 16 | 100.0 | 9 | 4 | US-09-359-304B-5 |
| 8 | 16 | 100.0 | 9 | 4 | US-09-359-304B-7 |
| 9 | 16 | 100.0 | 9 | 4 | US-09-000-217-2 |
| 10 | 16 | 100.0 | 9 | 4 | US-09-341-982-67 |
| 11 | 16 | 100.0 | 10 | 1 | US-08-277-007-1 |
| 12 | 16 | 100.0 | 10 | 1 | US-08-485-181-1 |
| 13 | 16 | 100.0 | 10 | 2 | US-08-964-338-1 |
| 14 | 16 | 100.0 | 10 | 3 | US-08-975-917-1 |
| 15 | 16 | 100.0 | 11 | 4 | US-09-817-310-5 |
| 16 | 16 | 100.0 | 11 | 5 | PCT-US92-01433A-6 |
| 17 | 16 | 100.0 | 12 | 1 | US-08-434-255-15 |
| 18 | 16 | 100.0 | 12 | 1 | US-08-459-967-15 |
| 19 | 16 | 100.0 | 12 | 1 | US-08-460-327-15 |
| 20 | 16 | 100.0 | 12 | 1 | US-08-459-871-15 |
| 21 | 16 | 100.0 | 12 | 4 | US-09-517-439-27 |
| 22 | 16 | 100.0 | 12 | 4 | US-09-428-082B-136 |
| 23 | 16 | 100.0 | 12 | 5 | PCT-US91-02942-70 |
| 24 | 16 | 100.0 | 13 | 4 | US-09-690-454-84 |
| 25 | 16 | 100.0 | 13 | 4 | US-10-053-485-55 |
| 26 | 16 | 100.0 | 13 | 4 | US-09-834-759-501 |
| 27 | 16 | 100.0 | 14 | 1 | US-07-620-426B-15 |

28 16 100.0 14 1 US-07-620-426B-16
29 16 100.0 14 1 US-07-662-007B-15
30 16 100.0 14 1 US-07-662-007B-15
31 16 100.0 14 1 US-07-824-247-15
32 16 100.0 14 1 US-07-824-247-16
33 16 100.0 14 2 US-08-695-412B-7
34 16 100.0 14 2 US-08-574-959A-18
35 16 100.0 14 3 US-08-470-204A-15
36 16 100.0 14 3 US-08-470-204A-16
37 16 100.0 14 3 US-08-622
38 16 100.0 14 3 US-09-357-014-18
39 16 100.0 14 4 US-09-165-922A-7
40 16 100.0 15 1 US-08-325-553-10
41 16 100.0 15 1 US-08-527-113-1
42 16 100.0 15 2 US-08-432-871C-88
43 16 100.0 15 2 US-08-934-222-52
44 16 100.0 15 2 US-08-394-152A-10
45 16 100.0 15 2 US-08-933-402-52

ALIGNMENTS

RESULT 1
US-08-197-792-25
; Sequence 25, Application US/08197792
; Patent No. 5525488
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin and
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,792
FILING DATE: 16-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/958414
FILING DATE: 08-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744207
FILING DATE: 12-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
FILING DATE: 05-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/906729
FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/783910
FILING DATE: 03-OCT-1985
ATTORNEY/AGENT INFORMATION:
NAME: Haak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 297P2D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881

TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 25;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-197-792-25

Query Match 100.0%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 4 FID 6

RESULT 2
US-08-459-850-25
; Sequence 25, Application US/08459850
; Patent No. 5665568

; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptides
; TITLE OF INVENTION: Using such Nucleic Acid
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,850
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/197792
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/958414
FILING DATE: 08-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744207
FILING DATE: 12-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
FILING DATE: 05-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/906729
FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/783910
FILING DATE: 03-OCT-1985
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 297P2D5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 25;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-850-25

Query Match 100.0%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 4 FID 6

RESULT 3

US-08-459-214-25
; Sequence 25, Application US/08459214
; Patent No. 5716810

; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptides
; TITLE OF INVENTION: Using such Nucleic Acid
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,214
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/197792
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/958414
FILING DATE: 08-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744207
FILING DATE: 12-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
FILING DATE: 05-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/906729
FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/783910
FILING DATE: 03-OCT-1985
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 297P2D6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 25.

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-214-25

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 7;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3-
Db 4 FID 6

RESULT 4
US-09-042-071-52
; Sequence 52, Application US/09042071
; Patent No. 6294372
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Kay, William W.
; TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM
; TITLE OF INVENTION: SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING
; TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,071
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.407
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-042-071-52

Query Match
Best Local Similarity 100.0%; Score 16; DB 3; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 2 FID 4

RESULT 5
US-09-946-678-8
; Sequence 8, Application US/09946678
; Patent No. 6541236
; GENERAL INFORMATION:
; APPLICANT: ITO, Kotaro
; APPLICANT: UMITSUKI, Genryou

; APPLICANT: KOYAMA, Yasuji
; TITLE OF INVENTION: Protein Having Glutaminase Activity and Gene Encoding the Same
; FILE REFERENCE: 0283-0158P
; CURRENT APPLICATION NUMBER: US/09/946,678
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: JP 2000-270371
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Cryptococcus nodaensis
US-09-946-678-8

Query Match
Best Local Similarity 100.0%; Score 16; DB 4; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 2 FID 4

RESULT 6
US-09-359-304B-2
; Sequence 2, Application US/09359304B
; Patent No. 6468745
; GENERAL INFORMATION:
; APPLICANT: FITZMAURICE, Wayne P.
; APPLICANT: LINDBO, John A.
; APPLICANT: PADGETT, Hal S.
; APPLICANT: POGUE, Gregory P.
; TITLE OF INVENTION: METHOD FOR EXPRESSING A LIBRARY OF
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE VARIANTS AND SELECTING DESIRED TRAITS
; FILE REFERENCE: 008010137US02
; CURRENT APPLICATION NUMBER: US/09/359,304B
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Tobacco mosaic virus
US-09-359-304B-2

Query Match
Best Local Similarity 100.0%; Score 16; DB 4; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 3 FID 5

RESULT 7
US-09-359-304B-5
; Sequence 5, Application US/09359304B
; Patent No. 6468745
; GENERAL INFORMATION:
; APPLICANT: FITZMAURICE, Wayne P.
; APPLICANT: LINDBO, John A.
; APPLICANT: PADGETT, Hal S.
; APPLICANT: POGUE, Gregory P.
; TITLE OF INVENTION: METHOD FOR EXPRESSING A LIBRARY OF
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE VARIANTS AND SELECTING DESIRED TRAITS
; FILE REFERENCE: 008010137US02
; CURRENT APPLICATION NUMBER: US/09/359,304B
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 9
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; TYPE: PRT
; ORGANISM: Tobacco mosaic virus
US-09-359-304B-5

Query Match 100.0%; Score 16; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 3 FID 5

RESULT 8
US-09-359-304B-7

; Sequence 7, Application US/09359304B
; Patent No. 6468745
; GENERAL INFORMATION:
; APPLICANT: FITZMAURICE, Wayne P.
; APPLICANT: LINDBO, John A.
; APPLICANT: PADGETT, Hal S.
; APPLICANT: POQUE, Gregory P.
; TITLE OF INVENTION: METHOD FOR EXPRESSING A LIBRARY OF
; FILE REFERENCE: 008010137US02
; CURRENT APPLICATION NUMBER: US/09/359,304B
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Tobacco mosaic virus
US-09-359-304B-7

Query Match 100.0%; Score 16; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 3 FID 5

RESULT 9
US-09-000-217-2

; Sequence 2, Application US/09000217A
; Patent No. 6521598
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Ils A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: The H-Y Antigen
; FILE REFERENCE: Sequence ID No. 6521598. 1-9 for 294-43
; Patent No. 6521598
; CURRENT APPLICATION NUMBER: US/09/000,217A
; CURRENT FILING DATE: 1998-06-26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-000-217-2

Query Match 100.0%; Score 16; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 1 FID 3

RESULT 10
US-09-341-982-67
; Sequence 67, Application US/09341982
; Patent No. 6586671
; GENERAL INFORMATION:
; APPLICANT: SLINGLUFF, Craig L.
; APPLICANT: HUNT, Donald F.
; APPLICANT: ENGELHARD, Victor H.
; APPLICANT: KITTELSEN, David
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
; FILE REFERENCE: SLINGLUFF=3B
; CURRENT APPLICATION NUMBER: US/09/341,982
; CURRENT FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: PCT/US98/01592
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/037,781
; EARLIER FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: human protein
US-09-341-982-67

Query Match 100.0%; Score 16; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 1 FID 3

RESULT 11

US-08-277-007-1
; Sequence 1, Application US/08277007
; Patent No. 5538883

; GENERAL INFORMATION:
; APPLICANT: NISHIMOTO, Tomoyuki
; APPLICANT: CHAEN, Hiroto
; APPLICANT: SUGIMOTO, Toshiyuki
; APPLICANT: MIYAKE, Toshio
; TITLE OF INVENTION: MALTOSE-TREHALOSE CONVERTING ENZYME, AND
; PREPARATION AND USES THEREOF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,007
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 199971/1993
; FILING DATE: 20-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 144092/1994
; FILING DATE: 03-JUN-1994

ATTORNEY/AGENT INFORMATION:
NAME: NEIMARK, Sheridan
REGISTRATION NUMBER: 20,520
REFERENCE/DOCKET NUMBER: NISHIMOTO-2
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-277-007-1

Query Match 100.0%; Score 16; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 8 FID 10

RESULT 13
US-08-964-338-1
Sequence 1, Application US/08964338
Patent No. 5965411
GENERAL INFORMATION:
APPLICANT: NISHIMOTO, Tomoyuki
APPLICANT: CHAEN, Hiroto
APPLICANT: SUGIMOTO, Toshiyuki
APPLICANT: MIYAKE, Toshio
TITLE OF INVENTION: MALTULOSE-TREHALOSE CONVERTING ENZYME, AND
TITLE OF INVENTION: PREPARATION AND USES THEREOF
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,338
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277,007
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 144092/1994
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: NEIMARK, Sheridan
REGISTRATION NUMBER: 20,520
REFERENCE/DOCKET NUMBER: NISHIMOTO-2
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-338-1

Query Match 100.0%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 8 FID 10

ATTORNEY/AGENT INFORMATION:
NAME: NEIMARK, Sheridan
REGISTRATION NUMBER: 20,520
REFERENCE/DOCKET NUMBER: NISHIMOTO-2
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-277-007-1

Query Match 100.0%; Score 16; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 8 FID 10

RESULT 12
US-08-485-181-1
Sequence 1, Application US/08485181
Patent No. 5736380
GENERAL INFORMATION:
APPLICANT: NISHIMOTO, Tomoyuki
APPLICANT: CHAEN, Hiroto
APPLICANT: SUGIMOTO, Toshiyuki
APPLICANT: MIYAKE, Toshio
TITLE OF INVENTION: MALTULOSE-TREHALOSE CONVERTING ENZYME, AND
TITLE OF INVENTION: PREPARATION AND USES THEREOF
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,181
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,007
FILING DATE: 19-JUL-1994
APPLICATION NUMBER: JP 199971/1993
FILING DATE: 20-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 144092/1994
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: NEIMARK, Sheridan
REGISTRATION NUMBER: 20,520
REFERENCE/DOCKET NUMBER: NISHIMOTO-2
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids

RESULT 14
US-08-975-917-1
; Sequence 1, Application US/08975917
; Patent No. 6090792
; GENERAL INFORMATION:
; APPLICANT: NISHIMOTO, Tomoyuki
; APPLICANT: CHAEN, Hiroto
; APPLICANT: SUGIMOTO, Toshiyuki
; APPLICANT: MIYAKE, Toshio
; TITLE OF INVENTION: MALTOSYL-TREHALOSE CONVERTING ENZYME, AND
; TITLE OF INVENTION: PREPARATION AND USES THEREOF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,917
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,007
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: JP 199971/1993
; FILING DATE: 20-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 144092/1994
; FILING DATE: 03-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: NEIMARK, Sheridan
; REGISTRATION NUMBER: 20,520
; REFERENCE/DOCKET NUMBER: NISHIMOTO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-975-917-1

Query Match 100.0%; Score 16; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No. 2.8e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;
QY 1 FID 3
Db 8 FID 10

RESULT 15
US-09-817-310-5
; Sequence 5, Application US/09817310
; Patent No. 6534311
; GENERAL INFORMATION:
; APPLICANT: Stewart, Mary
; APPLICANT: Kozma, Sarah
; APPLICANT: Thomas, George
; TITLE OF INVENTION: Drosophila Melanogaster P70 S6 Kinase

FILE REFERENCE: 4-20971/A
; CURRENT APPLICATION NUMBER: US/09/817,310
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 09/230,247
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mammalian
; OTHER INFORMATION: autoinhibitory domain
US-09-817-310-5
Query Match 100.0%; Score 16; DB 4; Length 11;
Best Local Similarity 100.0%; Pred.No. 3.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FID 3
Db 6 FID 8
Search completed: September 30, 2004, 06:38:21
Job time : 6.08475 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:20:22 ; Search time 7.5503 Seconds
(without alignments)
4799.922 Million cell updates/sec

Title: US-09-674-716B-17
Perfect score: 619
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO.spool_p/US09674716/runat_30092004_070257_25855/app_query.fasta_1.3164
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLCN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORW=ext -HEA=SIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09674716@cgn 1 1 82 @runat_30092004_070257_25855 -NCPUE=6 -ICPU=3
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|--------------|---------------------|
| 1 | 506 | 81.7 | 113 | 1 KV2D_HUMAN | P01617 homo sapien |
| 2 | 494 | 79.8 | 117 | 1 KV2E_HUMAN | P06309 homo sapien |
| 3 | 493.5 | 79.7 | 115 | 1 KV2A_HUMAN | P01614 homo sapien |
| 4 | 490 | 79.2 | 113 | 1 KV2C_MOUSE | P01628 mus musculus |
| 5 | 483 | 78.0 | 112 | 1 KV2A_MOUSE | P01626 mus musculus |
| 6 | 481 | 77.7 | 113 | 1 KV2B_HUMAN | P01615 homo sapien |
| 7 | 473 | 76.4 | 133 | 1 KV2F_HUMAN | P06310 homo sapien |
| 8 | 463.5 | 74.9 | 112 | 1 KV2C_HUMAN | P01616 homo sapien |
| 9 | 455 | 73.5 | 120 | 1 KV2B_MOUSE | P01627 mus musculus |
| 10 | 444 | 71.7 | 113 | 1 KV2G_MOUSE | P01631 mus musculus |
| 11 | 443 | 71.6 | 113 | 1 KV2F_MOUSE | P01630 mus musculus |
| 12 | 439 | 70.9 | 113 | 1 KV2E_MOUSE | P03976 mus musculus |
| 13 | 432 | 69.8 | 112 | 1 KV2D_MOUSE | P01629 mus musculus |
| 14 | 416.5 | 67.3 | 108 | 1 KV1_CANFA | P01618 canis famil |
| 15 | 415.5 | 67.1 | 134 | 1 KV4C_HUMAN | P06314 homo sapien |
| 16 | 403.5 | 65.2 | 114 | 1 KV4B_HUMAN | P01625 homo sapien |
| 17 | 388 | 62.7 | 133 | 1 KV4B_HUMAN | P06313 homo sapien |
| 18 | 379 | 61.2 | 109 | 1 KV3D_HUMAN | P01622 homo sapien |

| | | | | | |
|----|-------|------|-----|--------------|---------------------|
| 19 | 378 | 61.1 | 129 | 1 KV3L_HUMAN | P18135 homo sapien |
| 20 | 377 | 60.9 | 129 | 1 KV3M_HUMAN | P18136 homo sapien |
| 21 | 372 | 60.1 | 109 | 1 KV3B_HUMAN | P01620 homo sapien |
| 22 | 370.5 | 59.9 | 111 | 1 KV3M_MOUSE | P01665 mus musculus |
| 23 | 370 | 59.8 | 109 | 1 KV4D_HUMAN | P01623 homo sapien |
| 24 | 368.5 | 59.5 | 109 | 1 KV4D_MOUSE | P83593 homo sapien |
| 25 | 366 | 59.1 | 109 | 1 KV3F_HUMAN | P01624 homo sapien |
| 26 | 365.5 | 59.0 | 111 | 1 KV3O_MOUSE | P01667 mus musculus |
| 27 | 365 | 59.0 | 108 | 1 KV3A_HUMAN | P01619 homo sapien |
| 28 | 362 | 58.5 | 109 | 1 KV3G_HUMAN | P04206 homo sapien |
| 29 | 361.5 | 58.4 | 111 | 1 KV3N_MOUSE | P01666 mus musculus |
| 30 | 361 | 58.3 | 129 | 1 KV3H_HUMAN | P04207 homo sapien |
| 31 | 360.5 | 58.2 | 111 | 1 KV3L_MOUSE | P01664 mus musculus |
| 32 | 358.5 | 57.9 | 111 | 1 KV3O_MOUSE | P01669 mus musculus |
| 33 | 358.5 | 57.9 | 111 | 1 KV3K_HUMAN | P01673 mus musculus |
| 34 | 356.5 | 57.6 | 128 | 1 KV3K_MOUSE | P06311 homo sapien |
| 35 | 356 | 57.5 | 110 | 1 KV3P_MOUSE | P01668 mus musculus |
| 36 | 353.5 | 57.1 | 111 | 1 KV3S_MOUSE | P01671 mus musculus |
| 37 | 351.5 | 56.8 | 111 | 1 KV3R_MOUSE | P01670 mus musculus |
| 38 | 345.5 | 56.0 | 108 | 1 KV1M_HUMAN | P01605 homo sapien |
| 39 | 346.5 | 56.0 | 121 | 1 KV4O_HUMAN | P06312 homo sapien |
| 40 | 344.5 | 55.7 | 111 | 1 KV3T_MOUSE | P01672 mus musculus |
| 41 | 343.5 | 55.5 | 111 | 1 KV3H_MOUSE | P01660 mus musculus |
| 42 | 339.5 | 54.8 | 111 | 1 KV3C_MOUSE | P01656 mus musculus |
| 43 | 339.5 | 54.8 | 111 | 1 KV3J_MOUSE | P01662 mus musculus |
| 44 | 337.5 | 54.5 | 131 | 1 KV3I_MOUSE | P01661 mus musculus |
| 45 | 336.5 | 54.4 | 111 | 1 KV3A_MOUSE | P01654 mus musculus |

ALIGNMENTS

| RESULT 1 | | | | |
|------------|--|-----------|------|---------|
| KV2D_HUMAN | | | | |
| ID | KV2D_HUMAN | STANDARD; | PRT; | 113 AA. |
| AC | P01617; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) | | | |
| DE | Ig kappa chain V-II region TEW. | | | |
| OS | Homo sapiens (Human) | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE (BENCE-JONES PROTEIN TEW). | | | |
| RP | MEDLINE=74148480; PubMed=4596149; | | | |
| RA | Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.; | | | |
| RT | "Amino acid sequence of a kappa Bence Jones protein from a case of | | | |
| RT | Primary amyloidosis."; | | | |
| RL | Biochemistry 12:3763-3780(1973). | | | |
| RN | [2] | | | |
| RP | SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW). | | | |
| RP | MEDLINE=73166638; PubMed=4700495; | | | |
| RA | Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F., | | | |
| RA | Glenner G.G.; | | | |
| RT | "Structural identity of Bence Jones and amyloid fibril proteins in a | | | |
| RT | patient with plasma cell dyscrasia and amyloidosis."; | | | |
| RL | J. Clin. Invest. 52:1276-1281(1973). | | | |
| CC | -!- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL | | | |
| CC | WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT. | | | |
| CC | -!- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A | | | |
| CC | PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS. | | | |
| CC | -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) | | | |
| CC | MARKER. | | | |
| DR | PIR; A90370; K2HUTW. | | | |
| DR | HSSP; P01607; 1REI. | | | |
| DR | GO; GO:0005576; C:extracellular; NAS. | | | |
| DR | GO; GO:0003823; F:antigen binding; NAS. | | | |
| DR | GO; GO:0006955; P:immune response; NAS. | | | |
| DR | InterPro; IPR007110; IG-like. | | | |
| DR | InterPro; IPR003596; IG_v. | | | |
| DR | Pfam; PF00047; IG; 1. | | | |
| DR | SMART; SM00406; IGV; 1. | | | |

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DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 FRAMEWORK-2.
FT DOMAIN 40 54 FRAMEWORK-3.
FT DOMAIN 55 61 FRAMEWORK-4.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 103 112 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 113 117 BY SIMILARITY.
FT NON_TER 113 117
SQ SEQUENCE 113 AA; 12316 MW; 0C3C39F81F1843CA CRC64;

Alignment Scores:
Pred. No.: 1.2e-48 Length: 113
Score: 506.00 Matches: 95
Percent Similarity: 92.04% Conservatives: 9
Best Local Similarity: 84.07% Mismatches: 9
Query Match: 81.74% Indels: 0
DB: 1 Gaps: 0

US-09-674-716b-17 (1-348) x KV2D_HUMAN (1-113)
QY 1 GATATTGTGATCAGTCCTCCACTCTCCCTGCGGCTCAGCCCTGAGAGCGGCGCTCC 60
Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
QY 61 ATCTCTGCTGCTCGAGTAAGAGTCCTCTGTATAGGATGGAGACATACCTTGAATTGG 120
Db 21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAspGlyPheAspTyrLeuAsnTyr 40
QY 121 TACTCTGAGAACGAGGAGGAGTCCTCCAGCTCTCTGATCTATTTGATGTCAGAGTGG 180
Db 41 TyrLeuGlnLysProGlyGlnSerPro**LeuLeuIleTyrAlaLeuSerAsnArgAla 60
QY 181 TCAGGGTCCCTGACAGCTTCAGTGGGAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGGTGAGGATGTTGGGTTTATTTACTGTCAACAGCTGGTAGATATCCA 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMet**AlaLeuGlnAlaPro 100
QY 301 TTCAGGTTCGGCCAGGAGGACCAAGTGGAGTCAAAAGT 339
Db 101 IleThrPheGlyGlnGlyThrArgLeuGluLeuLysArg 113

RESULT 2
KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RL Nature 309:73-76(1984).
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CC -----
DR EMBL; Z00009; -; NOT ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSSP; P80362; LWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 27 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 65 FRAMEWORK-2.
FT DOMAIN 66 97 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 COMPLEMENTARITY-DETERMINING-4.
FT DISULFID 27 97 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Alignment Scores:
Pred. No.: 2.68e-47 Length: 117
Score: 494.00 Matches: 97
Percent Similarity: 91.15% Conservatives: 6
Best Local Similarity: 85.84% Mismatches: 10
Query Match: 79.81% Indels: 0
DB: 1 Gaps: 0

US-09-674-716b-17 (1-348) x KV2E_HUMAN (1-117)
QY 1 GATATTGTGATCAGTCCTCCACTCTCCCTGCGGCTCAGCCCTGAGAGCGGCGCTCC 60
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24
QY 61 ATCTCTGCTGCTCGAGTAAGAGTCCTCTGTATAGGATGGAGACATACCTTGAATTGG 120
Db 25 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTyr 44
QY 121 TACTCTGAGAACGAGGAGGAGTCTCCAGCTCTCTGATCTATTTGATGTCAGAGTGG 180
Db 45 TyrLeuGlnLysProGlnGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 64
QY 181 TCAGGGTCCCTGACAGTTCAGTGGGAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 84
QY 241 AGCAGAGTGGAGGTGAGGATGTTGGGTTTATTTACTGTCAACAGCTGGTAGATATCCA 300
Db 85 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyLeuGlnThrPro 104
QY 301 TTCAGGTTCGGCCAGGAGGACCAAGTGGAGTCAAAAGT 339
Db 105 GlnThrPheGlyGlnGlyThrLysValGluLeuLysArg 117

RESULT 3
KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E;
RT Amino acid sequence of the light chain variable region of MS11, a
RL phosphorylcholine-binding murine myeloma protein.;
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A01910; KVM551.
DR HSSP; P80362; IWL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Alignment Scores:
Pred. No.: 7,47e-47 Length: 113
Score: 490.00 Matches: 95
Percent Similarity: 90.23% Conservative: 7
Best Local Similarity: 84.23% Mismatches: 11
Query Match: 79.73% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x KV2C_MOUSE (1-113)

QY 1 GATATTGTCAGTCAGTCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 60
Db 2 AsplLeValMetThrGlnThrProLeuSerLeuProValThrProGlyValProAlaSer 21
QY 61 ATCTCTGTCGTCGAGTAAGAGTCCTCTGTATAAGGATGGGAAGACATCTGAAT 117
Db 22 IleSerCysArgSerSerGlnSerLeuLeuAspSerGlyAspGlyAsnThrTyLeuAsn 41
QY 118 TGTACTCTCAGAACGCGGAGCTCCACAGCTCCCTGATCTATTGATGTCACCCGG 177
Db 42 TrpTyLeuGlnLysAlaGlyGlnSerProGlnLeuLeuLeuLeuLeuLeuLeuLeu 61
QY 178 GCATCAGGGGTCCTCAGAGTTCTAGTCGACGTGATCAGGCACAGATTTTACACTGAAA 237
Db 62 AlaSerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLys 81
QY 238 ATCAGCAGAGTGGAGCTCAGATGTTGGGGTTTATTACTGTCACACAGCTGGTAGATAT 297
Db 82 IleSerArgValGlnAlaGlnAspValGlyValTyTyTyCysMetGlnArgLeuGluLeu 101
QY 298 CATTCACGTTCCGCCAAGGACCAAGGTGGAGATCAACGTT 339
Db 102 ProTyThrPheGlyGlnGlyThrLysLeuGluLeuArgArg 115

RESULT 4
KV2C_MOUSE
ID KV2C_MOUSE STANDARD; PRT; 113 AA.
AC P01628;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MOPC 511.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E;
RT Amino acid sequence of the light chain variable region of MS11, a
RL phosphorylcholine-binding murine myeloma protein.;
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A01910; KVM551.
DR HSSP; P80362; IWL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Alignment Scores:
Pred. No.: 3,04e-47 Length: 115
Score: 493.50 Matches: 96
Percent Similarity: 91.23% Conservative: 8
Best Local Similarity: 84.23% Mismatches: 9
Query Match: 79.73% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-17 (1-348) x KV2A_HUMAN (1-115)

QY 1 GATATTGTCAGTCAGTCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 60
Db 2 AsplLeValMetThrGlnThrProLeuSerLeuProValThrProGlyValProAlaSer 21
QY 61 ATCTCTGTCGTCGAGTAAGAGTCCTCTGTATAAG---GATGGGAAGACATCTGAAT 117
Db 22 IleSerCysArgSerSerGlnSerLeuLeuAspSerGlyAspGlyAsnThrTyLeuAsn 41
QY 118 TGTACTCTCAGAACGCGGAGCTCCACAGCTCCCTGATCTATTGATGTCACCCGG 177
Db 42 TrpTyLeuGlnLysAlaGlyGlnSerProGlnLeuLeuLeuLeuLeuLeuLeuLeu 61
QY 178 GCATCAGGGGTCCTCAGAGTTCTAGTCGACGTGATCAGGCACAGATTTTACACTGAAA 237
Db 62 AlaSerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLys 81
QY 238 ATCAGCAGAGTGGAGCTCAGATGTTGGGGTTTATTACTGTCACACAGCTGGTAGATAT 297
Db 82 IleSerArgValGlnAlaGlnAspValGlyValTyTyTyCysMetGlnArgLeuGluLeu 101
QY 298 CATTCACGTTCCGCCAAGGACCAAGGTGGAGATCAACGTT 339
Db 102 ProTyThrPheGlyGlnGlyThrLysLeuGluLeuArgArg 115

RESULT 5
KV2A_MOUSE
ID KV2A_MOUSE STANDARD; PRT; 112 AA.
AC P01626;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=79000273; PubMed=99160;
RA Rudikoff S., Potter M.;
RT "Kappa Chain variable region from M167, a phosphorylcholine binding
RL myeloma protein.";
RL Biochemistry 17:2703-2707(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY
CC CHAIN HAS ALSO BEEN DETERMINED.
DR PIR; A01908; KMS16.
DR HSSP; P80362; 1MTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00466; IgV_1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region.
DR DOMAIN 1 23
FT FRAMEWORK-1.
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 39
FT FRAMEWORK-2.
FT DOMAIN 40 54
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 55 61
FT FRAMEWORK-3.
FT DOMAIN 62 93
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 94 102
FT FRAMEWORK-4.
FT DISULFID 103 112
FT BY SIMILARITY.
FT NON TER 112 112
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;
Alignment Scores:
Pred. No.: 4,54e-46 Length: 112
Score: 483.00 Matches: 94
Percent Similarity: 90.18% Conservatives: 7
Best Local Similarity: 83.93% Mismatches: 11
Query Match: 78.03% Indels: 0
DB: 1 Gaps: 0
US-09-674-716B-17 (1-348) x KV2A_MOUSE (1-112)
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACTCCCTGGAGAGCGGCTCC 60
DB 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY 61 ATCTCTGTCTGCTGAGTAAGAGTCTCTGTATAAGGATGGGAGACATACCTTGAATTGG 120
DB 21 IleSerCysArgSerSerLysSerLeuLeuTyLysAspGlyLysThrTyLysAsnTrp 40
QY 121 TACTCTGAGAGGACGAGGAGTCTCCACAGTCTCTGATCTATTGATGTCACCGCGGCA 180
DB 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleSerLeuMetSerThrArgAla 60
QY 181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATTC 240
DB 61 SerGlyValSerAspArgPheSerGlySerGlySerArgThrAspPheThrLeuGluIle 80
QY 241 AGCAGAGTGGAGCTCAGAGTGTGGGTATTACTGTCACAGCTGGTAGAGTATCCA 300
DB 81 SerArgValIysAlaGluAspValGlyValTyTyCysGlnGlnLeuValGluTyPro 100
QY 301 TTCACGTTCGGCCACAGGACCAAGGTGGAGATCAA 336
DB 101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuLys 112
RESULT 6
KV2B_HUMAN
ID KV2B_HUMAN STANDARD; PRT; 113 AA.
AC F01615;
DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=76253627; PubMed=821524;
RA Riessen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenstroms Igm
RL with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR PIR; A01886; K2HUPR.
DR HSSP; P01607; IREI.
DR GO; GO:000576; Extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region.
DR DOMAIN 1 23
FT FRAMEWORK-1.
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 39
FT FRAMEWORK-2.
FT DOMAIN 40 54
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 55 61
FT FRAMEWORK-3.
FT DOMAIN 62 93
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 94 102
FT FRAMEWORK-4.
FT DISULFID 103 112
FT BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39B46DB96BE CRC64;
Alignment Scores:
Pred. No.: 7,63e-46 Length: 113
Score: 481.00 Matches: 88
Percent Similarity: 89.38% Conservatives: 13
Best Local Similarity: 77.88% Mismatches: 12
Query Match: 77.71% Indels: 0
DB: 1 Gaps: 0
US-09-674-716B-17 (1-348) x KV2B_HUMAN (1-113)
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACTCCCTGGAGAGCGGCTCC 60
DB 1 AspValValMetThrGlnSerProLeuPheLeuProValThrLeuGlyGluProAlaSer 20
QY 61 ATCTCTGTCTGCTGAGTAAGAGTCTCTGTATAAGGATGGGAGACATACCTTGAATTGG 120
DB 21 IleGlnCysArgSerSerGlnSerLeuValTyArg***Gly***ThrTyLys***Trp 40
QY 121 TACTCTGAGAGGACGAGGAGTCTCCACAGTCTCTGATCTATTGATGTCACCGCGGCA 180
DB 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyLysSerSerTyArgAsp 60
QY 181 TCAGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATTC 240
DB 61 SerGlyValProAspArgPheSerAspSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTCAGAGTGTGGGTATTACTGTCACAGCTGGTAGAGTATCCA 300
DB 81 ThrArgValGlnAlaGluAspValGlyValTyTyCysMetGlnAlaThr***SerPro 100
QY 301 TTCACGTTCGGCCACAGGACCAAGGTGGAGATCAAACGT 339
DB 101 TyThrPheGlyGlnGlyThrLysLeu***IleLysArg 113
RESULT 7

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KV2F_HUMAN          STANDARD;          PRT;          133 AA.
ID   P06310;
DI   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG kappa chain V-II region RPMI 6410 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=8604182; PubMed=2997711;
RA   Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT   "Human immunoglobulin kappa light chain genes of subgroups II and
RT   III.";
RL   Nucleic Acids Res. 13:6499-6513(1985).
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CC   or send an email to license@sib-sib.ch).
CC   -----
DR   EMBL; Z00020; CAA7315.1; --
DR   PIR; A01890; K2HURP.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003596; IG_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; Igv; 1.
DR   PROSITE; PS50835; IG LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1      20
FT   CHAIN           21     133
FT   DOMAIN          21     43
FT   DOMAIN          44     59
FT   DOMAIN          60     74
FT   DOMAIN          75     81
FT   DOMAIN          82     113
FT   DOMAIN          114     122
FT   DOMAIN          123     132
FT   DISULFID        43     133
FT   NON_TER         133
SQ   SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Alignment Scores:
Pred. No.:          6,2e-45          Length:          133
Score:              473.00          Matches:          90
Percent Similarity: 88.50%          Conservative:    10
Best Local Similarity: 79.65%          Mismatches:     13
Query Match:        76.41%          Indels:          0
DB:                  1                Gaps:            0

US-09-674-716B-17 (1-348) x KV2F_HUMAN (1-133)
QY   1 GATATTGTGACTGACTGCTCCACTCTCCCTGCCCGTCCACCCCTGGAGAGCGGCTCC 60
DB   21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40
QY   61 ATCTCTCTGCTCGAGTAAAGTCTCTCTGATTAAGGATGGGAACATCTTGAATTGG 120
DB   41 IleserCysArgSerSerGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 60
QY   121 TACCTGCAGAACCCAGGCGAGCTCCACAGCTCTGATCTATTGATGTCCACCCGGGCA 180
DB   61 PheGlnGlnArgProGlyGlnSerProArgGlnLeuIleTyrLysValSerAsnArgAsp 80

KV2C_HUMAN          STANDARD;          PRT;          112 AA.
ID   P01616;
DI   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG kappa chain V-II region MIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RA   Dreyer W.J., Gray W.R., Hood L.E.;
RT   "The genetic, molecular, and cellular basis of antibody formation:
RT   some facts and a unifying hypothesis.";
RL   Cold Spring Harb. Symp. Quant Biol. 32:353-367(1967).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01887; K2HUML.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003596; IG_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; Igv; 1.
DR   PROSITE; PS50835; IG LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN          1      23
FT   DOMAIN          24     38
FT   DOMAIN          39     53
FT   DOMAIN          54     60
FT   DOMAIN          61     92
FT   DOMAIN          93    101
FT   DOMAIN          102    111
FT   DISULFID        23     92
FT   NON_TER         112
SQ   SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Alignment Scores:
Pred. No.:          6,98e-44          Length:          112
Score:              463.50          Matches:          86
Percent Similarity: 89.38%          Conservative:    15
Best Local Similarity: 76.11%          Mismatches:     11
Query Match:        74.88%          Indels:          1
DB:                  1                Gaps:            1

US-09-674-716B-17 (1-348) x KV2C_HUMAN (1-112)
QY   1 GATATTGTGACTGACTGCTCCACTCTCCCGCCCGTCCACCCCTGGAGAGCGGCTCC 60
DB   1 AspIleValLeuThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
QY   61 ATCTCTCTGCTCGAGTAAAGTCTCTCTGATTAAGGATGGGAACATCTTGAATTGG 120
DB   21 IleserCysArgSerSerGlnAsnLeuLeu***Ser***Gly***---TyrLeuAspTrp 39
QY   121 TACCTGCAGAACCCAGGCGAGCTCCACAGCTCTGATCTATTGATGTCCACCCGGGCA 180
DB   40 TyrLeu***LysProGly***SerPro***LeuLeuIleTyrLeuGlySerAsnArgAla 59

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QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGCATCAGGCACAGATTTTACACTGAAATC 240
Db 60 SerGlyValProAsnArgPheSerGlySerGlyThr***PheThrLeuValle 79
QY 241 AGCAGAGTGGAGGTGAGAGTGGGTTTATTACTGTCACAGCTGGTAGATATCCA 300
Db 80 SerArgVal***Ala*****ValGlyValTyrCysMetGlnAlaLeuGlnThrPro 99
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAAAGT 339
Db 100 LeuThrPheGlyGlyThrAsnValGluLeuLysArg 112

RESULT 9
KV2B_MOUSE
ID KV2B_MOUSE STANDARD; PRT: 120 AA.
AC P01627;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region VKappa167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. PubMed=6791832;
RA MEDLINE=8200223;
RA Seising E., Storb U.;
RT "Somatic mutation of immunoglobulin light-chain variable-region
genes.";
RL Cell 25:47-58(1981).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; J05562; AAA39032.1; --
DR EMBL; K02415; AAA39051.1; --
DR PIR; A01909; KVM567.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 120 IG KAPPA CHAIN V-II REGION VKAPPA167.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 60 74 FRAMEWORK-2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 113 FRAMEWORK-3.
FT DOMAIN 114 120 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 113 BY SIMILARITY.
SQ SEQUENCE 120 AA; 13280 MW; 63B3571F0B4DE3E8 CRC64;

Alignment Scores:
Pred. No.: 6,34e-43 Length: 120
Score: 455.00 Matches: 88
Percent Similarity: 93.00% Conservative: 5
Best Local Similarity: 88.00% Mismatches: 7
Query Match: 73.51% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x KV2B_MOUSE (1-120)
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTACCCCTGGAGAGCGGCTCC 60
Db 1 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 20

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Db 21 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 40
QY 61 ATCTCTGTCGTCGAGTAAGAGTCTCTGATATAAGGATGGAGACATACTTGAATGG 120
Db 41 IleSerCysArgSerSerLysSerLeuLeuTyrLysAspGlyLysThrLeuAsnTrp 60
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTCATGTCACCCGGCA 180
Db 61 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleTyrLeuMetSerThrArgAla 80
QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGCATCAGGCACAGATTTTACACTGAAATC 240
Db 81 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLeu 100
QY 241 AGCAGAGTGGAGGTGAGAGTGGGTTTATTACTGTCACAGCTGGTAGATATCCA 300
Db 101 SerArgValLysAlaGluAspValGlyValTyrCysGlnGlnLeuValGluTyrPro 120

RESULT 10
KV2G_MOUSE
ID KV2G_MOUSE STANDARD; PRT: 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RA MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RT anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
CC PROTEIN THAT BINDS DIGOXIN.
DR PIR; A01914; KVM526.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Alignment Scores:
Pred. No.: 1.07e-41 Length: 113
Score: 444.00 Matches: 84
Percent Similarity: 86.73% Conservative: 14
Best Local Similarity: 74.34% Mismatches: 15
Query Match: 71.73% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x KV2G_MOUSE (1-113)
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTACCCCTGGAGAGCGGCTCC 60
Db 1 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 20

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QY 61 ATCTCTGCTGCTGAGTAAAGTCTCCCTGATTAAGGATGGGAAGACATACCTTGAATTGG 120
 Db 21 IleserCysArgSerSerGlnSerLeuValHisSerAsnGlyAsnThrTyrLeuAsnTrp 40
 QY 121 TACCTGCAAGCAGCAGGAGTCTCCACAGCTCCCTGATCTATTGATGTCCACCCGGGCA 180
 Db 41 TyrLeuGlnTysAlaGlyGlnSerProLysLeuLeuIleTyrLysValSerAsnArgPhe 60
 QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGAGTACAGGACAGCATTTTACACTGAAATC 240
 Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
 QY 241 AGCAGAGTGGAGCTGAGATGTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
 Db 81 SerArgValGluAlaGluAspLeuGlyIleTyrPheCysSerGlnThrHisValPro 100
 QY 301 TTCACCTTCGGCCCAAGGACCAAGTGGAGATCAAAAGT 339
 Db 101 ProThrPheGlyGlyThrLysLeuGluIleLysArg 113
 RESULT 11
 KV2F_MOUSE
 ID KV2F_MOUSE STANDARD; PRT; 113 AA.
 AC P01630;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-II region 7834.1.
 CS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83256427; PubMed=6409088;
 RA Chang J.-Y., Herbst H., Abersold R., Braun D.G.;
 RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
 RT light chains from a mouse hybridoma-derived anti-(streptococcal group
 RT A polysaccharide) antibody containing an additional cysteine residue.
 RT Application of the dimethylaminoazobenzene isothiocyanate technique
 RT for the isolation of peptides.";
 RL Biochem. J. 211:173-180(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
 CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
 DR PIR; A01913; KMS78.
 DR HSSP; P80362; IWT.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig_v.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT DOMAIN 40 54
 FT DOMAIN 55 61
 FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON TER 113 113
 SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91/CRC64;

Alignment Scores:
 Pred. No.: 1,39e-41 Length: 113
 Score: 443.00 Matches: 87
 Percent Similarity: 84.07% Conservative: 8
 Best Local Similarity: 76.99% Mismatches: 18
 Query Match: 71.57% Indels: 0
 DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x KV2F_MOUSE (1-113)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCCCTGAGAGCGCGCTCC 60
 Db 1 AspileValMetThrGlnThrAlaProSerAlaLeuValThrProGlyGluSerValSer 20
 QY 61 ATCTCTGCTGCTGAGTAAAGTCTCCCTGATTAAGGATGGGAAGACATACCTTGAATTGG 120
 Db 21 IleserCysArgSerSerLysSerLeuLeuHisSerAsnGlyAsnThrTyrLeuTrp 40
 QY 121 TACCTGCAAGCAGCAGGAGTCTCCACAGCTCCCTGATCTATTGATGTCCACCCGGGCA 180
 Db 41 PheLeuGlnArgProGlyGlnCysProGlnLeuLeuIleTyrArgMetSerAsnLeuAla 60
 QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGAGTACAGGACAGCATTTTACACTGAAATC 240
 Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAlaPheThrLeuArgIle 80
 QY 241 AGCAGAGTGGAGCTGAGATGTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
 Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlnArgGluTyrPro 100
 QY 301 TTCACCTTCGGCCCAAGGACCAAGTGGAGATCAAAAGT 339
 Db 101 TyrThrPheGlyGlyThrLysLeuGluIleLysArg 113
 RESULT 12
 KV2E_MOUSE
 ID KV2E_MOUSE STANDARD; PRT; 113 AA.
 AC P03976;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-II region 17829.1.
 CS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Hybridoma; PubMed=6441768;
 RA Abersold R., Herbst H., Grutter T., Chang J.-Y., Braun D.G.;
 RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
 RT origin: monoclonal antibodies 17S29.1 and 2S25.1 specific for the
 RT group A-streptococcal polysaccharide.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
 CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
 DR PIR; A01912; KMS17.
 DR HSSP; P01607; IRE1.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT DOMAIN 40 54
 FT DOMAIN 55 61
 FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON TER 113 113
 SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33/CRC64;

Alignment Scores:
 Pred. No.: 3.9e-41 Length: 113
 Score: 439.00 Matches: 87
 Percent Similarity: 84.07% Conservative: 8
 Best Local Similarity: 76.99% Mismatches: 18
 Query Match: 70.92% Indels: 0
 DB: 1 Gaps: 0

Blank sheet

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:27:18 ; Search time 44.0663 Seconds
(without alignments)
4983.418 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 619
Sequence: 1 gatattgtgactcagtc.....agatcaaacgtacgtggct 348

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q/cgn2_1/USPTO.spool_p/US09674716/runat_30092004_070258_25867/app_query.fasta_1.3164
-DB=SPTREMBL_25 -QWMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=51 -MATRIX=blom62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pcpt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09674716@cgn_1_1_499@runat_30092004_070258_25867 -NCPH=6 -ICPH=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SPTREMBL_25:

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Score | Query Match | Length | ID | Description |
|--------|-------|-------------|--------|----------|--------------------|
| 1 | 516 | 83.4 | 239 | 4 Q8NEK0 | Q8nek0 homo sapien |

ALIGNMENTS

RESULT 1

| ID | Q8NEK0 | PRELIMINARY; | PRT; | 239 | AA. |
|----|---|--------------|------|-----|-----|
| AC | Q8NEK0; | | | | |
| DT | 01-OCT-2002 (TrEMBLrel. 22, Created) | | | | |
| DT | 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) | | | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | | | | |
| DE | Hypothetical protein. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OX | NCBI_taxID=9606; | | | | |
| RN | [1]_taxID=9606; | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Prostate; | | | | |
| RA | Strausberg R.; | | | | |
| RL | Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases. | | | | |
| DR | EMBL; BC030814; AAH30814.1; .. | | | | |
| DR | PIR; S23638; S23638. | | | | |
| DR | PIR; S34091; S34091. | | | | |
| DR | PIR; S40357; S40357. | | | | |
| DR | InterPro; IPR007110; Ig-like. | | | | |
| DR | InterPro; IPR003597; Ig cl. | | | | |
| DR | InterPro; IPR003006; Ig MHC. | | | | |
| DR | InterPro; IPR003596; Ig_v. | | | | |

Q8tcd0 homo sapien
Q8vc55 mus musculu
Q9u180 homo sapien
Q99m37 mus musculu
Q8vc16 mus musculu
Q8k0f8 mus musculu
Q8k122 mus musculu
Q9j182 mus musculu
Q9u178 homo sapien
Q9u183 homo sapien
Q9u186 homo sapien
Q920e9 mus musculu
Q72473 homo sapien
Q9u179 homo sapien
Q8l1u6 mus musculu
Q9u175 homo sapien
Q9u185 homo sapien
Q8k1f2 mus musculu
Q9erz9 mus musculu
Q7sz36 xenopus lae
Q9u410 schistosoma
Q723y4 homo sapien
Q723y5 homo sapien
Q8k1f3 mus musculu
Q8k1f1 mus musculu
Q96sa9 homo sapien
Q9u181 homo sapien
Q9u170 homo sapien
Q9ria5 mus musculu
Q9qyf0 mus musculu
Q8vcp0 mus musculu
Q920e6 mus musculu
Q8vi10 mus musculu
Q8vdd0 mus musculu
Q7e998 mus musculu
Q8r062 mus musculu
Q7tmk3 mus musculu
Q8l1c3 mus musculu
Q9j180 mus musculu
Q9lws9 mus musculu
Q96pf6 homo sapien
Q9lwf8 mus musculu
Q7tmk0 mus musculu
Q9lwl2 mus musculu

DR DB; 1KN2; 13-MAR-02.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00061; ADH_SHORT; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR KW Hypothetical protein.
DR SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;

Alignment Scores:
Pred. No.: 5,25e-42 Length: 239
Score: 433.00 Matches: 83
Percent Similarity: 84.48% Conservative: 15
Best Local Similarity: 71.55% Mismatches: 18
Query Match: 69.95% Indels: 0
DB: 11 Gaps: 0

US-09-674-716B-17 (1-348) x Q8K0F8 (1-239)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGTCACCCCTGGAGAGCCGCCCTCC 60
DB 21 AspValValMetThrGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSer 40
QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCCCTGTATAGGATGGGAACACATCTTGAAATGG 120
DB 41 IleSerCysLysSerGlnSerLeuPheThrAsnGlyLysMetCysThrLeuSerTrp 60
QY 121 TACTCTGAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATCTCCACCCGGGCA 180
DB 61 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleSerLeuValSerLysLeuAsp 80
QY 181 TAGGGGTCTCGACAGGTTTCAGTGCAGTGCATGAGGACAGATTTTACACTGAAATC 240
DB 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 100
QY 241 AGCAGAGTGAGGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 101 SerArgValGluAlaGluAspLeuGlyValTyrCysLeuGlnSerThrHisPhePro 120
QY 301 TTCACGTTCCGCGCAAGGACCAAGGTGGAGATCAACAGCTACCGTGCT 348
DB 121 TyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAspAla 136

RESULT 8
Q8K122 PRELIMINARY; PRT; 148 AA.
ID Q8K122
AC Q8K122; 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206024; AAF69322.1; -.
DR PIR; S26334; S26334.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON TER 1

| | |
|----|--|
| DR | PIR; H30607; H30607. |
| DR | PIR; H30608; H30609. |
| DR | PIR; I30601; I30601. |
| DR | PIR; PH0963; PH0963. |
| DR | PIR; PH0965; PH0965. |
| DR | PIR; S34096; S34096. |
| DR | HSSP; P80362; LWL. |
| DR | InterPro; IPR007110; Ig-like. |
| DR | InterPro; IPR003596; IG_v. |
| DR | Pfam; PF00047; ig; 1. |
| DR | SMART; SM00406; IGV; 1. |
| DR | PROSITE; PS00835; IG_LIKE; 1. |
| FT | NON_TER 1_1 |
| FT | NON_TER 109 109 |
| SQ | SEQUENCE 109 AA; 11646 MW; 5F675C52EC7BE197 CRC64; |

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 3,066-35 | Length: | 109 |
| Score: | 375.00 | Matches: | 73 |
| Percent Similarity: | 79.65% | Conservative: | 17 |
| Best Local Similarity: | 64.68% | Mismatches: | 19 |
| Query Match: | 60.58% | Indels: | 4 |
| DB: | 4 | Gaps: | 1 |

US-09-674-716B-17 (1-348) x Q9UL78 (1-109)

| | | | |
|----|-----|---|-----|
| Qy | 1 | GATATTGTCAGTACCTCCACTCTCCCTGCCCGTCACCCTGGAGCGGCCTCC | 60 |
| Dd | 1 | GluiLevalLeuthrGlnSerProGlyThrLeuSerLeuSerProGlyGluArgAlaIthr | 20 |
| | | | |
| Qy | 61 | ATCTCTCTCGTCGAGTAAGAAGTCTCCTGTATAAGCATGGGAACACATACTTTGAATTGG | 120 |
| Dd | 21 | LeuSerCysArgAlaSerGlnSerVal-----SerSerSerTyrLeuAlaTip | 36 |
| | | | |
| Qy | 121 | TACCTGCAGAACCGAGGCAGTCCTCCACAGCTCTCTGATCTATTGTTGATGTCACCCGGCA | 180 |
| Dd | 37 | TyrGlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerSerArgAla | 56 |
| | | | |
| Qy | 181 | TCAGGGTGCCCTGCAGAGCTTCAGTGGCAGTCGGATCAGGCACAGACATTTTACACTGAAATC | 240 |
| Dd | 57 | ThrGlyIleProAspArgPheserGlySerGlySerGlyThraspPheThrLeuThrIle | 76 |
| | | | |
| Qy | 241 | ACGAGATGGAGGCTGAGAGTGTGGGGTTATTACTGTCTAACAGCTGGTAGACTATCCA | 300 |
| Dd | 77 | SerArgLeuProGluAspCysAlaValTyrTyrCysGlnGlnTyrGlySerSerPro | 96 |
| | | | |
| Qy | 301 | TTACAGTTCCGCCAAGGACCAAGTGCGAGATCAACGT | 339 |
| Dd | 97 | LeuThrPheGlyGlyThrLysValGluIleLysarg | 109 |

RESULT 11

Q9UL83 PRELIMINARY; PRT; 108 AA.

| | |
|----|---|
| ID | Q9UL83 |
| AC | Q9UL83; |
| DT | 01-MAY-2000 (TrEMBLrel. 13, Created) |
| DT | 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) |
| DE | Myosin-reactive immunoglobulin light chain variable region (Fragment). |
| DE | D.C.; |
| OS | Homo sapiens (Human). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. |
| OX | NCBI_TaxID=9606; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE=98277139; PubMed=9614934; |
| RA | Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M., Young D.C. |
| RT | "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."; |
| RL | Clin. Immunol. Immunopathol. 87:184-192 (1998). |
| DR | EMBL; AF035031; AAD56267.1; -. |
| DR | PIR; B30609; B30609. |

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DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Alignment Scores:
Pred. No.: 9,148-34 Length: 108
Score: 362.50 Matches: 70
Percent Similarity: 77.88% Conservative: 18
Best Local Similarity: 61.95% Mismatches: 20
Query Match: 58.56% Indels: 5
DB: 4 Gaps: 1

US-09-674-716B-17 (1-348) x Q9UL83 (1-108)
QY 1 GATATTGTGATCACTCAGTCTCCACTCTCCCTGCGCTCCAGCGTGGAGAGCCGCGCTCC 60
Db 1 GluileValMetThrGlnSerProAlaThrLeuSerValSerProGlyGluArgAlaThr 20
QY 61 ATCTCTGTCTGCTCGAGTAAGAGTCTCTCTGTAATAGGATGGGAACACATCTTGAATTGG 120
Db 21 LeuSerCysArgAlaSerGlnSerVal-----SerSerAsnLeuAlaTrp 35
QY 121 TACCTGCAGAAGCCAGGCGAGTCTCCAGCTCCTGATCTATTGTGATGTCCACCCGGGCA 180
Db 36 TyrGlnGlnLysProGlyGlnAlaProArgLeuLeuLeuTyrCysAlaSerThrArgAla 55
QY 181 TCAGGGTCCCTGCACAGGTTCAAGTTCAGTGCAGTACAGGACAGATTTACACTGAAAATC 240
Db 56 ThrGlyIleProAlaArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrile 75
QY 241 ACAGAGTCGAGGCTGAGGATGTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 76 SerSerLeuGlnPheGlnAspPheAlaValTyrCysGlnHisTyrAsnAsnTrpPro 95
QY 301 TTCACGTCGCGCAAGGACCAAGTGGAGTCAAAACGT 339
Db 96 PheThrPheGlyProGlyThrLysValAspIleLysArg 108

RESULT 12
Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
R Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSP; P80362; 1WTL.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Alignment Scores:
Pred. No.: 3,118-33 Length: 109
Score: 358.00 Matches: 71
Percent Similarity: 77.88% Conservative: 17
Best Local Similarity: 62.83% Mismatches: 21
Query Match: 57.84% Indels: 4
DB: 4 Gaps: 1

US-09-674-716B-17 (1-348) x Q9UL86 (1-109)
QY 1 GATATTGTGATCACTCAGTCTCCACTCTCCCTGCGCTCCAGCGTGGAGAGCCGCGCTCC 60
Db 1 GluileValLeuThrGlnSerProGlyThrLeuSerLeuPheProGlyGluArgAlaThr 20
QY 61 ATCTCTGTCTGCTCGAGTAAGAGTCTCTCTGTAATAGGATGGGAACACATCTTGAATTGG 120
Db 21 LeuSerCysArgAlaSerGlnSerVal-----SerSerSerTyrLeuAlaTrp 36
QY 121 TACCTGCAGAAGCCAGGCGAGTCTCCAGCTCCTGATCTATTGTGATGTCCACCCGGGCA 180
Db 37 TyrGlnGlnLysProGlyGlnAlaProArgLeuLeuLeuTyrGlyThrSerSerArgAla 56
QY 181 TCAGGGTCCCTGCACAGGTTCAAGTTCAGTGCAGTACAGGACAGATTTACACTGAAAATC 240
Db 57 ThrGlyIleProAspArgPheSerGlySerGlySerGlyThrGluThrAspPheThrLeuThrile 76
QY 241 ACAGAGTCGAGGCTGAGGATGTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 77 SerArgLeuGlnPheGlnAspPheAlaValTyrCysGlnGlnTyrGlySerSerIle 96
QY 301 TTCACGTCGCGCAAGGACCAAGTGGAGTCAAAACGT 339
Db 97 PheThrPheGlyProGlyThrLysValAspIleLysArg 109

RESULT 13
Q920E9 PRELIMINARY; PRT; 111 AA.
AC Q920E9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307935; AAL09419.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;

Alignment Scores:

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Pred. No.: 3,59e-33 Length: 111
Score: 357.50 Matches: 72
Percent Similarity: 75.00% Conservatives: 12
Best Local Similarity: 64.29% Mismatches: 27
Query Match: 57.75% Indels: 1
DB: 11 Gaps: 1

US-09-674-716B-17 (1-348) x Q920B9 (1-111)
QY 1 GATATTGTGACTCAGTCTCCACTCTCCCTGCCCTGAGAGAGCGGCTCC 60
D 1 AspileValLeuThrGlnSerProAlaSerLeuAlaValSerLeuGlnArgAlaThr 20
QY 61 ATCTCTGCTGCTCGAGTAGAGTCTCTGTATAGAGTGGGAGACATACCTGATGG 120
D 21 IleSerCysArgAlaSerLysSer--ValSerThrSerGlyTyrSerTyrMetHisTrp 39
QY 121 TACCTGAGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180
D 40 TyrGlnGlnLysProGlyGlnProLysLeuLeuLysLeuLysLeuLysLeuLysLeu 59
QY 181 TCAGGGGTCTCCAGAGGTTCACTGCGAGTGGATGACGACAGATTTTACATGAAATC 240
D 60 SerGlyValProAlaArgPheSerGlySerGlySerGlyThrAspPheThrLeuAsnLeu 79
QY 241 AGCAGAGTGGAGGCTGAGGATGTGGGGTTATTACTGTCAACAGCTGTAGAGTATCCA 300
D 80 HisProValGlnGluAlaPheAlaAlaThrTyrTyrCysGlnHisSerArgGluLeuPro 99
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAA 336
D 100 TyrThrPheGlyGlyGlyThrLysLeuGluLeuLys 111

RESULT 14
Q72473 ID Q72473 PRELIMINARY; PRT; 234 AA.
AC Q72473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Lung.
RC MEDLINE=22368257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.S., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Smith J.J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schmutz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;

```

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RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Alignment Scores:
Pred. No.: 4,25e-33 Length: 234
Score: 357.50 Matches: 71
Percent Similarity: 73.91% Conservatives: 14
Best Local Similarity: 61.74% Mismatches: 25
Query Match: 57.75% Indels: 5
DB: 4 Gaps: 1

US-09-674-716B-17 (1-348) x Q72473 (1-234)
QY 4 ATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGAGAGAGCGGCTCCATC 63
D 22 IleArgMetThrGlnSerProSerSerPheSerAlaSerThrGlyAspArgValThrIle 41
QY 64 TCCTGCTGCTCGAGTAGAGTCTCTGTATAGAGTGGGAGACATACCTGATGGTAC 123
D 42 ThrCysArgAlaSerGlnSerIle-----GlySerTyrLeuAlaTrpTyr 56
QY 124 CTGAGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGATCA 183
D 57 GlnGlnLysProGlyLysAlaProGlnLeuLeuLysLeuLeuLysLeuLeuSer 76
QY 184 GGGTCTCCAGAGGTTCACTGCGAGTGGATGACGACAGATTTTACATGAAATCAGC 243
D 77 GlyValProSerArgPheSerGlySerAlaSerGlyThrAspPheThrLeuSerIleSer 96
QY 244 AGCTGGAGGCTGAGGATGTGGGGTTATTACTGTCAACAGCTGTAGAGTATCCATTC 303
D 97 CysLeuGlnSerGluAspPheAlaThrTyrTyrCysGlnGlnTyrTyrThrThrProTrp 116

RESULT 15
Q9UL79 ID Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SMC0406; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Alignment Scores:

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Pred. No.: 4,1e-32 Length: 108
Score: 348.50 Matches: 69
Percent Similarity: 72.57% Conservative: 13
Best Local Similarity: 61.06% Mismatches: 26
Query Match: 56.30% Indels: 5
DB: 4 Gaps: 1

US-09-674-716B-17 (1-348) x Q9UL79 (1-108)

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QY 1 GATATTGTGATCACTCAGTCTCCCTGCGCCGTCACCCCTGGAGAGCCGGCCTCC 60
Db |||||
1 AspIleValMetThrGlnSerProSerLeuLeuSerAlaSerThrGlyAspArgValThr 20
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGAGACATCTTGAATTGG 120
Db |||||
21 IleSerCysArgMetSerGlnGlyLe-----SerSerTyLeuAlaTrp 35
QY 121 TACCTGCGAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGATCTCCACCCGGGCA 180
Db |||||
36 TyrGlnGlnLysProGlyLysAlaProGluLeuLeuTyrAlaAlaSerThrLeuGln 55
QY 181 TCAGGGGTCCTGACAGGTTCAAGTGGAGTGGATCAGGCACAGATTTTACACTGAATC 240
Db |||||
56 SerGlyValProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIle 75
QY 241 AGCAGAGTGGAGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db |||||
76 SerCysLeuGlnSerGluAspPheAlaThrTyrTyrcysGlnGlnTyrTyrcysPhePro 95
QY 301 TTCAGTTCGGCCAGGACCCAGGTGGAGATCAACGT 339
Db |||||
96 ProThrPheGlyGlnGlyThrLysValGluIleLysArg 108
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Search completed: September 30, 2004, 08:53:40
Job time : 45.0663 secs

Blank sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:19:42 ; Search time 41.458 Seconds
(without alignments)

4743.430 Million cell updates/sec

Title: US-09-674-716b-17

Perfect score: 619

Sequence: 1 gatattgtgactcagtc.....agatcaaacgtacgtggtc 348

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool_P/US09674716/runat_30092004_070257_25848/app_query.fasta_1.3164
-DB=A_Geneseq_29Jan04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=oct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=ptio -NORM=exc -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09674716@cgn_1.1.47@runat_30092004_070257_25848 -NCPUS=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 601 | 97.1 | 116 | 3 AAY32262 | Aay32262 Humanised |
| 2 | 522 | 84.3 | 239 | 7 ADE28461 | Ade28461 Human ant |
| 3 | 519.5 | 83.9 | 170 | 5 ABP64972 | Abp64972 Human pro |
| 4 | 519 | 83.8 | 239 | 3 AAY82615 | Aay82615 Human PTH |
| 5 | 519 | 83.8 | 239 | 7 ADE28405 | Ade28405 Human ant |
| 6 | 518 | 83.7 | 114 | 5 ABB57576 | Abb57576 HLA-DR-sp |
| 7 | 518 | 83.7 | 239 | 7 ADE28465 | Ade28465 Human ant |
| 8 | 516 | 83.4 | 145 | 3 AAY32261 | Aay32261 Mouse ant |
| 9 | 513 | 82.9 | 239 | 7 ADE28397 | Ade28397 Human ant |
| 10 | 512 | 82.7 | 239 | 7 ADE28421 | Ade28421 Human ant |

| | | | | | |
|----|-------|------|-----|------------|--------------------|
| 11 | 511 | 82.6 | 239 | 3 AAY82611 | Aay82611 Human PTH |
| 12 | 511 | 82.6 | 239 | 7 ADE28469 | Ade28469 Human ant |
| 13 | 510 | 82.4 | 238 | 4 AAB72235 | Aab72235 Humanised |
| 14 | 510 | 82.4 | 238 | 4 AAB72231 | Aab72231 Humanised |
| 15 | 510 | 82.4 | 238 | 4 AAB72227 | Aab72227 Humanised |
| 16 | 510 | 82.4 | 238 | 4 AAB72233 | Aab72233 Humanised |
| 17 | 510 | 82.4 | 239 | 3 AAY82617 | Aay82617 Human PTH |
| 18 | 510 | 82.4 | 239 | 7 ADE28521 | Ade28521 Human ant |
| 19 | 510 | 82.4 | 239 | 7 ADE28477 | Ade28477 Human ant |
| 20 | 507 | 81.9 | 114 | 2 AAW27544 | Aaw27544 Human Ab |
| 21 | 507 | 81.9 | 281 | 2 AAW27560 | Aaw27560 Consensus |
| 22 | 506 | 81.7 | 239 | 3 AAY82614 | Aay82614 Human PTH |
| 23 | 506 | 81.7 | 239 | 3 AAY82610 | Aay82610 Human PTH |
| 24 | 505 | 81.6 | 239 | 3 AAY82616 | Aay82616 Human PTH |
| 25 | 504 | 81.4 | 112 | 7 ADE28437 | Ade28437 Human ant |
| 26 | 504 | 81.4 | 113 | 7 ADD28282 | Add28282 Human het |
| 27 | 503 | 81.3 | 112 | 2 AAW53586 | Aaw53586 Light cha |
| 28 | 502.5 | 81.2 | 113 | 2 AAR88508 | Aar88508 Vlkappa f |
| 29 | 502 | 81.1 | 113 | 6 ABJ18680 | Abj18680 Antibody |
| 30 | 502 | 81.1 | 139 | 4 AAB99117 | Aab99117 Human pro |
| 31 | 501 | 80.9 | 112 | 7 ADE28487 | Ade28487 Human ant |
| 32 | 501 | 80.9 | 112 | 7 ADE28409 | Ade28409 Human ant |
| 33 | 501 | 80.9 | 137 | 5 AAU79809 | Aau79809 Light cha |
| 34 | 501 | 80.9 | 239 | 3 AAY82618 | Aay82618 Human PTH |
| 35 | 501 | 80.9 | 239 | 6 ABR48456 | Abr48456 Human Cal |
| 36 | 500 | 80.8 | 112 | 2 AAW54015 | Aaw54015 Human ant |
| 37 | 500 | 80.8 | 112 | 7 ADE28441 | Ade28441 Human ant |
| 38 | 500 | 80.8 | 125 | 5 ABG76926 | Abg76926 Humanised |
| 39 | 500 | 80.8 | 247 | 5 ABG70338 | Abg70338 Human MDD |
| 40 | 499.5 | 80.7 | 114 | 3 AAY95186 | Aay95186 Anti-plat |
| 41 | 499.5 | 80.7 | 131 | 3 AAY95226 | Aay95226 Anti-plat |
| 42 | 499 | 80.6 | 113 | 6 ADA89172 | Ada89172 Human ant |
| 43 | 499 | 80.6 | 219 | 6 ABR39484 | Abr39484 Humanised |
| 44 | 499 | 80.6 | 219 | 6 ABU08310 | Abu08310 Humanised |
| 45 | 499 | 80.6 | 219 | 6 ABR39792 | Abr39792 Humanised |

ALIGNMENTS

RESULT 1

AAAY32262

ID AAY32262 standard; protein; 116 AA.

AC AAY32262;

DT 15-FEB-2000 (first entry)

XX Humanised anti-CD23 MAb C11 light chain variable region.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;
XX monoclonal antibody; chimeric antibody; humanised antibody;
XX complementarity determining region; CDR; autoimmune disease;
XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;
XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
XX urticaria; nephrotic syndrome; glomerulonephritis;
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;
XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
XX graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
XX therapy.

OS Homo sapiens.

OS Synthetic.

| Key | Location/Qualifiers |
|--------|-----------------------------|
| Region | 1..23 |
| Region | /notes="framework region 1" |
| Region | 24..39 |
| Region | /note="CDR 1" |
| Region | 40..54 |
| Region | /note="framework region 2" |
| Region | 55..61 |
| Region | /note="CDR 2" |
| Region | 62..93 |

FT Region /note= "framework region 3"

FT 94.102

FT /note= "CDR 3"

FT 103.113

FT /note= "framework region 4"

WT0958679-A1.

PN

PD

PD 18-NOV-1999.

XX

XX

XX 07-MAY-1999; 99WO-GB001434.

XX

XX

XX 09-MAY-1998; 98GB-00009839.

XX

XX (GLAX) GLAXO GROUP LTD.

XX

XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX

XX WPI; 2000-053101/04.

DR

DR N-PSDB; AA234747.

XX

XX Cell receptor specific antibodies useful for treating e.g. arthritis,

PT diabetes, multiple sclerosis and psoriasis.

PT

XX

XX Claim 9; Fig 3; 81pp; English.

XX

XX This sequence represents the light chain variable region (VL) of

CC humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human

CC framework (HSICKVII) and the light chain complementarity determining

CC regions (see AY32254-56) of murine antibody C11. The DNA was constructed

CC by splice overlap PCR. The invention provides altered antibodies, such as

CC chimeric or humanised antibodies, which comprise sufficient of the amino

CC acid sequences of the C11 light and heavy chain complementarity

CC determining regions to render them capable of binding to the CD23 type II

CC molecule expressed on haematopoietic cells. The antibodies are used to

CC block soluble CD23 formation in human therapy, for the treatment of

CC arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple

CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic

CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative

CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,

CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-

CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic

CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell

CC malignancies (claimed). They are also useful for studying interactions

CC between CD23 and various ligands and determining the binding agents

XX

XX Sequence 116 AA;

SQ

Alignment Scores:

Pred. No.: 6.6e-56 Length: 116

Score: 601.00 Matches: 116

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 97.09% Indels: 0

DB: 3 Gaps: 0

US-09-674-716B-17 (1-348) x AAY32262 (1-116)

QY 1 GATATTGATGACTCAGTCTCCACTCTCCGCGCTCCCTGCGAGAGCGCGCTCC 60

DB 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20

QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTGTATAGGATGGGAACATACACTGATGG 120

DB 21 IleSerCysArgSerSerIysSerLeuLeuTyrLysAspGlyLysThrTyrLeuAsnTrp 40

QY 121 TACCTCGAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCGACCGCGGCA 180

DB 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuMetSerThrArgala 60

QY 181 TCAGGGGTCCCTCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

DB 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGCTAGATATCCA 300

DB 81 SerArgValGluAlaGluaspValGlyValTyrTyrCysGlnGlnLeuValGluTyrPro 100

QY 301 TTCAGTTCGGCCCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348

DB 101 PheThrPheGlyGlnGlyThrIysValGluIleLysArgThrValAla 116

RESULT 2

ADE28461

ID ADE28461 standard; protein; 239 AA.

XX

XX ADE28461;

XX

XX 29-JAN-2004 (first entry)

DT

XX Human anti-CD40 antibody 23-28-1 variable region light chain protein.

DE

XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;

XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;

KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;

KW human; variable region light chain; 23-28-1.

XX

XX Homo sapiens.

OS

XX WO2003040170-A2.

PN

XX 15-MAY-2003.

XX

XX 08-NOV-2002; 2002WO-US036107.

XX

XX 09-NOV-2001; 2001US-0348980P.

PR

XX (PFIZ) PFIZER PROD INC.

PA

XX (ABGE-) ABGENIX INC.

PA

XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

PI WPI; 2003-441521/41.

XX

XX N-PSDB; ADE28460.

DR

XX

XX New chimeric or human monoclonal antibody or its antigen-binding portion

PT that specifically binds to and activates human CD40, useful for enhancing

PT an immune response in a human, or treating cancer, HIV, neutropenia or

PT viral infections.

XX

XX Claim 1; SEQ ID NO 68; 177pp; English.

XX

XX The invention relates to a novel chimeric or human monoclonal antibody or

CC its antigen-binding portion that specifically binds to and activates

CC human CD40. The anti-CD40 antibody of the invention demonstrates

CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV

CC activities and may be useful for treating a hyperproliferative disorder

CC such as cancer, viral and bacterial infection or genetic, primary or

CC combined immunodeficiency conditions including neutropenia or HIV

CC infection. The anti-CD40 antibodies may also be useful for detecting CD40

CC in a biological sample in vitro or in vivo, as well as during gene

CC therapy procedures. The current sequence is that of the human anti-CD40

CC antibody variable region light chain protein of the invention.

XX

XX Sequence 239 AA;

SQ

Alignment Scores:

Pred. No.: 2.33e-47 Length: 239

Score: 522.00 Matches: 100

Percent Similarity: 93.10% Conservative: 8

Best Local Similarity: 86.21% Mismatches: 8

Query Match: 84.33% Indels: 0

DB: 7 Gaps: 0

US-09-674-716B-17 (1-348) x ADE28461 (1-239)

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 155 /note= "possible Ala"
 FT
 PN JP2000080100-A.
 XX
 XX 21-MAR-2000.
 XX
 XX 12-OCT-1998; 98JP-00304793.
 XX
 XX 17-JUN-1998; 98JP-00188196.
 PR
 XX 26-JUN-1998; 98JP-00196729.
 XX
 PA (NISR) JAPAN TOBACCO INC.
 XX
 XX WPI; 2000-286723/25.
 DR N-PSDB; AAA13925.
 XX
 XX A human monoclonal antibody to parathyroid hormone related protein. -
 PT useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain.
 XX
 XX Claim 31; Page 45-46; 88pp; Japanese.
 XX
 XX The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment of
 CC hypercalcemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a human
 CC PTHrP monoclonal antibody clone protein sequence from the present
 CC invention
 XX
 SQ Sequence 239 AA;

Alignment Scores:
 Pred. No.: 4,9e-47 Length: 239
 Score: 519.00 Matches: 99
 Percent Similarity: 92.24% Conservative: 8
 Best Local Similarity: 85.34% Mismatches: 9
 Query Match: 83.84% Indels: 0
 DB: 3 Gaps: 0

US-09-674-716B-17 (1-348) x AAY82615 (1-239)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGGAGAGCCGCTCC 60
 DB 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
 QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCCCTGATAAGGTGGGAGACATACCTGAATTGG 120
 DB 41 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyAsnThrLeuAspTyr 60
 QY 121 TACCTCAGAACCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCCGGGCA 180
 DB 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 80
 QY 181 TCAGGGTCCCTGCACAGTTCAGTGCAGTGCATGAGGACAGACATTTACACTGAAATC 240
 DB 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 100
 QY 241 AGCAGAGTGGAGCTGAGGATGTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
 DB 101 SerArgValGluAlaGluAspValGlyIleTyrTyrCysMetGlnAlaLeuGlnThrPro 120
 QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAACACGTACGGTGGCT 348

DB 121 PheThrPheGlyProGlyThrLysValAspIleLysArgThrValAla 136
 RESULT 5
 ADE28405
 ID ADE28405 standard; protein; 239 AA.
 XX
 XX ADE28405;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 XX Human anti-CD40 antibody 7-1-2 variable region light chain protein.
 DE
 XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
 KW human; variable region light chain; 7-1-2.
 XX
 XX Homo sapiens.
 XX
 XX WO2003040170-A2.
 PN
 XX 15-MAY-2003.
 PD
 XX 08-NOV-2002; 2002WO-US036107.
 PF
 XX 09-NOV-2001; 2001US-0348980P.
 PR
 XX (PRIZ) PRIZER PROD INC.
 PA (ABGE-) ABGENIX INC.
 XX
 XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
 PI WPI; 2003-441521/41.
 XX N-PSDB; ADE28404.
 DR
 XX New chimeric or human monoclonal antibody or its antigen-binding portion
 PT that specifically binds to and activates human CD40, useful for enhancing
 PT an immune response in a human, or treating cancer, HIV, neutropenia or
 PT viral infections.
 XX
 XX Claim 1; SEQ ID NO 12; 177pp; English.
 PS
 XX The invention relates to a novel chimeric or human monoclonal antibody or
 CC its antigen-binding portion that specifically binds to and activates
 CC human CD40. The anti-CD40 antibody of the invention demonstrates
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
 CC activities and may be useful for treating a hyperproliferative disorder
 CC such as cancer, viral and bacterial infection or genetic, primary or
 CC combined immunodeficiency conditions including neutropenia or HIV
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
 CC in a biological sample in vitro or in vivo, as well as during gene
 CC therapy procedures. The current sequence is that of the human anti-CD40
 CC antibody variable region light chain protein of the invention.
 XX
 SQ Sequence 239 AA;

Alignment Scores:
 Pred. No.: 4,9e-47 Length: 239
 Score: 519.00 Matches: 101
 Percent Similarity: 92.24% Conservative: 6
 Best Local Similarity: 87.07% Mismatches: 9
 Query Match: 83.84% Indels: 0
 DB: 7 Gaps: 0

US-09-674-716B-17 (1-348) x ADE28405 (1-239)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGGAGAGCCGCTCC 60
 DB 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
 QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCCCTGATAAGGTGGGAGACATACCTGAATTGG 120

Db 41 IleSerCysArgSerSerGlnSerLeuLeuTyrSerAsnGlyTyrAsnPheLeuAspTyr 60
QY 121 TACCTGCAGAGCCAGGCGACTCTCCACAGCTCCTGATCTATTGATGTCACCCCGGCA 180
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 80
QY 181 TCAGGGGTCCTGACAGCTTCAGTGGCAGTGGATCAGCAGACAGATTTTACACTGAAAATC 240
Db 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 100
QY 241 AGCAGAGTGGAGCTGAGAGTGGGTTTATTACTGTCAACAGCTGGTAGAGATATCCA 300
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 120
QY 301 TTCAGTTTCGGCCAGGACCAAGTGGAGATCAAACTACGGTGGCT 348
Db 121 ArgThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 136

RESULT 6
ABBS5756
ID ABB57576 standard; peptide; 114 AA.
XX
AC ABB57576;
XX
DT 18-MAR-2002 (first entry)
XX
DE HLA-DR-specific protein MS-GPC16 VL sequence.
XX
KW Immunomodulatory human MHC class II antigen-binding protein; HLA;
KW human leukocyte antigen; immune system; immunosuppression; antibody;
KW major histocompatibility complex; antiarthritis; antidiabetic; antipsoriatic;
KW neuroprotective; antiinflammatory; antithyroid; nephrotropic; psoriasis;
KW immunosuppressive; dermatological; immune response suppressor; narcolepsy;
KW thymomimetic; hepatotropic; immune response suppressor; narcolepsy;
KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;
KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
KW transplant rejection; graft versus host disease; pemphigus vulgaris;
KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
KW irritable bowel disease; Sjogren's syndrome.

XX Homo sapiens.
OS Synthetic.
XX WO200187338-A1.
XX
PD 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US015626.
XX
XX 12-MAY-2000; 2000EP-00110063.
PR 06-OCT-2000; 2000US-0238762P.
XX
XX (GPCB-) GPC BIOTECH AG.
PA (MORP-) MORPHOSYS AG.
XX
XX Nagy Z, Tessaar M, Thomassen-Wolf E;
PI WPI; 2002-075289/10.
XX
XX Composition for suppressing immune response, treating diseases of immune
PT system, has polypeptide comprising antibody-based antigen-binding domain
PT of human composition, which binds antigen expressed on a cell surface.
XX
XX Example; Fig 15; 139pp; English.
PS
XX The present invention describes a composition (I), comprising a
CC polypeptide comprising an antibody-based antigen-binding domain of human
CC composition with binding specificity for an antigen expressed on the
CC surface of a cell, where treating cells expressing the antigen with the
CC polypeptides leads to suppression of an immune response, and the IC50 for
CC the suppression of immune response is 1 microM or less. (I) has
CC antirheumatic, antiarthritis, neuroprotective, antiinflammatory,

CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,
CC antithyroid, nephrotropic, thymomimetic and hepatotropic activities, and
CC can be used as a suppressor of immune response. (I) is useful for
CC suppressing activation or proliferation of a cell of the immune system,
CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
CC immune system with another cell, immunosuppressing a patient and for
CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
CC the surface of the cell, where neither cytotoxic entities nor
CC immunological mechanisms are needed to cause or lead to the killing. (I)
CC (optionally linked to cytotoxic or immunogenic agent) is useful for
CC preparing a pharmaceutical preparation for the treatment of rheumatoid
CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
CC the exemplification of the present invention

XX
SQ Sequence 114 AA;
Alignment Scores:
Pred. No.: 5,61e-47 Length: 114
Score: 518.00 Matches: 101
Percent Similarity: 92.11% Conservative: 4
Best Local Similarity: 88.60% Mismatches: 9
Query Match: 83.68% Indels: 0
DB: Gaps: 0

US-09-674-716B-17 (1-348) x ABB57576 (1-114)
QY 1 GATATTGTGATGACTGATCTCCACTCTCCTCCGCTACCCCTCGAGAGCGGCTCC 60
Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
QY 61 ATCTCTCTGCTCGCTGATAGACTCTCTCTATATAGGATGGAGACATCTTGAATTGG 120
Db 21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTyr 40
QY 121 TACTGTCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCCACCCGGCA 180
Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 60
QY 181 TCAGGGGTCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 80
QY 241 AGCAGAGTGGAGCTGAGAGTGGGTTTATTACTGTCAACAGCTGGTAGAGATATCCA 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysGlnGlnTyrAsnSerTyrPro 100
QY 301 TTCAGTTTCGGCCAGGACCAAGTGGAGATCAAACTACGGTGGCT 342
Db 101 ArgThrPheGlyGlnGlyThrLysValGluLeuLysArgThr 114

RESULT 7
ADE28465
ID ADE28465 standard; protein; 239 AA.
XX
AC ADE28465;
XX
DT 29-JAN-2004 (first entry)
XX
XX Human anti-CD40 antibody 23-28-1 full length light chain protein.
XX
XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW human; light chain; 23-28-1.
XX
OS Homo sapiens.
XX

PN WO2003040170-A2.
 XX 15-MAY-2003.
 XX 08-NOV-2002; 2002WO-US036107.
 XX 09-NOV-2001; 2001US-0348980P.
 XX (PFIZ) PFIZER PROD INC.
 XX (ABGE-) ABGENIX INC.
 XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
 XX WPI: 2003-441521/41.
 XX N-PSDB; ADE28464.
 XX New chimeric or human monoclonal antibody or its antigen-binding portion
 PT that specifically binds to and activates human CD40, useful for enhancing
 PT an immune response in a human, or treating cancer, HIV, neutropenia or
 PT viral infections.
 XX
 XX Claim 7; SEQ ID NO 72; 177bp; English.
 XX
 CC The invention relates to a novel chimeric or human monoclonal antibody or
 CC its antigen-binding portion that specifically binds to and activates
 CC human CD40. The anti-CD40 antibody of the invention demonstrates
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
 CC activities and may be useful for treating a hyperproliferative disorder
 CC such as cancer, viral and bacterial infection or genetic, primary or
 CC combined immunodeficiency conditions including neutropenia or HIV
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
 CC in a biological sample in vitro or in vivo, as well as during gene
 CC therapy procedures. The current sequence is that of the human anti-CD40
 CC antibody full length light chain protein of the invention.
 XX
 XX Sequence 239 AA;
 SQ
 Alignment Scores:
 Pred. No.: 6,28e-47 Length: 239
 Score: 518.00 Matches: 101
 Percent Similarity: 91.38% Conservative: 5
 Best Local Similarity: 87.07% Mismatches: 10
 Query Match: 83.68% Indels: 0
 DB: 7 Gaps: 0
 US-09-674-716b-17 (1-348) x ADE28465 (1-239)
 QY 1 GATATTGTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGCGCTCC 60
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
 QY 61 ACTCTCTGCTGCTGAGTAAAGTCTCTGTTAGGATGGGAACATACCTGTAATGG 120
 Db 41 IleSerCysArgSerSerGlnSerLeuLeuTyrSerAsnGlyTyrAsnTyrLeuAspTrp 60
 QY 121 TACCTGCAGAACGAGGAGTCTCAGACGCTCTGATCTATTCTGATGTCACCGCGGCA 180
 Db 61 TyrLeuGlnLysProGlyGlnSerProHisLeuLeuLeuTyrLeuGlySerAsnArgAla 80
 QY 181 TAGGGGTCCTCAGAGTTCAGTGGCTGAGTGGATCAGGACAGATTTACCTGAAATC 240
 Db 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 100
 QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGTTAGAGTATCCA 300
 Db 101 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnAlaLeuGlnThrPro 120
 QY 301 TTCAGTTCGGCCAGGGACCAAGGTGGAGATCAACGTTACGTGGCT 348
 Db 121 ArgThrPheGlyGlnGlyThrLysValGluLysValGluLysArgThrValAla 136
 RESULT 8
 AAY32261

ID AAY32261 standard; protein; 145 AA.
 XX
 AC AAY32261;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Mouse anti-CD23 MAb C11 light chain variable region.
 XX
 KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 55..70
 FT /note= "CDR L1"
 FT Region 83..92
 FT /note= "CDR L2"
 FT Region 125..134
 FT /note= "CDR L3"
 XX
 PN WO9958679-A1.
 XX 18-NOV-1999.
 PD
 XX 07-MAY-1999; 99WO-GB001434.
 PF
 XX 09-MAY-1998; 98GB-00009839.
 PR
 XX (GLAX) GLAXO GROUP LTD.
 PA
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 FI
 XX WPI: 2000-053101/04.
 XX N-PSDB; AAZ34746.
 DR
 XX
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis.
 XX
 PS Claim 8; Fig 2; 81pp; English.
 CC This sequence represents the light chain variable region (VL) of murine
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies (see
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid
 CC sequences of the C11 light and heavy chain complementarity determining
 CC regions (see AAY32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies are
 CC used to block soluble CD23 formation in human therapy for the treatment
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX
 SQ Sequence 145 AA;
 Alignment Scores:
 Pred. No.: 9,55e-47 Length: 145
 Score: 516.00 Matches: 99
 Percent Similarity: 92.98% Conservative: 7

| | | | |
|-----|---|-----|----|
| 1 | GATATTGTGATGACTACGTCTCCACTCTCCCTGCCGCTACCCCTGGAGAGCGCGCTCC | 60 | QY |
| 21 | Asp11eValMetThrGlnSerProLeuSerLeuProValThrProGlyLeuProAlaThr | 40 | Db |
| 61 | ATCTCCTCTCGCTCGAGTAAGAGTCTCTGTATTAAGGATGGGAAGACATACTTGAATTGG | 120 | QY |
| 41 | IleSerCysArgSerSerGlnSerLeuLeuHisArgAsnGlyAsnAsnTyrLeuAspTyr | 60 | Db |
| 121 | TACTTCGAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTTGATGTCCACCCGGCA | 180 | QY |
| 61 | PheLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla | 80 | Db |
| 181 | TACGGGGTCCCTGCACAGGTTCCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC | 240 | QY |
| 81 | SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysLeu | 100 | Db |
| 241 | AGCAGATGGAGGCTGAGGATCTGGGGTTATTACTGTCAACAGCTGGTAGAGTATCCA | 300 | QY |
| 101 | SerArgValGluAlaGluAspValGlyLeuTyrTyrCysMetGlnAlaLeuGlnIlePro | 120 | Db |
| 301 | TTACGTTTCGGCCAAAGGACCAAGAGTGGAGATCAACAGTACGGTGGCT | 348 | QY |

Human; parathyroid hormone related protein; pHRP; monoclonal antibody; KW
 hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain; KW
 fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis; KW

```
Db      121 PheThrPheGlyProGlyThrLysValAspLeuLysArgThrValAla 136
RESULT 12
ADE28469
ID      ADE28469 standard; protein; 239 AA.
XX
AC      ADE28469;
XX
DT      29-JAN-2004 (first entry)
XX
DE      Human anti-CD40 antibody 23-29-1 variable region light chain protein.
XX
DE      anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
XX      immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
XX      bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
XX      human; variable region light chain; 23-29-1.
XX
OS      Homo sapiens.
XX
XX      WO2003040170-A2.
XX
XX      15-MAY-2003.
XX
XX      08-NOV-2002; 2002WO-US036107.
XX
XX      09-NOV-2001; 2001US-0348980P.
XX
XX      (PFIZ ) PFIZER PROD INC.
XX
XX      (ABGE-) ABGENIX INC.
XX
XX      Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX
XX      WPI: 2003-441521/41.
XX      N-PSDB; ADE28468.
XX
XX      New chimeric or human monoclonal antibody or its antigen-binding portion
XX      that specifically binds to and activates human CD40, useful for enhancing
XX      an immune response in a human, or treating cancer, HIV, neutropenia or
XX      viral infections.
XX
XX      Claim 1; SEQ ID NO 76; 177pp; English.
XX
XX      The invention relates to a novel chimeric or human monoclonal antibody or
XX      its antigen-binding portion that specifically binds to and activates
XX      human CD40. The anti-CD40 antibody of the invention demonstrates
XX      cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
XX      activities and may be useful for treating a hyperproliferative disorder
XX      such as cancer, viral and bacterial infection or genetic, primary or
XX      combined immunodeficiency conditions including neutropenia or HIV
XX      infection. The anti-CD40 antibodies may also be useful for detecting CD40
XX      in a biological sample in vitro or in vivo, as well as during gene
XX      therapy procedures. The current sequence is that of the human anti-CD40
XX      antibody variable region light chain protein of the invention.
XX
XX      Sequence 239 AA;
XX
Alignment Scores:
Pred. No.:      3,56e-46      Length:      239
Score:      511.00      Matches:      101
Percent Similarity:      91.38%      Conservative:      5
Best Local Similarity:      87.07%      Mismatches:      10
Query Match:      82.55%      Indels:      0
DB:      7      Gaps:      0
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Db      21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProLaser 40
QY      61 ATCTCTGTCGTCGAGTGAAGTCTCTCTGATATAAGGATGGGAAGACATCTGTAATCG 120
Db      41 IleSerCysArgSerGlnSerLeuLeuProGlyAsnGlyTyrAsnTyrLeuAspTrp 60
QY      121 TACTCAGAACGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGTATGTCACCCCGGCA 180
Db      61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLysArgThrValAla 80
QY      181 TCAGGGTCCCTCAGAGTTCAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAAAATC 240
Db      81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
QY      241 AGCAGAGTGGAGGCTCAGGATGTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db      101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 120
QY      301 TTCAGTTGGCCCAAGGACCGAGGTCGAGATCAACAGTACGCTGGCT 348
Db      121 ArgThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 136
RESULT 13
AAB72235
ID      AAB72235 standard; protein; 238 AA.
XX
AC      AAB72235;
XX
DT      10-MAY-2001 (first entry)
XX
DE      Humanised 323/A3 (IgG2cys) antibody kappa light chain amino acid.
XX
XX      Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
XX      chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
XX      light chain.
XX
XX      Mus sp.
XX      Homo sapiens.
XX
XX      WO200107082-A1.
XX
XX      01-FEB-2001.
XX
XX      23-JUL-1999; 99WO-EP005271.
XX
XX      23-JUL-1999; 99WO-EP005271.
XX
XX      (GLAX ) GLAXO GROUP LTD.
XX
XX      Knick VC, Stimmel JB, Thurmond LM;
XX
XX      WPI; 2001-182729/18.
XX
XX      Combination for treating cancer (e.g. breast, gastric or prostate
XX      cancers), or in the manufacture of a medicament for anti-cancer therapy,
XX      comprises an anti-Ep-cyclic adenosine monophosphate antibody with a
XX      chemotherapeutic agent.
XX
XX      Example 8; Fig 13; 103pp; English.
XX
XX      This invention relates to a combination of an anti-Ep-CAM (cyclic
XX      adenosine monophosphate) antibody with a chemotherapeutic agent, that is
XX      capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
XX      phase or the second growth phase (M) of cell enlargement (G2)/DNA
XX      replication. The antibody exhibits cytostatic activity and is useful in
XX      the manufacture of a medicament for use in anti-cancer therapy.
XX      characterised in that a chemotherapeutic agent, which is capable of
XX      arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-
XX      administered to a patient with an anti-Ep-CAM antibody. The combination
XX      is useful for treating cancer, particularly colorectal cancer, breast
XX      cancer, gastric cancer, prostate cancer or non-small-cell lung cancer.
XX      The present sequence represents the kappa light chain of anti-Ep-CAM
XX      antibody known as humanised 323/A3 (IgG2cys) which can be used in the
XX      combination of the invention
XX
XX      Sequence 238 AA;
XX
Alignment Scores:
```


XX (GLAXO) GLAXO GROUP LTD.
 PA
 XX Knick VC, Stimmel JB, Thurmond LM;
 PI
 XX WPI; 2001-182729/18.
 DR N-PSDB; AAF63373.
 DR
 XX
 PT Combination for treating cancer (e.g. breast, gastric or prostate
 PT cancers), or in the manufacture of a medicament for anti-cancer therapy,
 PT comprises an anti-Ep-cyclic adenosine monophosphate antibody with a
 PT chemotherapeutic agent.
 XX
 XX Disclosure; Fig 15; 103pp; English.
 PS
 XX
 XX This invention relates to a combination of an anti-Ep-CAM (cyclic
 CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
 CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
 CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
 CC replication. The antibody exhibits cytostatic activity and is useful in
 CC the manufacture of a medicament for use in anti-cancer therapy,
 CC characterised in that a chemotherapeutic agent, which is capable of
 CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-
 CC administered to a patient with an anti-Ep-CAM antibody. The combination
 CC is useful for treating cancer, particularly colorectal cancer, breast
 CC cancer, gastric cancer, prostate cancer or non-small-cell lung cancer.
 CC The present sequence represents the light chain of anti-Ep-CAM antibody
 CC known as humanised 323/A3 (IgG1) which can be used in the combination of
 CC the invention
 CC
 XX
 SQ Sequence 238 AA;

Alignment Scores:
 Pred. No.: 4,566-46 Length: 238
 Score: 510.00 Matches: 101
 Percent Similarity: 90.52% Conservative: 4
 Best Local Similarity: 87.07% Mismatches: 11
 Query Match: 82.39% Indels: 0
 DB: 4 Gaps: 0

US-09-674-716B-17 (1-348) x AAB72227 (1-238)

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| Db | 20 | AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProLase | 39 |
| QY | 61 | ATCTCTGTGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAGACATCTTGAATTGG | 120 |
| Db | 40 | IleSerCysArgSerSerIlysAsnLeuHisSerAsnGlyIleThrTyrLeuTyrTrp | 59 |
| QY | 121 | TACCTGCAGACGCGGAGCTCCAGCTCCTGATCTATTTGATGCTCCACCCGGGCA | 180 |
| Db | 60 | TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrGlnMetSerAsnLeuAla | 79 |
| QY | 181 | TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAATC | 240 |
| Db | 80 | SerGlyValProAspArgPheSerSerSerGlySerGlyThrAspPheThrLeuLysIle | 99 |
| QY | 241 | AGCAGAGTGGAGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA | 300 |
| Db | 100 | SerArgValGluAlaGluAspValGlyValTyrTyrCysAlaGlnAsnLeuGluIlePro | 119 |
| QY | 301 | TTACGTTCTGGCCAGGGACCAAGGTGGAGATCAACAGTACGGTGGCT | 348 |
| Db | 120 | ArgThrPheGlyGlnGlyThrLysValGluIleLysArgThrValAla | 135 |

Search completed: September 30, 2004, 08:40:57
 Job time : 45.458 secs

Blank sheet

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:54:09 ; Search time 45.645 Seconds
(without alignments)

4906.833 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 619

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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 2702124

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications AA.*

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|-------|-------|--------|----|-------------|
| ----- | | | | | |

| | | | | | | |
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| 1 | 522 | 84.3 | 239 | 12 | US-10-292-088-40 | Sequence 40, Appl |
| 2 | 519 | 83.8 | 239 | 12 | US-10-292-088-16 | Sequence 16, Appl |
| 3 | 518 | 83.7 | 114 | 15 | US-10-275-046-83 | Sequence 83, Appl |
| 4 | 518 | 83.7 | 239 | 12 | US-10-292-088-56 | Sequence 56, Appl |
| 5 | 516 | 83.4 | 238 | 16 | US-10-663-244-149 | Sequence 149, App |
| 6 | 513 | 82.9 | 238 | 16 | US-10-663-244-145 | Sequence 145, App |
| 7 | 513 | 82.9 | 239 | 12 | US-10-292-088-8 | Sequence 8, Appl |
| 8 | 512 | 82.7 | 239 | 12 | US-10-292-088-32 | Sequence 32, Appl |
| 9 | 511 | 82.6 | 239 | 12 | US-10-292-088-64 | Sequence 64, Appl |
| 10 | 510 | 82.4 | 239 | 12 | US-10-292-088-80 | Sequence 80, Appl |
| 11 | 510 | 82.4 | 239 | 12 | US-10-292-088-102 | Sequence 102, App |
| 12 | 510 | 82.4 | 239 | 12 | US-10-404-724-12 | Sequence 12, Appl |
| 13 | 505 | 81.6 | 113 | 15 | US-10-453-698-177 | Sequence 177, App |
| 14 | 505 | 81.6 | 113 | 15 | US-10-308-817-177 | Sequence 177, App |
| 15 | 505 | 81.6 | 238 | 16 | US-10-663-244-148 | Sequence 148, App |
| 16 | 504 | 81.4 | 112 | 12 | US-10-292-088-36 | Sequence 36, Appl |
| 17 | 504 | 81.4 | 112 | 12 | US-10-292-088-103 | Sequence 103, App |
| 18 | 504 | 81.4 | 112 | 12 | US-10-292-088-111 | Sequence 111, App |
| 19 | 504 | 81.4 | 113 | 15 | US-10-364-743-60 | Sequence 60, Appl |
| 20 | 504 | 81.4 | 238 | 16 | US-10-663-244-144 | Sequence 144, App |
| 21 | 503 | 81.3 | 112 | 12 | US-10-292-088-104 | Sequence 104, App |
| 22 | 502 | 81.1 | 113 | 14 | US-10-125-687-9 | Sequence 9, Appl |
| 23 | 501 | 80.9 | 112 | 12 | US-10-292-088-12 | Sequence 12, Appl |
| 24 | 501 | 80.9 | 112 | 12 | US-10-292-088-94 | Sequence 94, Appl |
| 25 | 501 | 80.9 | 127 | 16 | US-10-380-092-4 | Sequence 4, Appl |
| 26 | 501 | 80.9 | 239 | 10 | US-09-992-600A-8 | Sequence 8, Appl |
| 27 | 501 | 80.9 | 239 | 10 | US-09-924-340-8 | Sequence 8, Appl |
| 28 | 501 | 80.9 | 239 | 10 | US-09-992-095B-8 | Sequence 8, Appl |
| 29 | 501 | 80.9 | 239 | 10 | US-09-999-570-8 | Sequence 8, Appl |
| 30 | 501 | 80.9 | 239 | 14 | US-10-000-489-8 | Sequence 8, Appl |
| 31 | 501 | 80.9 | 239 | 14 | US-10-000-986-8 | Sequence 8, Appl |
| 32 | 501 | 80.9 | 239 | 14 | US-10-154-678-8 | Sequence 8, Appl |
| 33 | 500 | 80.8 | 112 | 12 | US-10-292-088-52 | Sequence 52, Appl |
| 34 | 500 | 80.8 | 112 | 12 | US-10-292-088-112 | Sequence 112, App |
| 35 | 500 | 80.8 | 125 | 14 | US-10-010-942B-6 | Sequence 6, Appl |
| 36 | 500 | 80.8 | 125 | 16 | US-10-388-389-6 | Sequence 6, Appl |
| 37 | 500 | 80.8 | 125 | 16 | US-10-703-713-6 | Sequence 6, Appl |
| 38 | 500 | 80.8 | 125 | 16 | US-10-704-070-6 | Sequence 6, Appl |
| 39 | 500 | 80.8 | 247 | 12 | US-10-468-164-69 | Sequence 69, Appl |
| 40 | 499.5 | 80.7 | 237 | 16 | US-10-663-244-146 | Sequence 146, App |
| 41 | 499.5 | 80.7 | 237 | 16 | US-10-663-244-146 | Sequence 153, App |
| 42 | 499 | 80.6 | 113 | 12 | US-10-371-942-16 | Sequence 16, Appl |
| 43 | 499 | 80.6 | 219 | 12 | US-10-226-435A-11 | Sequence 11, Appl |
| 44 | 499 | 80.6 | 238 | 16 | US-10-663-244-147 | Sequence 147, App |
| 45 | 498 | 80.5 | 112 | 16 | US-10-663-244-75 | Sequence 75, Appl |

ALIGNMENTS

RESULT 1
US-10-292-088-40
; Sequence 40, Application US/10292088
; Publication NO. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-Pf/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-40

Alignment Scores:
 Pred. No.: 3,83e-45 Length: 239
 Score: 522.00 Matches: 100
 Percent Similarity: 93.10% Conservative: 8
 Best Local Similarity: 86.21% Mismatches: 8
 Query Match: 84.33% Indels: 0
 DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-292-088-40 (1-239)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACCCCTGGAGAGCCGCGCTCC 60
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
 QY 61 ATCTCTCTGTCGCTCAGTAAAGTCTCCTGTATAAGATGGGAGACACATCTTGAATTGG 120
 Db 41 IleSerCysArgSerSerGlnSerValLeuTyrSerAsnGlyTyrAsnTyrLeuAspTrp 60
 QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCGCGGCA 180
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLeuGlySerAsnArgala 80
 QY 181 TCAGGGGTCCCTCAGAGTTCAGTGGCAGTGGATGAGATCAACAGTACGATGAAATC 240
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
 Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnValLeuGlnThrPro 120
 QY 301 TTCACGTTGGCCAGGACCAAGGTGGAGATCAACAGTACGCTGGCT 348
 Db 121 PheThrPheGlyProGlyThrLysValAspIleLysArgThrValAla 136

RESULT 2

US-10-292-088-16

; Sequence 16, Application US/10292088
 ; Publication No. US2003021100A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BEDIAN, VAHE
 ; APPLICANT: GLADUE, RONALD P.
 ; APPLICANT: CORVALAN, JOSE
 ; APPLICANT: JIA, XIAO-CHI
 ; APPLICANT: PENG, XIAO
 ; TITLE OF INVENTION: ANTIBODIES TO CD40
 ; FILE REFERENCE: ABX-PF/3 US
 ; CURRENT APPLICATION NUMBER: US/10/292,088
 ; CURRENT FILING DATE: 2003-03-14
 ; PRIOR APPLICATION NUMBER: 60/348,980
 ; PRIOR FILING DATE: 2001-11-09
 ; NUMBER OF SEQ ID NOS: 147
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-292-088-16

Alignment Scores:

Pred. No.: 7.81e-45 Length: 239
 Score: 519.00 Matches: 101
 Percent Similarity: 92.24% Conservative: 6
 Best Local Similarity: 87.07% Mismatches: 9
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 DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-292-088-16 (1-239)

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 QY 61 ATCTCTCTGTCGCTCAGTAAAGTCTCCTGTATAAGATGGGAGACACATCTTGAATTGG 120

Db 41 IleSerCysArgSerSerGlnSerLeuTyrSerAsnGlyTyrAsnPheLeuAspTrp 60
 QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCGCGGCA 180
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLeuGlySerAsnArgala 80
 QY 181 TCAGGGGTCCCTCAGAGTTCAGTGGCAGTGGATGAGATCAACAGTACGCTGGCT 240
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
 Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 120
 QY 301 TTCACGTTGGCCAGGACCAAGGTGGAGATCAACAGTACGCTGGCT 348
 Db 121 ArgThrPheGlyGlnGlyThrLysValGluLysArgThrValAla 136

RESULT 3

US-10-275-046-83

; Sequence 83, Application US/10275046
 ; Publication No. US20040019187A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nagy et al.
 ; TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPTIDES
 ; FILE REFERENCE: GPCG-P01-260
 ; CURRENT APPLICATION NUMBER: US/10/275,046
 ; CURRENT FILING DATE: 2002-10-31
 ; PRIOR APPLICATION NUMBER: 00110063.5
 ; PRIOR FILING DATE: 2000-05-12
 ; NUMBER OF SEQ ID NOS: 97
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 83
 ; LENGTH: 114
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: MS-GPC16 VL
 ; US-10-275-046-83

Alignment Scores:

Pred. No.: 9.04e-45 Length: 114
 Score: 518.00 Matches: 101
 Percent Similarity: 92.11% Conservative: 4
 Best Local Similarity: 88.60% Mismatches: 9
 Query Match: 83.68% Indels: 0
 DB: 15 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-275-046-83 (1-114)

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 QY 61 ATCTCTCTGTCGCTCAGTAAAGTCTCCTGTATAAGATGGGAGACACATCTTGAATTGG 120
 Db 21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 40
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 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
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 QY 301 TTCACGTTGGCCAGGACCAAGGTGGAGATCAACAGTACGCTAGC 342


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; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PR/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-56
Alignment Scores:
Pred. No.: 9,91e-45 Length: 239
Score: 518.00 Matches: 101
Percent Similarity: 91.38% Conservative: 5
Best Local Similarity: 87.07% Mismatches: 10
Query Match: 83.68% Indels: 0
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Db 41 IleSerCysArgSerSerGlnSerLeuLeuTyrSerAsnGlyTyrAsnTyrLeuAspTyr 60
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCAGCTCTCTGATCTATTGATGTCACCCGGCA 180
Db 61 TyrLeuGlnLysProGlyGlnSerProHisLeuLeuIleTyrLeuGlySerAsnArgAla 80
QY 181 TCAGGGGTCCCTGCACAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
QY 241 AGCAGAGTGGAGCTGAGAGTCTGGGGTTTATTACTCTCAACAGCTGGTAGAGTATCCA 300
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 120
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAACTACGGTGGCT 348
Db 121 ArgThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 136
RESULT 5
US-10-663-244-149
; Sequence 149, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-145
```

```
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide.
US-10-663-244-149
Alignment Scores:
Pred. No.: 1.59e-44 Length: 238
Score: 516.00 Matches: 100
Percent Similarity: 92.24% Conservative: 7
Best Local Similarity: 86.21% Mismatches: 9
Query Match: 83.36% Indels: 0
DB: 16 Gaps: 0
US-09-674-716B-17 (1-348) x US-10-663-244-149 (1-238)
QY 1 GATATTGTGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60
Db 20 AspileGlnMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 39
QY 61 ATCTCTGCTCGTTCGAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
Db 40 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTyr 59
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCAGCTCTCCAGCTCTCTGATCTATTGATGTCACCCGGCA 180
Db 60 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 79
QY 181 TCAGGGGTCCCTGCACAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
Db 80 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 99
QY 241 AGCAGAGTGGAGCTGAGAGTCTGGGGTTTATTACTCTCAACAGCTGGTAGAGTATCCA 300
Db 100 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 119
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAACTACGGTGGCT 348
Db 120 TrpThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 135
RESULT 6
US-10-663-244-145
; Sequence 145, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-145
```

```

Alignment Scores:
Pred. No.: 3,25e-44 Length: 238
Score: 513.00 Matches: 99
Percent Similarity: 92.24% Conservative: 8
Best Local Similarity: 85.34% Mismatches: 9
Query Match: 82.88% Indels: 0
DB: 16 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-663-244-145 (1-238)

QY 1 GATATTGTGATCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCCGGCTCC 60
Db 20 AspIleGlnMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 39
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAACACATACTTGAATTGG 120
Db 40 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTirp 59
QY 121 TCACCTGCAGAGCCAGGCGAGTCTCCAGCTCCTGATCTATTTACTGTCAACAGCTGGTAGATATCCA 180
Db 60 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLeuGlySerAsnArgAla 79
QY 181 TCAGGGTCCCTGACAGCTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 80 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 99
QY 241 AGCAGAGTGGAGCTGAGGATTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 100 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnAlaLeuGlnThrPro 119
QY 301 TTCACGTTCCGCGCAAGGACCAAGGTGGAGATCAACAGTACGGTGGCT 348
Db 120 TrpThrPheGlyGlnGlyThrLysLeuGluLeuLysArgThrValAla 135

RESULT 7
; Sequence 8, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-8

Alignment Scores:
Pred. No.: 3,25e-44 Length: 239
Score: 513.00 Matches: 99
Percent Similarity: 92.24% Conservative: 8
Best Local Similarity: 85.34% Mismatches: 9
Query Match: 82.88% Indels: 0
DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-292-088-8 (1-239)

QY 1 GATATTGTGATCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCCGGCTCC 60
Db 21 AspIleValLeuThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAACACATACTTGAATTGG 120
Db 41 IleSerCysArgSerSerGlnSerLeuLeuHisThrAsnGlyTyrAsnTyrPheAspTirp 60
QY 121 TCACCTGCAGAGCCAGGCGAGTCTCCAGCTCCTGATCTATTTACTGTCAACAGCTGGTAGATATCCA 180
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLeuGlySerAsnArgAla 80
QY 181 TCAGGGTCCCTGACAGCTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
QY 241 AGCAGAGTGGAGCTGAGGATTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 101 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnAlaLeuGlnThrPro 120

US-09-674-716B-17 (1-348) x US-10-292-088-32 (1-239)

QY 1 GATATTGTGATCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCCGGCTCC 60
Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAACACATACTTGAATTGG 120
Db 41 IleSerCysArgSerSerGlnSerLeuLeuHisThrAsnGlyTyrAsnTyrPheAspTirp 60
QY 121 TCACCTGCAGAGCCAGGCGAGTCTCCAGCTCCTGATCTATTTACTGTCAACAGCTGGTAGATATCCA 180
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLeuGlySerAsnArgAla 80
QY 181 TCAGGGTCCCTGACAGCTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
QY 241 AGCAGAGTGGAGCTGAGGATTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 101 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnAlaLeuGlnThrPro 120

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QY 301 TTCAGTTCCGCGCAGGACCAAGTGGAGATCAAACTACGTGGCT 348
Db 121 TyrSerPheGlyGlnGlyThrLysLeuGluLeuLysArgThrValAla 136

RESULT 9

US-10-292-088-64
; Sequence 64, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD.RES
; LOCATION: (156)
; OTHER INFORMATION: Variable amino acid
US-10-292-088-64

Alignment Scores:
Pred. No.: 5,248-44 Length: 239
Score: 511.00 Matches: 101
Percent Similarity: 91.38% Conservative: 5
Best Local Similarity: 87.07% Mismatches: 10
Query Match: 82.55% Indels: 0
DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-292-088-64 (1-239)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGACCGGCTCC 60
Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTGTATAGGATGGAGACATCTTGAATTGG 120
Db 41 IleSerCysArgSerSerGlnSerLeuLeuProGlyAsnGlyTyrAsnTyrLeuAspTrp 60
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGATCTCCACCGGGCA 180
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLeuGlySerAsnArgAla 80
QY 241 AGCAGAGTGGAGCTCAGGATCTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 101 SerArgValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
QY 301 TTCAGTTCCGCGCAGGACCAAGTGGAGATCAAACTACGTGGCT 348
Db 121 ArgThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 136

RESULT 10

US-10-292-088-80
; Sequence 80, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.

; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-80

Alignment Scores:
Pred. No.: 6,648-44 Length: 239
Score: 510.00 Matches: 100
Percent Similarity: 91.38% Conservative: 6
Best Local Similarity: 86.21% Mismatches: 10
Query Match: 82.39% Indels: 0
DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-292-088-80 (1-239)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGACCGGCTCC 60
Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTGTATAGGATGGAGACATCTTGAATTGG 120
Db 41 IleSerCysArgSerSerGlnSerLeuLeuProGlyAsnGlyTyrAsnTyrLeuAspTrp 60
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGATCTCCACCGGGCA 180
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuTyrLeuGlySerAsnArgAla 80
QY 181 TCAGGGTCCCTCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
QY 241 AGCAGAGTGGAGCTCAGGATCTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 101 SerArgValGluAlaGluAspValGlyIleTyrTyrCysMetGlnAlaLeuGlnThrPro 120
QY 301 TTCAGTTCCGCGCAGGACCAAGTGGAGATCAAACTACGTGGCT 348
Db 121 ArgThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAla 136

RESULT 11

US-10-292-088-102
; Sequence 102, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-292-088-102

Alignment Scores:

Pred. No.: 6,64e-44 Length: 239
 Score: 510.00 Matches: 100
 Percent Similarity: 91.38% Conservative: 6
 Best Local Similarity: 86.21% Mismatches: 10
 Query Match: 82.39% Indels: 0
 DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-292-088-102 (1-239)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCCGCGCTCC 60
 DB 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
 QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
 DB 41 IleSerCysArgSerGlnSerLeuLeuProGlyAsnGlyTyAsnTyLeuAspTrp 60
 QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCCGCGCA 180
 DB 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyLeuGlySerAsnArgala 80
 QY 181 TCAGGGGTCCTTCACAGGTTTCAGTGGCAGTGGATCAGGCACACAGATTTACACTGAAATC 240
 DB 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100
 QY 241 AGCAGAGTGGAGCTCAGAGTGTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
 DB 101 SerArgValGluAlaGluAspValGlyIleTyTyTyCysMetGlnAlaLeuGlnThrPro 120
 QY 301 TTCACGTTCCGCAAGGACCAAGTGGAGATCAACAGTACCGTGGCT 348
 DB 121 ArgThrPheGlyGlnGlyThrLysValGluLysArgThrValAla 136

RESULT 12

US-10-404-724-12
 ; Sequence 12, Application US/10404724
 ; Publication No. US20030203447A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horwitz, Arnold H.
 ; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
 ; FILE REFERENCE: Polypeptides
 ; CURRENT APPLICATION NUMBER: US/10/404,724
 ; PRIOR APPLICATION NUMBER: 2003-03-31
 ; PRIOR FILING DATE: 2002-03-29
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 12
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-404-724-12

Alignment Scores:

Pred. No.: 6,64e-44 Length: 239
 Score: 510.00 Matches: 100
 Percent Similarity: 90.52% Conservative: 5
 Best Local Similarity: 86.21% Mismatches: 11
 Query Match: 82.39% Indels: 0
 DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-404-724-12 (1-239)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCCGCGCTCC 60
 DB 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProGlySer 40
 QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCCTGTATAGGATGGGAAGACATACCTTGAATTGG 120

Db 41 IleSerCysArgSerSerLysSerLeuLeuHisSerAsnGlyIleThrTyLeuTyTrp 60
 QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCCGCGCA 180
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyGlnMetSerAsnArgala 80
 QY 181 TCAGGGTCTCCTGCACAGGTTTCAGTGGAGTGGATCAGGCACACAGATTTACACTGAAATC 240
 Db 81 SerGlyValProAspArgPheSerSerSerGlySerGlyThrAspPheThrLeuLysile 100
 QY 241 AGCAGAGTGGAGCTCAGGATGTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
 Db 101 SerArgValGluAlaGluAspValGlyValTyTyTyCysAlaGlnAsnLeuGluLeuPro 120
 QY 301 TTCACGTTCCGCAAGGACCAAGTGGAGATCAACAGTACCGTGGCT 348
 Db 121 ArgThrPheGlyGlnGlyThrLysLeuGluMetLysArgThrValAla 136

RESULT 13

US-10-453-698-177
 ; Sequence 177, Application US/10453698
 ; Publication No. US20040038308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rother, Russell
 ; TITLE OF INVENTION: HYBRID ANTIBODIES
 ; FILE REFERENCE: 82 CIP (1087-37 CIP)
 ; CURRENT APPLICATION NUMBER: US/10/453,698
 ; CURRENT FILING DATE: 2003-06-03
 ; NUMBER OF SEQ ID NOS: 196
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 177
 ; LENGTH: 113
 ; TYPE: PRT
 ; ORGANISM: human
 US-10-453-698-177

Alignment Scores:

Pred. No.: 1,99e-43 Length: 113
 Score: 505.00 Matches: 98
 Percent Similarity: 92.04% Conservative: 6
 Best Local Similarity: 86.73% Mismatches: 9
 Query Match: 81.58% Indels: 0
 DB: 12 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-453-698-177 (1-113)

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCCGCGCTCC 60
 Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
 QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
 Db 21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyAsnTyTrLeuAspTrp 40
 QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCCGCGCA 180
 Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyLeuGlySerAsnArgala 60
 QY 181 TCAGGGTCTCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACACAGATTTACACTGAAATC 240
 Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 80
 QY 241 AGCAGAGTGGAGCTCAGGATGTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
 Db 81 SerArgValGluAlaGluAspValGlyValTyTyTyCysMetGlnAlaLeuGlnThrPro 100
 QY 301 TTCACGTTCCGCAAGGACCAAGTGGAGATCAACAGT 339
 Db 101 GlnThrPheGlyGlnGlyThrLysValGluLysArg 113

RESULT 14

US-10-308-817-177
 ; Sequence 177, Application US/10308817

100 Sep 30 15:10:30 2004

```
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 177
; LENGTH: 113
; TYPE: PRT
; ORGANISM: human
US-10-308-817-177

Alignment Scores:
Pred. No.: 1,996-43 Length: 113
Score: 505.00 Matches: 98
Percent Similarity: 92.04% Conservative: 6
Best Local Similarity: 86.73% Mismatches: 9
Query Match: 81.58% Indels: 0
DB: 15 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-308-817-177 (1-113)
QY 1 GATATTGTGATGACAGTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGCGCTCC 60
DB 1 AsplleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCCTGTATAGGATGGGAGACATACCTGGAATTGG 120
DB 21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 40
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCAGCTCCTGATCTATTGATGTCCACCCGGGCA 180
DB 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 60
QY 181 TCAGGGGTCCTTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 80
QY 241 ACCAGATGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
DB 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 100
QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAAACGT 339
DB 101 GlnThrPheGlyGlnGlyThrLysValGluLysArg 113

RESULT 15
US-10-663-244-148
; Sequence 148, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-148

Alignment Scores:
Pred. No.: 2,186-43 Length: 238
Score: 505.00 Matches: 99
Percent Similarity: 90.52% Conservative: 6
Best Local Similarity: 85.34% Mismatches: 11
Query Match: 81.58% Indels: 0
DB: 16 Gaps: 0

US-09-674-716B-17 (1-348) x US-10-663-244-148 (1-238)
QY 1 GATATTGTGATGACAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGCGCTCC 60
DB 20 AsplleGlnMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 39
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCCTGTATAGGATGGGAGACATACCTGGAATTGG 120
DB 40 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 59
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCAGCTCCTGATCTATTGATGTCCACCCGGGCA 180
DB 60 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 79
QY 181 TCAGGGGTCCTTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 80 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 99
QY 241 AGCAGATGGAGCTCAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
DB 100 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnThrPro 119
QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAAACGTACGTTGGCT 348
DB 120 ArgThrPheGlyGlyThrLysValGluLysArgThrValAla 135

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Job time : 47.645 secs
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ALIGNMENTS

RESULT 1
US-09-025-769B-15
; Sequence 15, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Illeg, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Pluckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: September 30, 2004, 08:41:28 ; Search time 8.51124 Seconds
(without alignments)
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Perfect score: 619
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778928

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 507 | 81.9 | 114 | 4 | US-09-025-769B-29 Sequence 29, Appl |
| 3 | 507 | 81.9 | 114 | 4 | US-09-025-769B-45 Sequence 45, Appl |
| 4 | 507 | 81.9 | 281 | 4 | US-09-025-769B-178 Sequence 178, Appl |
| 5 | 505 | 81.6 | 112 | 1 | US-08-053-171-16 Sequence 16, Appl |
| 6 | 502.5 | 81.2 | 113 | 1 | US-08-264-093-10 Sequence 10, Appl |
| 7 | 500 | 80.8 | 112 | 1 | US-08-478-039-88 Sequence 88, Appl |
| 8 | 500 | 80.8 | 112 | 1 | US-08-476-349A-88 Sequence 88, Appl |
| 9 | 498 | 80.5 | 116 | 1 | US-08-482-882-66 Sequence 66, Appl |
| 10 | 498 | 80.5 | 116 | 2 | US-08-483-389-66 Sequence 66, Appl |
| 11 | 498 | 80.5 | 116 | 2 | US-08-487-113D-66 Sequence 66, Appl |
| 12 | 498 | 80.5 | 116 | 2 | US-08-473-503-66 Sequence 66, Appl |

; ZIF: 100Z1

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-45

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Pred. No.: 6,518-55 Length: 114
Score: 507.00 Matches: 100
Percent Similarity: 91.23% Conservative: 4
Best Local Similarity: 87.72% Mismatches: 10
Query Match: 81.91% Indels: 0
DB: 4 Gaps: 0

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QY 61 ATCTCTGCTGCTGAGTAAAGTCTCTGTATAGGATGGAGACATATCTGAATTGG 120
Db 21 IleSerCysArgSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 40
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTGATCTATTGATCTCCACCCGGGCA 180
Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 60
QY 181 TCAGGGTCCCTGACAGGTTCACTGCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysGlnGlnHisTyrThrThrPro 100
QY 301 TTCAGTTCGGCCCAAGGACCAAGTGGAGATCAAAACGTAGC 342
Db 101 ProThrPheGlyGlnGlyThrLysValGluIleLysArgThr 114

RESULT 4
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-178

Alignment Scores:
Pred. No.: 9,318-55 Length: 281
Score: 507.00 Matches: 100
Percent Similarity: 91.23% Conservative: 4
Best Local Similarity: 87.72% Mismatches: 10
Query Match: 81.91% Indels: 0
DB: 4 Gaps: 0

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QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTGATCTATTGATCTCCACCCGGGCA 180
Db 206 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 225
QY 181 TCAGGGTCCCTGACAGGTTCACTGCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 240
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QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300
Db 246 SerArgValGluAlaGluAspValGlyValTyrTyrCysGlnGlnHisTyrThrThrPro 265
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Db 266 ProThrPheGlyGlnGlyThrLysValGluIleLysArgThr 279

RESULT 5
US-08-053-171-16
; Sequence 16, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Leibner

;; TITLE OF INVENTION: Antibody Derivatives
;; NUMBER OF SEQUENCES: 32
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourie and Crew
;; STREET: 379 Lytton Avenue
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: US
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/053,171
;; FILING DATE: 22-APR-1993
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-54-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 112 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..112
;; OTHER INFORMATION: /note= "Sequence of Tew antibody
;; Patent No. 5562903
;; OTHER INFORMATION: fragment"
;; NAME/KEY: Peptide
;; LOCATION: 1..112
;; OTHER INFORMATION: /note= "E.A. Kabat, et al.,
;; OTHER INFORMATION: Sequences of Protein of Immunological Interest,
;; OTHER INFORMATION: 4th Ed. (1987), US Dept. of Health and Human Services
US-08-053-171-16

Alignment Scores:
Pred. No.: 1,15e-54 Length: 112
Score: 505.00 Matches: 96
Percent Similarity: 91.96% Conservative: 7
Best Local Similarity: 85.71% Mismatches: 9
Query Match: 81.58% Indels: 0
DB: 1 Gaps: 0

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QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTGTATAGGATGGAGACACATCTTGAATTGG 120
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QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGTCTCGATCTATTGATGTCACCCCGGCA 180
Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrAlaLeuSerAsnArgAla 60
QY 181 TCAGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGATGGAGGCTGAGGAGTTCGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300

Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnAlaPro 100
QY 301 TTCACGTTCCGCCAAGGGCAAGGTCAGGATCAAA 336
Db 101 IleThrPheGlyGlnGlyThrArgLeuGluLeuLys 112
RESULT 6
US-08-264-093-10
; Sequence 10, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; ADDRESSEE: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-10
Alignment Scores:
Pred. No.: 2,37e-54 Length: 113
Score: 502.50 Matches: 98
Percent Similarity: 92.04% Conservative: 6
Best Local Similarity: 86.73% Mismatches: 8
Query Match: 81.18% Indels: 1
DB: 1 Gaps: 1
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QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTCTG---TATAAGGATGGGAAGACATCTTGAAT 117
Db 21 IleSerCysArgSerSerGlnSerLeuLeuAspSerAspGlyAsnThrTyrLeuAsp 40
QY 118 TGGTACTCTCAGAACCCAGGCGAGTCTCCACAGTCTCGATCTATTGATGTCACCCCGG 177
Db 41 TrpTyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrThrLeuSerTyrArg 60
QY 178 GCATCAGGGGTCCTCGTACAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAA 237

Db 61 AlaSerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLys 80
QY 238 ATCAGCAGAGTGGAGGTGGAGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTAT 297
Db 81 IleSerArgValGluAlaGluAspValGlyValTyrCysMetGlnArgIleGluPhe 100
QY 298 CCATTCAGTTCGCCCAAGGACCAAGTGGAGATCAAA 336
Db 101 ProPheThrPheGlyGlyThrLysValGluIleLys 113
RESULT 7
US-08-478-039-88
; Sequence 88, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VK2 consensus
US-08-478-039-88
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Score: 500.00 Matches: 95
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Query Match: 80.78% Indels: 0
DB: 1 Gaps: 0
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QY 121 TACCTCAGAAAGCCAGGCGAGTCTCCAGAGCTCTCTGATCTATTTGATGTCCACCCGGGCA 180
Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 60
QY 181 TCAGGGCTCCCTGACAGAGTTCAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCA 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnSerPro 100
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RESULT 8
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; Sequence 88, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE: 07-JUN-1995
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; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
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; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VK2 consensus
US-08-476-349A-88

Alignment Scores:
Pred. No.: 4,85e-54 Length: 112
Score: 500.00 Matches: 95
Percent Similarity: 91.96% Conservative: 8
Best Local Similarity: 84.82% Mismatches: 9
Query Match: 80.78% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x US-08-476-349A-88 (1-112)
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGCGCTCC 60
Db 1 AsplleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTGTAAGAGTGGGAAGACATCTGAATTGG 120
Db 21 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAsnThrTyrLeuAsnTrp 40
QY 121 TACCTGCAGAACCGAGGCGAGTCTCCACAGCTCCGTGATCTATTGATCTCCACCGCGCA 180
Db 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 60
QY 181 TCAGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 80
QY 241 AGCAGAGTGGGCGTGGAGTCTGGGTATTACTCTCAACAGCTGGTAGATATCCA 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaLeuGlnSerPro 100

RESULT 9
US-08-482-882-66
; Sequence 66, Application US/08482882
; Patent No. 5773218
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,882
; FILING DATE: 07-JUN-1995
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5773218and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-882-66

Alignment Scores:
Pred. No.: 8,75e-54 Length: 116
Score: 498.00 Matches: 95
Percent Similarity: 91.07% Conservative: 7
Best Local Similarity: 84.82% Mismatches: 10
Query Match: 80.45% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-17 (1-348) x US-08-482-882-66 (1-116)
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGCGCTCC 60
Db 5 AsplleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTGTAAGAGTGGGAAGACATCTGAATTGG 120
Db 25 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44
QY 121 TACCTGCAGAACCGAGGCGAGTCTCCACAGCTCCGTGATCTATTGATCTCCACCGCGCA 180
Db 45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 64
QY 181 TCAGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 84
QY 241 AGCAGAGTGGGCGTGGAGTCTGGGTATTACTCTCAACAGCTGGTAGATATCCA 300
Db 85 SerArgValGluAlaGluAspValGlyValTyrCysSerGlnSerThrHisValPro 104
QY 301 TTCAGTTTCGGCCAGGACCAAGTGGAGATCAAA 336
Db 105 TyrThrPheGlyGlnGlyThrLysValGluIleLys 116

RESULT 10
US-08-483-389-66
; Sequence 66, Application US/08483389
; Patent No. 5811517
; GENERAL INFORMATION:
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QY 181 TCAGGGGTCCTGACAGAGTTCAGTGGCAGTGGATCAGGCAGACAGATTTTACACTGAAATC 240
Db 65 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 84
QY 241 AGCAGAGTGGAGGCTGAGGATGTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 85 SerArgValGluAlaGluAspValGlyValTyrTyrCysSerGlnSerThrHisValPro 104
QY 301 TTCACGTTGGCCAGGAGGACCAAGTGGAGATCAAA 336
Db 105 TyrThrPheGlyGlnGlyThrLysValGluIleLys 116
RESULT 11
US-08-487-113D-66
; Sequence 66, Application US/08487113D
; Patent No. 5837822
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,113D
; FILING DATE: 05-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5837822and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-113D-66
Alignment Scores: 8.75e-54 Length: 116
Pred. No.: 8.75e-54

APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-RELATED PROTEIN
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,389
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Suh, Young J.
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/32760
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-389-66
Alignment Scores:
Pred. No.: 8.75e-54 Length: 116
Score: 498.00 Matches: 95
Percent Similarity: 91.07% Conservative: 7
Best Local Similarity: 84.82% Mismatches: 10
Query Match: 80.45% Indels: 0
DB: 2 Gaps: 0
US-09-674-716B-17 (1-348) x US-08-483-389-66 (1-116)
QY 1 GATATGTCAGTCACTTCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 60
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyLeuProAlaSer 24
QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCCCTGATAAGGATGGGAACATACCTGAAATGG 120
Db 25 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44
QY 121 TACCTGACAGACCGAGGAGTCTCCACAGCTCCCTGATCTATTGTCATGTCACCCGGCA 180
Db 45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 64

| | | | |
|------------------------|--------|----------------|----|
| Score: | 498.00 | Matches: | 95 |
| Percent Similarity: | 91.07% | Conservatives: | 7 |
| Best Local Similarity: | 84.82% | Mismatches: | 10 |
| Query Match: | 80.45% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-09-674-716B-17 (1-348) X US-08-487-113D-66 (1-116)

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| 60 | QY | 1 | GATATTGTGATCACTCAGTCTCCACTCTCCCTGCGCCGTACCCCTGGAGAGCCGGCTCC | |
| 60 | Db | 5 | AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaIleSer | |
| 120 | QY | 61 | ATCTCCTGTCGTCGAGTAAGAGTCTCCTGTATTAAGGATGGGAAGACATACTTGAATTGG | |
| 120 | Db | 25 | IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp | |
| 180 | QY | 121 | TACCTGCAGAAAGCGAGGCAGTCTCCAGAGTCTGTATTTGATGTCACCCCGGCA | |
| 180 | Db | 45 | TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe | |
| 240 | QY | 181 | TCAGGGGTCCTTCAGAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC | |
| 240 | Db | 65 | SerGlyValproAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle | |
| 300 | QY | 241 | ACGACAGTGGAGGCTCAGGATCTTGGGGTTTACTGTCTCAACAGCTGTGAGAGTATCCA | |
| 300 | Db | 85 | SerArgValGluAlaSerLysValGlyValTyrTyrCysSerGlnSerThrHisValPro | |
| 360 | QY | 301 | TTACAGTTTCGGCCAAAGGCACCAAGTGGAGATCAAA | 336 |
| 360 | Db | 105 | TyrThrPheGlyGlnGlyThrLysValGluIleLys | 116 |

RESULT 12

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US-08-473-503--66
; Sequence 66, Application US/08473503
; Patent No. 5869262
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,503
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,754
; FILING DATE: 05-AUG-1994
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/869,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689

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APPLICATION NUMBER: US/08/483,932
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5880268and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856-
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-932-66

Alignment Scores:
Pred. No.: Length: 116
Score: 498.00 Matches: 95
Percent Similarity: 91.07% Conservative: 7
Best Local Similarity: 84.82% Mismatches: 10
Query Match: 80.45% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-17 (1-348) x US-08-483-932-66 (1-116)

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCAGCCCTGGAGAGCGGCTCC 60
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24
Qy 61 ATCTCTGCTGCTCGAGTAAGAGTCTCCTGTATAGGAGGAGACATATCTGAATTGG 120
Db 25 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44
Qy 121 TACCTGCAGAGCCAGGGAGTCTCCAGCTCCTGATCTATTGATCTCCACCGGGCA 180
Db 45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 64
Qy 181 TCAGGGGTCCTGACAGGTTAGTGGAGTGGAGCAGACAGATTTTACACTGAAATC 240
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 84
Qy 241 ACCAGAGTGGAGGCTCAGGATCTGGGTTTATTACTCTCAACAGCTGGTAGATCCA 300
Db 85 SerArgValGluAlaGluAspValGlyValTyrTyrCysSerGlnSerThrHisValPro 104
Qy 301 TTCAGGTTGGCAGAGGACCAAGTGGAGATCAA 336
Db 105 TyrThrPheGlyGlnGlyThrLysValGluIleLys 116

RESULT 14

US-08-720-420A-66

; Sequence 66, Application US/08720420A

Patent No. 5999843
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,420A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 33282
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856-
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-420A-66

Alignment Scores:
Pred. No.: Length: 116
Score: 498.00 Matches: 95
Percent Similarity: 91.07% Conservative: 7
Best Local Similarity: 84.82% Mismatches: 10
Query Match: 80.45% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-17 (1-348) x US-08-720-420A-66 (1-116)

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCAGCCCTGGAGAGCGGCTCC 60
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24

QY 61 ATCTCTGTCGCTCAGTAAAGTCTCCTGTATAGGATGGGAACACATACCTGTAATGG 120
Db 25 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44
QY 121 TACCTCAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACACCGGGCA 180
Db 45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 64
QY 181 TCAGGGGTCCCTGACAGGTTACGTGCGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 84
QY 241 AGCAGAGTGGAGCTGAGGATGTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 85 SerArgValGluAlaGluAspValGlyValTyrTyrCysSerGlnSerThrHisValPro 104
QY 301 TTCACGTTCCGCAAGGACCAAGTGGAGATCAAA 336
Db 105 TyrThrPheGlyGlnGlyThrLysValGluIleLys 116

RESULT 15

US-08-714-017-66
; Sequence 66, Application US/08714017
; Patent No. 6040176
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,754
; FILING DATE:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/899,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6040176and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-714-017-66
Alignment Scores:
Pred. No.: 8,75e-54 Length: 116
Score: 498.00 Matches: 95
Percent Similarity: 91.07% Conservative: 7
Best Local Similarity: 84.82% Mismatches: 10
Query Match: 80.45% Indels: 0
DB: 3 Gaps: 0
US-09-674-716B-17 (1-348) x US-08-714-017-66 (1-116)
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCTCCCTGACCCCTCGAGAGCGGCTCC 60
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24
QY 61 ATCTCTGTCGCTCAGTAAAGTCTCCTGTATAGGATGGGAAGACATACCTGTAATGG 120
Db 25 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAspThrTyrLeuHisTrp 44
QY 121 TACCTCAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACACCGGGCA 180
Db 45 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLysValSerAsnArgPhe 64
QY 181 TCAGGGGTCCCTGACAGGTTACGTGCGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 65 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 84
QY 241 AGCAGAGTGGAGCTGAGGATGTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 85 SerArgValGluAlaGluAspValGlyValTyrTyrCysSerGlnSerThrHisValPro 104
QY 301 TTCACGTTCCGCAAGGACCAAGTGGAGATCAAA 336
Db 105 TyrThrPheGlyGlnGlyThrLysValGluIleLys 116
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Job time : 11.5112 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:29:27 ; Search time 52.926 Seconds

(without alignments)
4852.647 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 2405

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2/USPTC_spool_p/US09674716/runat_30092004_070259_25882/app_query.fasta_1.3164
-DB=PIR_78 -QFMT=fastan -SUFFIX=pr -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09674716 -CGEN 1 1 152 @runat_30092004_070259_25882 -NCPU=6 -ICPU=3
-NO_WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREAS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 78:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------|---------------------|
| 1 | 1756 | 73.0 | 330 | 1 GHUU | Ig gamma-1 chain C |
| 2 | 1619.5 | 67.3 | 377 | 2 A23511 | Ig gamma-3 chain C |
| 3 | 1617.5 | 67.3 | 377 | 2 A60764 | Ig gamma-3 chain C |
| 4 | 1608 | 66.9 | 326 | 1 G2HU | Ig gamma-2 chain C |
| 5 | 1579.5 | 65.7 | 327 | 1 G4HU | Ig gamma-4 chain C |
| 6 | 1563 | 65.0 | 444 | 2 PC4436 | monoclonal antibody |
| 7 | 1450.5 | 60.3 | 470 | 2 S22080 | Ig heavy chain pre |
| 8 | 1430.5 | 59.5 | 374 | 2 S69339 | Ig heavy chain V r |
| 9 | 1419 | 59.0 | 469 | 2 S37483 | Ig gamma-2a chain |
| 10 | 1415.5 | 58.9 | 472 | 2 S31459 | Ig gamma-1 chain - |
| 11 | 1400.5 | 58.2 | 446 | 2 S40295 | Ig gamma-2a chain |
| 12 | 1361.1 | 56.6 | 474 | 1 G2MS11 | Ig gamma-2b chain |
| 13 | 1351 | 56.2 | 475 | 2 S01321 | Ig gamma-2b chain |
| 14 | 1259 | 52.3 | 328 | 2 I47159 | Ig gamma 2a chain |

ALIGNMENTS

RESULT 1

GHUU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999
C;Accession: A93433; S33887; B90563; A90564; B91668; A31723; A02146
R;Ellison J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: EMBL:Z17370

A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, 1

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: EMBL:Z17370

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A;Reference number: S33887; MUID:83001943; PMID:6811139

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: EMBL:Z17370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A;Reference number: A90563; MUID:71064024; PMID:5489771

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

Ig gamma 2b chain
Ig gamma-1 chain C
Ig gamma chain C r
Ig gamma 1 chain c
Ig gamma 3 chain c
Ig gamma chain C r
Ig gamma-2 chain C
Ig heavy chain C r
Ig gamma-1 chain C
Ig gamma-3 heavy C
Ig gamma-1 chain C
Ig gamma-1 chain C
Ig gamma-2b chain
Ig gamma-3 chain C
Ig gamma-3 chain C
Ig gamma-2a chain
Ig gamma-2 chain C
Ig gamma-2b chain
Ig gamma 4 chain c
Ig epsilon chain C
Ig heavy chain pre
Ig heavy chain VHI
Ig y heavy chain (r
Ig heavy chain V-I
Ig gamma-1 heavy c
Ig heavy chain (DO
Ig heavy chain (Ma

A;Residues: 1-96, 'R', 98-135 <CUN>
A;Note: this sequence has the Gln(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequence
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu

A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, 242
A;Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie).
igen Primärstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668

A;Molecule type: protein
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A;Note: this sequence has the Gln(17) and Gln(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723

A;Molecule type: protein
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A;Note: this sequence has the Gln(3) and Gln(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds

R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enamide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:

A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar
tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83, 144-204, 250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Alignment Scores:
Pred. No.: 4, 73e-89 Length: 330
Score: 1756.00 Matches: 328
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 2
Query Match: 73.01% Indels: 0
DB: 1 Gaps:

US-09-674-716b-18 (1-1335) x GHU (1-330)

QY 343 GCCTCCACAGGGCCATCGGTCTTCCCGTGCACCTCCGACCTCCGACAGACCTCTGGG 402
Db 1 AlaserThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 20
QY 403 GGCACAGCGGCCCTGGGCTGCCTCGCTCAAGGACTACTTCCCGGACCGGTGACGGTGTGC 462

Db 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 463 TGGAACTCAGGCGCCCTGACCGAGCGGTGCACACCTCCCGCTGTCTCAGAGCTCTCA 522
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 523 GGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTCCAGCAGCTTGGGACCAGACC 582
Db 61 GlyLeuTyrSerLeuSerValThrValProSerSerSerLeuGlyThrGlnThr 80
QY 583 TACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGCACAAGAAAGTGGAGCC 642
Db 81 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100
QY 643 AAATCTGTGCAAAAACCTCACATGCCACCGTGCACAGCAGCTCCGCGGGGCA 702
Db 101 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuGlyGly 120
QY 703 CCGTCACTTCTCTCTCCCGCCCAACCCAGGACACCTCATGATCTCCCGGACCCCT 762
Db 121 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 140
QY 763 GAGGTCACTGCGTGTGTGTGACGTGACGTGCACAGCAGCCCTGAGGTCAAGTTCAC 822
Db 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 160
QY 823 TAGCTGGAGCGGTGTGAGTGTGATATCCACAGACAAAGCCGCGGAGGAGCAGTACAC 882
Db 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnThrAsn 180
QY 883 AGCAGCTACCGTGTGTGTGACGTCTCCACCGTCTGCACAGCAGCTGGGTGAATGGCA 942
Db 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200
QY 943 GAGTCAAGTGAAGTCTTCCAAAGCCCTCCAGCGCCCATCGAGAAACCATCTCC 1002
Db 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 220
QY 1003 AAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTCCCGCCCATCCCGGATG 1062
Db 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240
QY 1063 CTGACCAAGAACCCAGCTCAGCTGACCTGCCTGGTCAAGAGTCTTATCCCGACATC 1122
Db 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260
QY 1123 GCGTGTGAGTGGAGAGCAATGGGAGCGGAGACAACTACAGACCGCTCCCGT 1182
Db 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 280
QY 1183 CTGGACTCCGAGCGGTCTCTTCTCTACACAGAGCTCACCGTGCACAAGACAGGTGG 1242
Db 281 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300
QY 1243 CAGCAGGGAAGCTTCTCTCATGCTCCGCTGATGATGAGGTCTCTGCACACCATACAG 1302
Db 301 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 320
QY 1303 CAGAAGAGCTCTCCCTGTCTCCGGTAAA 1332
Db 321 GlnLysSerLeuSerLeuSerProGlyLys 330

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Buck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con
A;Reference number: A23511; MUID:86148507; PMID:3081877

A:Accession: A23511
 A:Molecule type: DNA
 A:Residues: 1-377 <HUC>
 A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
 C:Genetics:
 A:Gene: GDB:IGHG3
 A:Cross-references: GDB:119339; OMIM:147120
 A:Map position: 14q32.33-14q32.33
 A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 1,39e-81 Length: 377
 Score: 1617.50 Matches: 307
 Percent Similarity: 84.08% Conservative: 10
 Best Local Similarity: 81.43% Mismatches: 13
 Query Match: 67.34% Indels: 47
 DB: 2 Gaps: 1

US-09-674-716B-18 (1-1335) x A23511 (1-377)

```

QY 343 GCCTCCACCAAGGGCCCATCGTCTTCCCTGGCACTCTCTCCAGAGCACCTCTGGG 402
DB 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGly 20
QY 403 GGCACAGCGGCGCTCGGTGCTGTCAGGACTACTTCCCGAACCGGTGACGGTGTG 462
DB 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 463 TGGAACTGAGCGCGCTGACAGCGCGGTGCACACCTTCCCGGTGCTCTACAGTCTCA 522
DB 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 523 GGACTCTACTCTCCAGAGCGGTGTGACCGTGGCTCCAGCAGTTCGGGACCCAGACC 582
DB 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80
QY 583 TACATCTGCAAGTGAATCAAGCCGACACACACCAAGGTGGACAAAGTG----- 636
DB 81 TyrThrCysAsnValAsnHisLysProSerAnThrLysValAspLysArgValGluLeu 100
QY 636 ----- 636
DB 101 LysThrProLeuGlyAspThrThrHisThrCysProArgCysProGluProLysSerCys 120
QY 636 ----- 636
DB 121 AspThrProProCysProArgCysProGluProLysSerCysAspThrProProPro 140
QY 637 -----GAGCCCAATCTGTGACAAACTCACATGCCCGCGGCCA 681
DB 141 CysProArgCysProGluProLysSerCysAspThrProProCysProArgCysPro 160
QY 682 GCACCTGAATCTCGCGGGGCACCGTCAGTCTTCTCTTCCCGCCAAACCCCAAGGACACC 741
DB 161 AlaProGluLeuLeuGlyGlyProSerValPheLeuPheProLysProLysAspThr 180
QY 742 CTCATGATCTCCGAGCCCTGAGTCACATCGGTGGTGGTGGAGTGCAGCAGCACAGAC 801
DB 181 LeuMetIleSerArgThrProGluValThrCysValValValAspValSerHisGluAsp 200
QY 802 CTGAGGTCAAGTCAACTGAGTACGTGGACGGCGGTGGAGTGCATAATGCCAAGACAAAG 861
DB 201 ProGluValGlnPheLysTyrTyrValAspGlyValGluValHisAlaLysThrLys 220
QY 862 CCGCGGGAGAGCAGTACAAACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 921
DB 221 ProArgGluGluGlnTyrAsnSerThrPheArgValValSerValLeuThrValLeuHis 240
QY 922 CAGGACTGCTGAATGGCAAGGAGTCAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCC 981

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DB 241 GlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAla 260
QY 982 CCCATCGAGAAAACCATCTCCAAAAGCAAGGCGCCCGGAGAACACACAGGTGTACACC 1041
DB 261 ProIleGluLysThrIleSerLysThrLysGlyGlnProArgGluProGlnValTyrThr 280
QY 1042 CTCGCCCATCCCGGATGAGCTGACCAAGAACAGGTCAGCTGACCTGACCTGCTGCTCAA 1101
DB 281 LeuProProSerArgGluMetThrLysAsnGlnValSerLeuThrCysLeuValLys 300
QY 1102 GGTCTTATCCACGACATCGCGTGGAGTGGAGCAATGGGAGCGGAGGAGACAAC 1161
DB 301 GlyPheTyrProSerAspIleAlaValGluTyrGluSerSerGlyGlnProGluAsnAsn 320
QY 1162 TACAAGACACGCTCCCGTGTGACTCCGAGCGGTCTCTTCTCTTACACAGCTC 1221
DB 321 TyrAsnThrThrProProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeu 340
QY 1222 ACCGTGCACAAGAGCAGGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGATGAG 1281
DB 341 ThrValAspLysSerArgTrpGlnGlnGlyAsnIlePheSerCysSerValMetHisGlu 360
QY 1282 GCTCTGCACAACCATACACGCAAGAGCGCTCTCCCTGTCTCCGGGTAAA 1332
DB 361 AlaLeuHisAsnArgPheThrGlnLysSerLeuSerLeuSerProGlyLys 377

```

RESULT 3

A60764
 Ig gamma-3 chain C region, form IAT - human
 C:Species: Homo sapiens (man)
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
 C:Accession: A60764
 R:Huck, S.; Lefranc, G.; Lefranc, M.P.
 Immunogenetics 30, 250-257, 1989
 A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
 A:Reference number: A60764; MUID:90007613; PMID:2571587
 A:Accession: A60764
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-377 <HUC>
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 1,79e-81 Length: 377
 Score: 1617.50 Matches: 307
 Percent Similarity: 84.08% Conservative: 10
 Best Local Similarity: 81.43% Mismatches: 13
 Query Match: 67.26% Indels: 47
 DB: 2 Gaps: 1

US-09-674-716B-18 (1-1335) x A60764 (1-377)

```

QY 343 GCCTCCACCAAGGGCCCATCGTCTTCCCGTGGCACTCTCTCCAGAGCACCTCTGGG 402
DB 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGly 20
QY 403 GGCACAGCGGCGCTCGGTGCTGTCAGGACTACTTCCCGAACCGGTGACGGTGTG 462
DB 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 463 TGGAACTGAGCGCGCTGACAGCGCGGTGCACACCTTCCCGGTGCTCTACAGTCTCA 522
DB 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 523 GGACTCTACTCTCCAGAGCGGTGTGACCGTGGCTCCAGCAGTTCGGGACCCAGACC 582
DB 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80
QY 583 TACATCTGCAAGTGAATCAAGCCGACACACCAAGGTGGACAAAGTG----- 636
DB 81 TyrThrCysAsnValAsnHisLysProSerAnThrLysValAspLysArgValGluLeu 100

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QY 636 ----- 636
 Db 101 LysThrProLeuGlyAspThrThrHisThrCysProArgCysProGluProLysSerCys 120
 QY 636 ----- 636
 Db 121 AspThrProProCysProArgCysProGluProLysSerCysAspThrProPro 140
 QY 637 ----- 637
 Db 141 CysProArgCysProGluProLysSerCysAspThrProProCysProArgCysPro 160
 QY 682 GCACCTGAATCCGGGGGACCGTCAGTCTCTCCCTCCCAAAACCCAGGACACC 741
 Db 161 AlaProGluLeuGlyGlyProSerValPheLeuPheProLysPheProLysAspThr 180
 QY 742 CTGATGATCTCCGGACCCCTGAGTCAATCGTGGTGGAGCTGAGCCAGGAC 801
 Db 181 LeuMetIleSerArgThrProGluValThrCysValValValAspValSerHisGluAsp 200
 QY 802 CCTGAGTCAAGTCAACTGAGTGGAGCGGCGTGGAGTGCATAATGCCAAGCAAG 861
 Db 201 ProGluValGlnPheLysIleThrValAspGlyValGluValHisAsnAlaLysThrLys 220
 QY 862 CCGCGGAGGAGCAGTACACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 921
 Db 221 ProArgGluGluGlnIleThrAsnSerThrPheArgValValSerValLeuThrValLeuHis 240
 QY 922 CAGGACTGGCTGAATGGCAGGAGTCAAGTCAAGTGGTGGTGGTGGTGGTGGTGGTGG 981
 Db 241 GlnAspTrpLeuAsnGlyLysGluTrpLysCysLysValSerAsnLysAlaLeuProAla 260
 QY 982 CCATCGAGAAACCATCTCCAAAGCAAGGCGACCCCGGAGACCCAGGAGTGGTGGTGGTGG 1041
 Db 261 ProIleGluLysThrIleSerLysThrLysGlyGlnProArgGluProGlnValThr 280
 QY 1042 CTGCCCCCATCCCGGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1101
 Db 281 LeuProSerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLys 300
 QY 1102 GCGTCTATCCAGCAGCATCCCGTGGAGTGGAGCAATGGCGAGCAATGGCGAGCAAC 1161
 Db 301 GlyPheTrpProSerAspIleAlaValGluTrpGluSerGlyGlnProGluAsn 320
 QY 1162 TACAAGACACCGCTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1221
 Db 321 TyrAsnThrThrProProValLeuAspSerAspGlySerPhePheLeuTySerArgLeu 340
 QY 1222 ACGTGGCAGCAGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1281
 Db 341 ThrValAspLysSerArgTrpGlnGluGlyAsnValPheSerCysSerValMethisGlu 360
 QY 1282 GCTCTCAACACCTACACGAGAGAGCCCTCTCCCTGCTCCCGGTAAG 1332
 Db 361 AlaLeuHisAsnArgPheThrGlnLysSerLeuSerLeuSerProGlyLys 377

RESULT 4

G2HU
 Ig gamma-2 chain C region - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000
 C:Accession: A93906; A92809; A90752; A93132; A02148
 R:Ellison, J.; Hood, L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
 A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
 A:Reference number: A93906; MUID:182197621; PMID:6804948
 A:Accession: A93906
 A:Molecule type: DNA
 A:Residues: 1-326 <ELL>
 A:Cross-references: GB:V00554; GB:J00230; NID:q32759; PIDN:CA58438.1; PID:g6066056
 A:Note: Lys-326 is probably removed posttranslationally
 R:Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980
 A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fi
 A:Reference number: A92809; MUID:81007873; PMID:6774012
 A:Contents: myeloma protein T11
 A:Accession: A92809
 A:Molecule type: protein
 A:Residues: 1-19, 'Q', '21-57', 'Z', '59', 'A', '61-193', 'D', '195-325 <WAN>
 A:Note: Trp-156 is at or near the complement-binding site
 R:Connell, G.E.; Parr, D.M.; Hofmann, T.
 Can. J. Biochem. 57, 758-767, 1979
 A:Title: The amino acid sequences of the three heavy chain constant region domains of a
 A:Reference number: A90752; MUID:80001357; PMID:113060
 A:Contents: myeloma protein Zie
 A:Accession: A90752
 A:Molecule type: protein
 A:Residues: 1-24, 'E', '26-57', 'EV', '60-85', '132-171', 'ZZZ', '175', 'B', '177-193', 'D', '195-196', 'Q', '198-2
 A:Note: this sequence has since been revised
 R:Hofmann, T.; Parr, D.M.
 Mol. Immunol. 16, 923-925, 1979
 A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
 A:Reference number: A93132; MUID:80114419; PMID:118920
 A:Contents: Zie
 A:Accession: A93132
 A:Molecule type: protein
 A:Residues: 238-275 <HOP>
 R:Hofmann, T.; Parr, D.M.
 submitted to the Atlas, March 1980
 A:Reference number: A94591
 A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
 A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
 red
 R:Milstein, C.; Frangione, B.
 Biochem. J. 121, 217-225, 1971
 A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
 A:Reference number: A90253; MUID:72033500; PMID:4940472
 A:Contents: annotation; myeloma protein Sa, disulfide bonds
 R:Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A:Title: Structural studies of immunoglobulin G.
 A:Reference number: A93157; MUID:69064124; PMID:5782707
 A:Contents: annotation; Sa, disulfide bonds
 C:Genetics:
 A:Gene: GDB:IGHG2
 A:Cross-references: GDB:119338; OMIM:147110
 A:Map position: 14q32.33-14q32.33
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM1>
 F:133-202/Domain: immunoglobulin homology <IM2>
 F:239-306/Domain: immunoglobulin homology <IM3>
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:27-83,140-200,246-304/Disulfide bonds: #status experimental
 F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores: 6.07e-81 Length: 326
 Pred. No.: 1608.00 Matches: 302
 Score: 95.15% Conservative: 12
 Percent Similarity: 91.52% Mismatches: 12
 Best Local Similarity: 66.86% Indels: 4
 Query Match: 1 Gaps: 2
 DB:

US-09-674-716B-18 (1-1335) x G2HU (1-326)

Qy 343 GCCTCCACCAAGGCGCCATCGGTCTTCCCGCTGGCAGCCCTCTCCAGAGCACCTCTGGG 402

Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 20

Qy 403 GGCACAGCGCGCCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 462

Db 21 SerThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 463 TGGAACTCAGCGCCCTGACAGCGCGTGCACACCTTCCTCCGGCTGCTCCTACAGTCTCA 522
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 60
QY 523 GGACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTGGGACCCAGACC 582
Db 61 GlyLeuTyrSerLeuSerSerValThrValProSerSerAsnPheGlyThrGlnThr 80
QY 583 TACATCTGCAAGCTGAATCAAGCCCAAGCAACCAAGGTGGACAGAAAGTGGAGCCC 642
Db 81 TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLysThrValGluArg 100
QY 643 AAATCTGTGACAAAACACTCACATGCCACCGTCCAGCAGCTGAACCTCGCGGGGCA 702
Db 101 LysCysCysValGlu-----CysProProCysProAlaProProValAlaGly--- 116
QY 703 CGCTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCGGACCCCT 762
Db 117 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 136
QY 763 GAGTTCATCGTGGTGGTGGACGTGACCCAGCAGACCTGAGTCAAGTTCACATCGG 822
Db 137 GluValThrCysValValAspValSerHisGluAspProGluValGlnPheAsnTrp 156
QY 823 TACGTGGACGGGTGGAGTGCATATGCAAGCAAAAGCCCGGGAGGACGATACAA 882
Db 157 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnPheAsn 176
QY 883 AGCAGTACCGTGGTGGTGGTCTCAGCTCCTCAGTCCCTGACAGGACTGCTGAAATGGCAG 942
Db 177 SerThrPheArgValValSerValLeuThrValValHisGlnAspTrpLeuAsnGlyLys 196
QY 943 GAGTCAAGTGAAGTGTCTCCAAAGACCTCCAGCCCTCCAGCCCTCGAGAAACCATCTCC 1002
Db 197 GluTyrLysCysLysValSerAsnLysGlyLeuProAlaProIleGluLysThrIleSer 216
QY 1003 AAAGCCAAAGGACACCCCGAGAAACACAGTGTATACACCTGCCCCCTCCCGGATAG 1062
Db 217 LysThrLysGlnProArgGluProGlnValTyrThrLeuProProSerArgGluGlu 236
QY 1063 CTGACCAAGAACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1122
Db 237 MetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 256
QY 1123 GCCGTGGAGTGGAGCAATCGGAGCGGAGAGAACTCAAGACCAACGCTCCCGGTG 1182
Db 257 AlaValGluTyrGlnLysAsnGlyGlnProGluAsnAsnTyrLysThrThrProProMet 276
QY 1183 CTGGACTCGAGCGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGG 1242
Db 277 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 296
QY 1243 CAGCAGGGAAGCTCTCTCATGCTCCGTCGATGATGAGCTCTGCACAAACCATACACG 1302
Db 297 GlnGlnGlnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 316
QY 1303 CAGAGAGCCTTCCTGCTCTCCGGTAAA 1332
Db 317 GlnLysSerLeuSerLeuSerProGlyLys 326

RESULT 5
G4HU

Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 16-Jul-1999
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299662
A:Accession: A90933

A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant re
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30,81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/binding site: carbohydrate (Asn) (covalent) #status predicted
Alignment Scores:
Pred. No.: 2 21e-79 Length: 327
Score: 1579.50 Matches: 298
Percent Similarity: 93.94% Conservative: 12
Best Local Similarity: 90.30% Mismatches: 17
Query Match: 65.68% Indels: 3
DB: 1 Gaps: 1
US-09-674-716B-18 (1-1335) x G4HU (1-327)

QY 343 GCCTCCACCAAGGCGCCATCGCTCTCCCTCCGACCTCTCCAGAGCAGCTCTGGG 402
Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 20
QY 403 GGACACGCGCCCTCGGCTCCCTGGTCAAGGACTACTTCCCGAAACCGGTGAGCGTGTG 462
Db 21 SerThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 463 TGGAACTCAGCGCCCTGACAGCGCGTGCACACCTTCCCGGTGCTCTACAGTCTCTCA 522
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 523 GGACTCTACTCCTCAGCAGCGTGGTACCGTCCCTCCAGCAGCTTGGGACCCAGACC 582
Db 61 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrLysThr 80
QY 583 TACATCTGCAAGCTGAATCAAGCCCAAGCAACCAAGGTGGACAGAAAGTGGAGCCC 642
Db 81 TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLysArgValGluSer 100
QY 643 AAATCTGTGACAAAACACTCACATGCCACCGTCCAGCAGCTGAACCTCGCGGGGCA 702
Db 101 Lys-----TyrGlyProProCysProSerCysProAlaProGluPheLeuGlyGly 117
QY 703 CGCTCAGTCTTCTCTTCTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 762
Db 118 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 137
QY 763 GAGTTCATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 822
Db 138 GluValThrCysValValAspValSerGlnGluAspProGluValGlnPheAsnTrp 157
QY 823 TACGTGGACGGGTGGAGTGCATATGCAAGCAAAAGCCCGGGAGGACGATACAA 882
Db 158 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnPheAsn 177

QY 883 AGCAGTACCGTGTGGTACGCGTCTCCACCGCTCTGCACCGAGCTGGCTGAATGCGAAG 942
 Db 178 SerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 197
 QY 943 GAGTACAGTGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCC 1002
 Db 198 GluTyLysCysLysValSerAsnLysGlyLeuProSerSerLeuLysThrIleSer 217
 QY 1003 AAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTACACCTCCGCCATCCCGGATGAG 1062
 Db 218 LysAlaLysGlyGlnProArgGluProGlnValTyThrLeuProProSerGlnGlu 237
 QY 1063 CTGACCAAGAACAGGTCTGAGCTGAGCTCCCTCGGTCAAGGTTTATCCAGCAGATC 1122
 Db 238 MetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAspIle 257
 QY 1123 GCGGTGAGTGGAGAGCAATGGCAGCGGAGAACACTCAAGACACACGCTCCCGTG 1182
 Db 258 AlaValGluTrpLeuSerAsnGlyGlnProGluAsnAsnTyLysThrThrProVal 277
 QY 1183 CTGGACTCCGACGGCTCTCTCTCTACAGCAAGCTCACCGTGGACAAAGAGCGTGG 1242
 Db 278 LeuAspSerAspGlySerPhePheLeuTySerArgLeuThrValAspLysSerArgTrp 297
 QY 1243 CAGCAGGGAAGCTCTCTCTCTGCTCCGTGATGATGAGCTCTGCACACCACTACAG 1302
 Db 298 GlnGluGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyThr 317
 QY 1303 CAGAAGAGCTCTCCCTGTCTCCGGTAA 1332
 Db 318 GlnLysSerLeuSerLeuSerLeuGlyLys 327

RESULT 6

PC4436
 monoclonal antibody 13-1 heavy chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
 C:Accession: PC4436
 R:Kashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kanachi, M.; Harada, A.
 Biochem. Biophys. Res. Commun. 240, 566-572, 1997
 A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
 A:Reference number: JCS810; PMID:98063277; PMID:9398605
 A:Accession: PC4436
 A:Molecule type: protein
 A:Residues: 1-444 <EKA>
 C:Comment: This catalytic antibody has peroxidase activity. It is directed against
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:251-320/Domain: immunoglobulin homology <IM>
 F:22/Disulfide bonds: interchain (to 98) #status predicted
 F:99/Disulfide bonds: interchain (to 109) #status predicted

Alignment Scores:
 Pred. No.: 1,69e-78 Length: 444
 Score: 1563.00 Matches: 288
 Percent Similarity: 78.76% Conservative: 68
 Best Local Similarity: 63.72% Mismatches: 80
 Query Match: 64.99% Indels: 16
 DB: 2 Gaps: 6

US-09-674-716b-18 (1-1335) x PC4436 (1-444)

QY 1 GAGGTGACGTGGTGGAGTCTGGGGAGCTTGGTAAAGCCCGGGGTCCCTTAGATC 60
 Db 1 GluValGln**ValGluThrGlyGlyLeuValArgProGlyAsnSerLeuLysLeu 20
 QY 61 TCCTGTCAGCTAGCGATTCTACTTCTAGTGGCTACTGATCTCTGGTCCGCGAGGCT 120
 Db 21 SerCysLeuThrSerGlyPheThrPheSerAsnTyArgMetHisTrpLeuArgGlnPro 40
 QY 121 CAGGGAAGGGCTCGAGTGGGTCTGAAATAGATTGAAATCTGAAATATTGCAACA 180
 Db 41 ProGlyLysArgLeuGluTrpIleAlaValIleThrValLysSerAspAsnTyGlyAla 60

QY 181 CATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
 Db 61 LysTyAlaGluSerValArgGlyArgPheThrIleSerArgAspSerLysSerSer 80
 QY 241 CTGTATCTGAAATGAAACAGCCCTGAAACCGAGGACACAGCCGTGTATTACTGT----- 294
 Db 81 ValTyLeuGlnMetAsnArgLeuArgGluGluAspThrAlaThrTyTyTyCysArg 100
 QY 295 ACAGATTTCATA-----GACTGGGGCCAGGAAACACTAGTCTACCGTCTCTCA 342
 Db 101 ThrProTrpValTyAlaMetAspCysTrpGlyGlnGlyThrSerValIleValSerSer 120
 QY 343 GCCTTCACCAAGGGCCATCGGTCTTCCCTGGCACCTCTCTCCAGAGACCTCTCGG 402
 Db 121 AlaLysThrThrProProSerValTyProLeuAlaProGlySerAlaAlaGlnThrAsn 140
 QY 403 GGCACAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGC 462
 Db 141 SerMetValThrLeuGlyCysLeuValLysGlyTyPheProGluProValThrValThr 160
 QY 463 TGAACCTCAGCGCCCTGACCCAGCGCGTGCACACCTTCCCGCTGTCTCAGACTCTCA 522
 Db 161 TrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGlnSerAsp 180
 QY 523 GGAATCTACTCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGAC 582
 Db 181 ---LeuTyThrLeuSerSerSerValThrValProSerSerThrTrpProSerGluThr 199
 QY 583 TACATCTGCAACGTGAATCACAAAGCCAGCAACACCAAGGTGCACAAAGAAAGTGGAGCC 642
 Db 200 ValThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysIleValPro 219
 QY 643 AATCTTGTGACAAACTCACATGCCACCG-----TGCCAGCAGCTGAATCGCG 696
 Db 220 ArgAspCysGly-----CysLysProCysIleCysThrValProGluValSer 235
 QY 697 GGGCAGCCGTCAGTCTCTCTTCTCCCAACCAAGCACACCTCATGATCTCCCG 756
 Db 236 -----SerValPheIlePheProProLysProLysAspValLeuThrLeu 252
 QY 757 ACCCTGAGTGCATCGGTGGTGGAGCGTGCAGCCAGCAACACCTCAGGTCAAGTTC 816
 Db 253 ThrProLysValThrCysValValValAspIleSerLysAspProGluValGlnPhe 272
 QY 817 AACTGTGTCAGTGCAGCGCTGGAGGTGCATTAATGCCAAGCAAGCCGCGGAGGAGCAG 876
 Db 273 SerTrpPheValAspAspValGluValHisThrAlaGlnThrGlnProArgGluGluGln 292
 QY 877 TACAACAGCAGCTAGTGGTGTGTCAGCGTCTCCTCAGCTCCTGCACAGCACTGGTGAAT 936
 Db 293 PheAsnSerThrPheArgSerValSerGluLeuProIleMetHisGlnAspTrpLeuAsn 312
 QY 937 GGCAGAGGTACAAGTCAAGTCTCCAACAAAGCCCTCCAGCCCTCCGAAACCC 996
 Db 313 GlyLysGluPheLysCysArgValAsnSerAlaAlaPheProAlaProIleGluLysThr 332
 QY 997 ATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCGCCATCCCG 1056
 Db 333 IleSerLysThrLysGlyArgProLysAlaProGlnValTyThrIleProProLys 352
 QY 1057 GATGAGTGCACGAAGAACAGGTGACCTGCTGCTGCTCAAGGCTTCTATCCAGC 1116
 Db 353 GluGlnMetAlaLysAspLysValSerLeuThrCysMetIleThrAspPhePheProGlu 372
 QY 1117 GACATCGCGTGGAGTGGAGCAATGGCGAGCCCGAGAACCAACTACAAAGACCCAGCCT 1176
 Db 373 AspIleThrValGluTrpGlnTrpAsnGlyGlnProAlaGluAsnTyLysAsnThrGln 392
 QY 1177 CCGTGTGAGCTCCGACCGCTCTCTCTCTCCTACAGCAAGCTCACCGTGGAGAGAC 1236
 Db 393 ProIleMetAspThrAspGlySerTyPheValTySerLysLeuAsnValGlnLysSer 412

| | | |
|------------------------|---------|------------------|
| Alignment Scores: | | |
| Pred. No.: | 1.3e-70 | Length: 469 |
| Score: | 1419.00 | Matches: 269 |
| Percent Similarity: | 74.45% | Conservative: 69 |
| Best Local Similarity: | 59.25% | Mismatches: 102 |

Query Match: 59.00% Indels: 14
DB: 2 Gaps: 6
US-09-674-716B-18 (1-1335) x S37483 (1-469)

| | | | |
|----|-----|--|-----|
| QY | 1 | GAGGTGACGTGCTGGAGTCTGGGGGAGGCTTGGTAAAGCCGGGGGCTCCCTTAGACTC | 60 |
| DB | 20 | GlnIleGlnLeuGlnGlnSerGlyProGluLeuValValProGlyAlaSerValIysIle | 39 |
| QY | 61 | TCCTGTGCAGCTACGGATTCACTTTCAGTGGCTACTGATCTCTGGGTCCGACGCT | 120 |
| DB | 40 | SerCysIysAlaSerGlyThrPheThrAspTyrTyrIleAsnTyrValIysGlnLys | 59 |
| QY | 121 | CCAGGGAAGGGCTCGAGTGGTTCGAAATTAGATTGAATCTGTAATTATGCAACA | 180 |
| DB | 60 | ProGlyGlnGlyLeuLysTrpIleGlyTrpIleTyrProAlaSerGlyAsn-----Thr | 77 |
| QY | 181 | CATTATGCGGAGTCTGTCAAGGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGA | 240 |
| DB | 78 | LysTyrAsnGluAsnPheLysGlyLysAlaThrLeuThrValAspThrSerSerThr | 97 |
| QY | 241 | CTGTATCTGCAAAATGAACAGCTGAAACCGAGGACACAGCGGTGATTACTGT----- | 294 |
| DB | 98 | AlaTyrMetGlnLeuSerSerLeuThrSerGluAspThrAlaValTyrPheCysAlaArg | 117 |
| QY | 295 | -----ACAGATTTCAATAGAC---TGGGGCCAGGGAACACTAGTCAACGCTC | 336 |
| DB | 118 | AlaMetGlyAlaThrAlaThrLeuLeuAspTyrTrpGlyGlnGlyThrThrLeuThrVal | 137 |
| QY | 337 | TCCTCAGCGCTCCACCAAGGGCCATCGGTCTTCCCTCGCCCTCTCCCAAGAGCACC | 396 |
| DB | 138 | SerSerAlaLysThrThrAlaProSerValTyrProLeuAlaProValCysGlyAspThr | 157 |
| QY | 397 | TCTGGGGCACAGCGGCCCTGGGTGCTGCTCAAGACTACTTCCCGAACCCTGGTACG | 456 |
| DB | 158 | ThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThr | 177 |
| QY | 457 | GTGTGCTGGAATCTCAGGCGCCCTCACCAGCGGGGTGCACACCTTCCGCGCTCTCTCAG | 516 |
| DB | 178 | LeuThrTrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGln | 197 |
| QY | 517 | TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCACGACTTGGGCACC | 576 |
| DB | 198 | SerAsp---LeuTyrThrLeuSerSerSerValThrValThrSerSerThrTrpProSer | 216 |
| QY | 577 | CAGACCTACATCTGCAGCTGAATCACAGCCAGCAACACCAAGGTGCACAGAAGATG | 636 |
| DB | 217 | GlnSerIleThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysIle | 236 |
| QY | 637 | GAGCCCAATCTGTGACAAAACCTCACACATGCCACCG-----TGCCCGACACCTGAA | 690 |
| DB | 237 | GluProArgGly---ProThrIleLysProCysProProCysLysCysProAlaProAsn | 255 |
| QY | 691 | CTGCGGGGGCACCGTCACTTCTCTTCTCCCGCAACCCCAAGACACCTCATGATC | 750 |
| DB | 256 | LeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeuMetIle | 275 |
| QY | 751 | TCCCGGACCCCTGAGGTCACTGCTGGTGTGGACGTGAGCCAGCCACAGACCCCTGAGTCT | 810 |
| DB | 276 | SerLeuSerProIleValThrCysValValValAspValSerGluAspAspProAspVal | 295 |
| QY | 811 | AGTTCAACTGTGATCGTGGACGGCGTGGAGTGCATATCCCAAGACAAGCCGGCGGAG | 870 |
| DB | 296 | GlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArg | 315 |
| QY | 871 | GAGCAGTACAACAGACACGTACCGTGTGGTCAAGCTCTCACCGTCTCTGCACAGACTGG | 930 |
| DB | 316 | GluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrp | 335 |
| QY | 931 | CTGAATGGCAAGGATACAAGTGAAGTCTCCCAACAAAGCCCTCCAGCCGCCCATCGAG | 990 |
| DB | 336 | MetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleGlu | 355 |

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Db      115 ValAspTyrAspSerSerHisAlaPheAlaTyrAlaSerTyrAspPhe-----TrpGly 132
QY      316 CAGGAACTAGTACCGTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCG 375
Db      133 ProGlyLeuLeuLeuSerValLeuSerAlaSerThrThrProProlysValTyrProLeu 152
QY      376 GCACCTCTCTCCAGAGACCTCTGGGGCCACAGCGCCCTGGTGGTCTGCTCAAGAC 435
Db      153 ThrSerCysCysGlyAspThrSerSerIleValThrLeuGlyCysLeuValSerSer 172
QY      436 TACTTCCCGAACCGGTGTCGTGGAACCTCAGCGCCCTCAGCAGCGCGCTGCAC 495
Db      173 TyrMetProGluProValThrValThrTrpAsnSerGlyAlaLeuThrSerGlyValHis 192
QY      496 ACCTTCCCGCTGCTCAGTCCCTCAGACCTACTCCTCAGCAGCGTGTGACCGTG 555
Db      193 ThrPheProAlaIleLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrVal 212
QY      556 CCCTCAGCAGCTTGGCCACCCAGACCTACATCTGCAACGTGAATCAACAAGCCCAAC 615
Db      213 ProAlaSerThrSerGlyAlaGlnThrPheIleCysAsnValAlaHisProAlaSerSer 232
QY      616 ACAAGGTGACAGAAAGTGGAGCCCAAAATCTGTGACAAACTCACACATGCCCAACG 675
Db      233 ThrLysValAspLysArgValGluProGlyCysProAspProCysLysHisCys---Arg 251
QY      676 TGCCACGACCTGAACCTCGCGGGGACCGCTCAGTCTCTCTCCCGCCCAAAACCCAAAG 735
Db      252 CysProProProGluLeuProGlyGlyProSerValPheIlePheProProlysProlys 271
QY      736 GACACCTCATGATCTCCCGGACCCCTGAGGTGCATCGGTGGTGGTGGAGCTGAGCCAC 795
Db      272 AspThrLeuThrIleSerGlyThrProGluValThrCysValValValAspValGlyGln 291
QY      796 GAAGACCTGAGTCAAGTCAACTGGTACGTGGAGCGCGGTGGAGTGCATAATGCCAAG 855
Db      292 AspAspProGluValGlnPheSerIrrPheValAspAsnValGluValArgThrAlaArg 311
QY      856 ACAAGCCCGGAGAGCAGTACACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGT 915
Db      312 ThrLysProArgGluGlnPheAsnSerThrPheArgValValSerAlaLeuProIle 331
QY      916 CTGCACCGAGTGGTGAATGGAGAGTACAGTCAAGTCTCAAGAGCCCTC 975
Db      332 GlnHisGlnAspTrpThrGlyLysGluPheLysCysLysValHisAsnGluAlaLeu 351
QY      976 CCAGCCCTCATCAGAAACCATCTCCAAAGCCAAAGCCAGCCCGGAGACCCAGACGAGTG 1035
Db      352 ProAlaProIleValArgThrIleSerArgThrLysGlyGlnAlaArgGluProGlnVal 371
QY      1036 TACACCTGCCCCATCCCGGATGAGTGCACCAAGACAGGTGAGCTGACCTGCTGCTG 1095
Db      372 TyrValLeuAlaProGlnGluLeuSerLysSerThrLeuSerValThrCysLeu 391
QY      1096 GTCAAGAGGCTTCTATCCAGACATCCCGTGGAGTGGAGAGCAATGGCAGCCG--- 1152
Db      392 ValThrGlyPheTyrProAspTyrIleAlaValGluTrpGlnLysAsnGlyGlnProGlu 411
QY      1153 ---GAGAACAACTACAGACCAAGCCCTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1209
Db      412 SerGluAspLysTyrGlyThrThrThrSerGlnLeuAspAlaAspGlySerTyrPheLeu 431
QY      1210 TACACAGCTCACCGTGGACAGAGTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1269
Db      432 TyrSerArgLeuArgValAspLysAsnSerTrpGlnGluGlyAspThrTyrAlaCysVal 451
QY      1270 GTGATGATAGGCTCTGCACAAACCTACACGACGAGAGGAGGAGGAGGAGGAGGAGGAG 1329
Db      452 ValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerIleSerLysProGly 471
QY      1330 AAA 1332

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Db      472 Lys 472
RESULT 11
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bit
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446<KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-95,144-139,261-321,367-425/Disulfide bonds: #status predicted
F:132/disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:237/binding site: carboxylate (Asn) (covalent) #status experimental
Alignment Scores:
Pred. No.: 1 35e-69 Length: 446
Score: 1400.50 Matches: 267
Percent Similarity: 73.89% Conservative: 67
Best Local Similarity: 59.07% Mismatches: 103
Query Match: 58.23% Indels: 15
DB: 2 Gaps: 6
US-09-674-716B-18 (1-1335) x S40295 (1-446)

```

```

QY      1 GAGTGCAGTGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db      1 GlnIleGlnLeuGlnSerGlyProGluLeuValArgProGlyAlaSerValLysile 20
QY      61 TCTGTGTCAGTACGCGATTCTTTCAGTGGCTACTGGATGCTCTGGGTCCGCGAGGCT 120
Db      21 SerCysLysAlaSerGlyTyrThrPheThrAspTyrTyrIleHisTrpValLysGlnArg 40
QY      121 CCAGGAAAGGGCTCGAGTGGTGTCTGAAATAGATTGAAATCTGATAATTATGCAACA 180
Db      41 ProGlyGluGlyLeuGluTrpIleGlyTrpIleTyrProGlySerGlyAsn-----Thr 58
QY      181 CATTATGCCGAGTCTGTGAAGGGAAATTCACATCTCAAGAGTGAATTCAAAATCTAGA 240
Db      59 LysTyrAsnGlnLysPheLysGlyLysAlaThrLeuThrValAspThrSerSerThr 78
QY      241 CTGTATCTCAATGAACACCGCTGAAACCCAGGACACAGCCGCTGTATTACTGTACA--- 297
Db      79 AlaTyrMetGlnLeuSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArg 98
QY      298 -----CATTTTCATAGTCTGGGCGAGGAGACACTAGTACCGCTTCCC 339
Db      99 GlyGlyLysPheAlaMetAspTyr-----TrpGlyGlnGlyThrSerValThrValSer 116
QY      340 TCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCTCTCCCAAGAGCACCTCT 399
Db      117 SerAlaLysThrAlaProSerValTyrProLeuAlaProValCysGlyAspThrThr 136
QY      400 GGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGGAGCCGTCGAGGTG 459

```

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <F1S>
A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from mouse
A:Reference number: A02157; MUID:80120716; PMID:6766534
A:Contents: a allele
A:Accession: A02157
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A:Cross-references: GB:J00461
A:Note: the sequence was determined from the germline gene
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy chain gene
A:Reference number: A26235; MUID:80081501; PMID:117548
A:Contents: MPC 11
A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
A:Note: Lys-474 is probably removed posttranslationally
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin
A:Reference number: A26232; MUID:80081502; PMID:117549
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
A:Note: Lys-474 is probably removed posttranslationally
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin
A:Reference number: A26233; MUID:82173203; PMID:6803173
A:Contents: b allele
A:Accession: A26233
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLI>
A:Cross-references: GB:J00461
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J.
J. Biol. Chem. 269, 12345-12350, 1994
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A:Reference number: A53598; MUID:94216359; PMID:7512967
A:Accession: A53598
A>Status: preliminary
A:Molecule type: protein
A:Residues: 234-251 <KIM>
C:Comment: The a allele sequence is shown.
C:Genetics:
A:Introns: 138/1; 236/1; 258/1; 368/1
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobulin
F:157-222/Domain: immunoglobulin homology <IM1>
F:236-257/Region: hinge
F:281-350/Domain: immunoglobulin homology <IM2>
F:387-454/Domain: immunoglobulin homology <IM3>
F:152/Disulfide bonds: interchain (to light chain) #status predicted
F:164-220, 394-452/Disulfide bonds: #status predicted
F:247, 250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 1.83e-67 Length: 474
Score: 1361.50 Matches: 259
Percent Similarity: 71.33% Conservative: 67
Best Local Similarity: 56.67% Mismatches: 116
Query Match: 56.61% Indels: 15
DB: 1 Gaps: 4

US-09-674-716B-18 (1-1335) x G2MS11 (1-474)

US-09-674-716B-18 (1-1335) x G2MS11 (1-474)

QY 1 GAGGTGCACTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
 DB 20 GluValGlnLeuGlnSerGlyProGluLeuValAsnProGlyAlaSerVallysMet 39
 QY 61 TCTGTGCACTAGGGATTACTTTCAGTGGCTACTGGATGCTCGGTCGCGAGGCT 120
 DB 40 SerCysLysAlaSerGlyThrPheIleThrValMetHisTrpVallysGlnLys 59
 QY 121 CCAGGAAGGGGCTCGAGTGGGTGTGTAATATTAGATTGAAATCTGATAATTATCAACA 180
 DB 60 ProGlyGlnGlyLeuGluTrpIleGlyTyrlleAsnProAsnLysAsp-----GlyThr 77
 QY 181 CATTATCGGAGTCTGTGAAGGGAAATTCACATCTCAGAGATGATCAAAATCTAGA 240
 DB 78 LysPheAsnGlnLysPheLysGlyLysAlaThrLeuThrSerAspLysSerSerAsnThr 97
 QY 241 CTGTATCTCAATGAACAGCTGCTTCCCGGACACAGCGCTGTATTACTGTACAGAT 300
 DB 98 AlaTyMetGluLeuSerSerLeuThrSerGluAspSerAlaValTyTrpCysAlaArg 117
 QY 301 -----TTCTATAGCTGGGCGCCAGGAACACTAGTCACTGCTCTCTCA 342
 DB 118 AspTyAspTyAspTrpPheAlaTyTrpGlyGlnGlyThrLeuValThrValSerAla 137
 QY 343 GCTCCACCAAGGGCCATCGTCTTCCCGGACACCTCTCCCAAGAGACCTCTGG 402
 DB 138 AlaLeuThrThrProSerValTyProLeuAlaProGlyCysGlyAspThrThrGly 157
 QY 403 GGCACAGCGGCGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 462
 DB 158 SerSerValThrSerGlyCysLeuValLysGlyTyTrpPheProGluSerValThrValThr 177
 QY 463 TGGAACTAGCGGCGCTGACAGCGGCTGACACCTTCCCGGCTGCTGCTGCTGCTGCT 522
 DB 178 TrpAsnSerGlySerLeuSerSerValHisThrLeuSerGlnAlaLeuLeuGlnSer 197
 QY 523 GGACTTACTCTCCCTCAGCAGCGTGTGACCGTCCCTCAGCAGCTTGGGACCCAGACC 582
 DB 198 GlyLeuTyThrMetSerSerValThrValProSerSerThrTrpProSerGlnThr 217
 QY 583 TACATCTGAAGTGAATCAAGCCGACACACACAGGTCGACAAAGAGTGGAGCC 642
 DB 218 ValThrCysSerValAlaHisProLaserSerThrValAspLysLysLeuGluPro 237
 QY 643 AAATCTGTGACAAAACCT---CACACATCCCGCCACCG-----TGCCCA 681
 DB 238 SerGlyProIleSerThrIleAsnProCysProProCysLysGluCysHisLysCysPro 257
 QY 682 GCACTGAACTCGGGGGGACCGTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 741
 DB 258 AlaProAsnLeuGluGlyProSerValPheIlePheProProAsnIleLysAspVal 277
 QY 742 CTCATGATCTCCGGACCCCTCAGGTTCATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 801
 DB 278 LeuMetIleSerLeuThrProLysValThrCysValValValValSerGluAspAsp 297
 QY 802 CTGAGGTCAAGTTCATGTTGACCGGCGTGGAGGTGATTAATGCAAGACAAAG 861
 DB 298 ProAspValGlnIleSerTrpPheValAsnAenValGluValHisThrAlaGlnThrGln 317
 QY 862 CCGGGGAGGACGATGACACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 921
 DB 318 ThrHisArgGluAspTrpAsnSerThrIleArgValValSerThrLeuProIleGlnHis 337
 QY 922 CAGGACTGTGCTGAATGGCAAGGATCAAGTGAAGGTCTCAACAAAGCCCTCCAGCC 981
 DB 338 GlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProSer 357
 QY 982 CCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGACACACAGGTGTACACC 1041
 DB 358 ProIleGluArgThrIleSerLysLysLysGlyLeuValAlaGalaProGlnValTyTrp 377
 QY 1042 CTGCCCCCATCCCGGATGAGCTGACCAAGAACACAGGTCAGCTGACCTGCTGCTGCTCAA 1101

DB 378 LeuProProAlaGluGlnLeuSerArgLysAspValSerLeuThrCysLeuValVal 397
 QY 1102 GGTTCCTATCCAGCAGCATCGCGTGGAGTGGAGCAATGGGAGCGGAGCAAC 1161
 DB 398 GlyPheAsnProGlyAspIleSerValGluTrpThrSerAsnGlyHisThrGluGluAsn 417
 QY 1162 TACAAGACACAGCTCCCGTGTGGACTCCGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 1221
 DB 418 TyrlleAspThrAlaProValLeuAspSerAspGlySerTyrlleThrSerLysLeu 437
 QY 1222 ACCTGTGACAAAGAGCTGGCAGCAGGAGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1281
 DB 438 AsnMetLysThrSerLysTrpGluLysThrAspSerPheSerCysAsnValArgHisGlu 457
 QY 1282 GCTCTGCACACCACTACACGACAGAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
 DB 458 GlyLeuLysAsnTyrlleLeuLysLysThrIleSerArgSerProGlyLys 474

RESULT 13
 S01321
 Ig gamma-2b chain precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
 C/Accession: S01321
 R/de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Piers, W.
 A/Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed at
 A/Reference number: S01320; MUID:88329081; PMID:3138116
 A/Accession: S01321
 A/Molecule type: mRNA
 A/Residues: 1-475 <DB1>
 A/Cross-references: EMBL:X13188; NID:G51780; PIDN:CAA31580.1; PID:G51781
 A/Note: this sequence was determined from the differentiated gene
 C/Superfamily: immunoglobulin C region; immunoglobulin homology
 C/Keywords: immunoglobulin
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-475/Product: Ig gamma-2b chain #status predicted <MAT>
 F/159-223/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 6,89e-67 Length: 475
 Score: 1351.00 Matches: 260
 Percent Similarity: 71.90% Conservative: 70
 Best Local Similarity: 56.64% Mismatches: 111
 Query Match: 56.17% Indels: 18
 DB: 2 Gaps: 5

US-09-674-716B-18 (1-1335) x S01321 (1-475)

QY 1 GAGGTGCACTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
 DB 20 GluValGlnLeuGlnSerGlyProGluLeuValAsnProGlyAlaSerVallysMet 39
 QY 61 TCTGTGCACTAGGGATTACTTTCAGTGGCTACTGGATGCTCGGTCGCGAGGCT 120
 DB 40 SerCysLysAlaSerGlyThrPheIleThrValMetHisTrpVallysGlnLys 59
 QY 121 CCAGGAAGGGGCTCGAGTGGGTGTGTAATATTAGATTGAAATCTGATAATTATCAACA 180
 DB 60 ProGlyGlnGlyLeuGluTrpIleGlyTyrlleAsnProAsnLysAsp-----GlyThr 77
 QY 181 CATTATCGGAGTCTGTGAAGGGAAATTCACATCTCAGAGATGATCAAAATCTAGA 240
 DB 78 LysPheAsnGlnLysPheLysGlyLysAlaThrLeuThrSerAspLysSerSerAsnThr 97
 QY 241 CTGTATCTCAATGAACAGCTGCTTCCCGGACACAGCGCTGTATTACTGTACAGAT 300
 DB 98 AlaTyMetGluLeuSerSerLeuThrSerGluAspSerAlaValTyTrpCysAlaArg 117
 QY 298 -----TTCTATAGCTGGGCGCCAGGAACACTAGTCACTGCTCTCTCA 342
 DB 118 AspTyAspTyAspTrpPheAlaTyTrpGlyGlnGlyThrLeuValThrValSerAla 137

337 TCCTCAGGCTCCACCAAGGGCCCATCGGTCTTCCCTGGACCCCTCTCTCAAGAGCACC 396
|||||
138 SerAlaAlaThrThrProSerValThrProLeuAlaProGlyCysGlyAspThr 157
|||||
397 TCTGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGCAACCGGTGACG 456
|||||
158 ThrGlySerSerValThrLeuGlyCysLeuValValGlyTyrPheProGluSerValThr 177
|||||
457 GTGTGCTGAAGTCAAGCGCCCTGACACAGCGGTGACACCTTCCCGGTGCTCTCAAG 516
|||||
178 ValThrTrpAsnSerGlySerLeuSerSerValHisThrPheProAlaLeuLeuGln 197
|||||
517 TCCTCAGGACTTACTCTCCCTCAGCAGCGTGTGACCGTGTGCTCCAGCAGCTTGGGAC 576
|||||
198 ---SerGlyLeuThrTrpMetSerSerValThrValProSerSerThrTrpProSer 216
|||||
577 CAGACTCATCTGCAAGCTGAATCACAAGCCGACCAACCAAGGTGACCAAGAAAGT 636
|||||
217 GlnThrValThrCysSerValAlaHisProAlaSerSerThrValAspLysLysLeu 236
|||||
637 GAGCCCAATCTGTGACAAACT---CACATGCCCCACCG----- 675
|||||
237 GluProSerGlyProThrSerThrIleAsnProCysProCysLysGluCysHisLys 256
|||||
676 TGCCCAGCACCTGAACTCGCGGGGACCGTCAGTCTTCTCTTCCCGCCCAAAACCCAAAG 735
|||||
257 CysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheProProAsnIleLys 276
|||||
736 GACACCTCATGATCTCCGGAGCCCTGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 795
|||||
277 AspValLeuMetIleSerLeuThrProLysValThrCysValValValAspValSerGlu 296
|||||
796 GAAGACCTGAGTCAAGTCAACTGCTGACGTGACGCGGTGGAGTGCATCAATGCCAAG 855
|||||
297 AspAspProAspValGlnIleSerTrpPheValAsnAsnValGluValLeuThrAlaGln 316
|||||
856 ACAAGCCCGGGAGGACGACGTACACAGCAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTG 915
|||||
317 ThrGlnThrHisArgGluAspTyrAsnSerThrIleArgValValSerAlaLeuProIle 336
|||||
916 CTGACACGAGGCTGCTGAATGGCAGGAGTACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 975
|||||
337 GlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeu 356
|||||
976 CCAGCCCGCATCGAAGAACCATCTCCAAAGCCAAAGGCGCAGCCCGGAGAACCCAGAGTG 1035
|||||
357 ProAlaProIleGluArgThrIleSerLysIleLysGlyIleValArgAlaProGlnVal 376
|||||
1036 TACACCTGCCCCATCCCGGATGAGTGTGACCAAGACAGGTCAGCTCAGCTCAGCTGCTG 1095
|||||
377 TyrIleLeuSerProProGluGlnLeuSerArgLysAspValSerLeuThrCysLeu 396
|||||
1096 GTCAAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGGAGCAATGGCGAGCCGGAG 1155
|||||
397 AlaValGlyPheSerProGluAspIleSerValGluTrpThrSerAsnGlyHisThrGlu 416
|||||
1156 AACAACTCAAGACCAAGCTCCCGTGTGACTCCGACCGCTCTCTCTCTCTCTCTCTCTCT 1215
|||||
417 GluAsnTyrLysAspThrAlaProValLeuAspSerAspGlySerTyrPheIleTyrSer 436
|||||
1216 AGCTCACCCTGGACAGGAGGTGGCAGGAGGAGGACGCTCTCTCTCTCTCTCTCTCTCTCT 1275
|||||
437 LysLeuAsnMetLysThrSerLysTrpGluLysThrAspSerPheSerCysAsnValArg 456
|||||
1276 CATGAGGCTCTGCACCAACCATACAGCAGCAGAGAGCCCTCTCTCTCTCTCTCTCTCTCT 1332
|||||
457 HisGluGlyLeuLysAsnTyrTyrLeuLysLysThrIleSerArgSerProGlyLys 475
|||||

RESULT 14

147159

Ig gamma 2a chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IGH identified from the cDNA sequences of a si
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124
C:Genetics:
A:Gene: IGG2a
C:Superfamily: immunoglobulin C region; immunoglobulin.homology
F:133-202/Domain: immunoglobulin homology <IM>

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 7,966-62 | Length: | 328 |
| Score: | 1259.00 | Matches: | 233 |
| Percent Similarity: | 82.83% | Conservative: | 42 |
| Best Local Similarity: | 70.18% | Mismatches: | 51 |
| Query Match: | 52.35% | Indels: | 6 |
| DB: | 2 | Gaps: | 3 |

US-09-674-716B-18 (1-1335) x I47159 (1-328)

QY 343 GCCTCCACCAAGGCGCCATCGGTCTTCCCTGGACCCCTCTCTCAAGAGCACCCTCTGGG 402
|||||
Db 1 AlaProLysThrAlaProSerValTyrProLeuAlaProCysSerArgAspThrSerGly 20
QY 403 GGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGACGCTGTCG 462
|||||
Db 21 ProAsnValAlaLeuGlyCysLeuAlaSerSerTyrPheProGluProValThrValThr 40
QY 463 TGAACCTCAGGCGCCCTGACCGCGCGTGCACACCTTCCCGGCTCTCTACAGTCTCTCA 522
|||||
Db 41 TrpAsnSerGlyAlaLeuSerSerGlyValHisThrPheProSerValLeuGlnProSer 60
QY 523 GGCCTCTACTCTCCCTCAGCAGCGTGTGACCGTGTGCTCCAGCAGCTTGGGACCCAGACC 582
|||||
Db 61 GlyLeuTyrSerLeuSerSerMetValThrValProAlaSerSerLeuSerSerLysSer 80
QY 583 TACATCTGCACCTGATCACAAGCCCGACCAACCAAGGTGGACAGAAAGTGGAGCCC 642
|||||
Db 81 TyrThrCysAsnValAsnHisProAlaThrThrLysValAspLysArgValGlyThr 100
QY 643 AATCTTGTGACAAAACCTCACACATGCCACCGTCCCGCAGCAGCTGAACCTCGCGGGGCA 702
|||||
Db 101 LysThr-----LysProProCysProIleCysProAlaCysGluSerProGly--- 116
QY 703 CGCTCAGTCTTCTCTTCTCCCGCCAAACCCAGGACACCTCATGATCTCCCGGACCCCT 762
|||||
Db 117 ProSerValPheIlePheProLysProLysAspThrLeuMetIleSerArgThrPro 136
QY 763 GAGTCACATGCTGCTGTGGTGGACGAGCCAGACACCTGAGGTCAAGTTCAACTGG 822
|||||
Db 137 GlnValThrCysValValValAspValSerGlnGluAsnProGluValGlnPheSerTrp 156
QY 823 TACGTGACCGCTGGAGGTGCATAATGCAAGACAAAGCCGCGGAGGAGCAGTACAAC 882
|||||
Db 157 TyrValAspGlyValGluValHisThrAlaGlnThrArgProLysGluGluGlnPheAsn 176
QY 883 AGCAGCTACCGTGTGCTCAGCTCCTCACCGTCTCCACCGAGGAGTGGCTGAATGCAAG 942
|||||
Db 177 SerThrTyrArgValValSerValLeuProIleGlnHisGlnAspTrpLeuAsnGlyLys 136
QY 943 GAGTCAAGTGCAGGTCTCCAAACAAAGCCCTCCCGAGCCCGCCATCGAGAAACCATCTCC 1002
|||||
Db 197 GluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleThrArgIleIleSer 216
QY 1003 AAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTACACCTGCCCCCATCCCCGGATGAG 1062
|||||
Db 217 LysAlaLysGlyGlnThrArgGluProGlnValThrThrLeuProHisAlaGluGlu 236
|||||

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:20:22 ; Search time 28.9645 Seconds
(without alignments)
4799.922 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 2405
Sequence: 1 gaggtgcagctgtgagtc.....ccctgtctccggtaaatga 1335

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model p/US09674716/runat_30092004_070257_25855/app_query.fasta_1.3.64
-Q=/cgn2_1/USPTO_spool_p/US09674716/runat_30092004_070257_25855/app_query.fasta_1.3.64
-DB=SwissProt 42 -OPMT=fastan -SUFFIX=rs -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=EPC -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09674716@cgn 1 1 82 @runat_30092004_070257_25855 -NCPU=3
-NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1756 | 73.0 | 330 | 1 | GCI_HUMAN |
| 2 | 1608 | 66.9 | 326 | 1 | GC2_HUMAN |
| 3 | 1579.5 | 65.7 | 327 | 1 | GC4_HUMAN |
| 4 | 1219.5 | 50.7 | 323 | 1 | GC_FABIT |
| 5 | 1205.5 | 50.1 | 329 | 1 | GC2_CAVPO |
| 6 | 1154 | 48.0 | 326 | 1 | GCI_RAT |
| 7 | 1153.5 | 48.0 | 290 | 1 | GC3_HUMAN |
| 8 | 1144 | 47.6 | 324 | 1 | GCI_MOUSE |
| 9 | 1139 | 47.4 | 393 | 1 | GCI_MOUSE |
| 10 | 1135.5 | 47.2 | 333 | 1 | GC_B_RAT |
| 11 | 1130 | 47.0 | 329 | 1 | GC3_MOUSE |
| 12 | 1119 | 46.5 | 398 | 1 | GC3_MOUSE |
| 13 | 1115 | 46.4 | 330 | 1 | GC3_MOUSE |
| 14 | 1114.5 | 46.3 | 329 | 1 | GCC_RAT |
| 15 | 1114 | 46.3 | 322 | 1 | GCA_RAT |
| 16 | 1112.5 | 46.3 | 335 | 1 | GCA_MOUSE |
| 17 | 1110 | 46.2 | 399 | 1 | GCAM_MOUSE |
| 18 | 1083 | 45.0 | 336 | 1 | GC_B_MOUSE |

ALIGNMENTS

RESULT 1

| ID | GCI_HUMAN | STANDARD; | PRT; | 330 AA. |
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| AC | P01857; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 15-MAR-2004 (Rel. 43, Last annotation update) | | | |
| DE | IG gamma-1 chain C region. | | | |
| GN | IGHG1 | | | |
| OS | Homo sapiens (Human) | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=82274238; PubMed=6287432; | | | |
| RA | Ellison J.W.; Berson B.J.; Hood L.E.; | | | |
| RT | "The nucleotide sequence of a human immunoglobulin C gamma gene." | | | |
| RL | Nucleic Acids Res. 10:4071-4079(1982). | | | |
| RN | [2] | | | |
| RP | SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). | | | |
| RX | MEDLINE=71064024; PubMed=5489771; | | | |
| RA | Cunningham B.A.; Rutishauser U.; Gall W.E.; Gottlieb P.D.; | | | |
| RA | Waxdal M.J.; Edelman G.M.; | | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4." | | | |
| RL | Biochemistry 9:3161-3170(1970). | | | |
| RN | [3] | | | |
| RP | SEQUENCE OF 136-329 (EU). | | | |
| RX | MEDLINE=71064025; PubMed=5530842; | | | |
| RA | Rutishauser U.; Cunningham B.A.; Bennett C.; Konigsberg W.H.; | | | |
| RA | Edelman G.M.; | | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7." | | | |
| RL | Biochemistry 9:3171-3181(1970). | | | |
| RN | [4] | | | |
| RP | SEQUENCE (MYELOMA PROTEIN NIE). | | | |
| RX | MEDLINE=770265; PubMed=826475; | | | |
| RA | Ponstingl H.; Hilschmann N.; | | | |
| RT | "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic | | | |

P01867 mus musculu
P01801 mus musculu
P01854 homo sapien
P01799 mus musculu
P01855 rattus norv
P01796 mus musculu
P01802 mus musculu
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P01872 mus musculu
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P01873 mus musculu
P20768 suncus muri
P01874 canis famil
P01786 mesocricetu
P06337 mesocricetu
P01768 homo sapien
P01770 homo sapien
P01791 mus musculu
P01790 mus musculu


```

RT peptides and discussion of the complete structure."
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
RN CC
CC -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC G1M(3) marker and the G1M (non-1) markers.
CC -!- MISCELLANEOUS: Nie also differs in the amidation states of
CC 35, 116, 198, 269 and 272.
CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -!- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
CC -----
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CC -----
CC EMBL; J00228; AAC82527.1; ALT_INIT.
CC PIR; A83433; GHVU.
CC PDB; 1FC1; 15-JUL-92.
CC PDB; 1FC2; 15-JUL-92.
CC PDB; 1A77; 12-NOV-97.
CC PDB; 1D5B; 09-FEB-00.
CC PDB; 1D5B; 09-FEB-00.
CC PDB; 1D5V; 04-OCT-00.
CC PDB; 1D22; 17-MAY-00.
CC PDB; 1E4K; 06-JUN-01.
CC PDB; 1FCC; 20-JUL-95.
CC PDB; 1H2H; 12-JUN-02.
CC PDB; 1H7Z; 08-AUG-01.
CC PDB; 1IIS; 16-MAY-01.
CC PDB; 1IIX; 16-MAY-01.
CC PDB; 1L6X; 10-APR-02.
CC PDB; 2RCS; 12-NOV-97.
CC MIM; 147100; -.
CC GO; GO:0005624; C:membrane fraction; NAS.
CC GO; GO:0003823; F:antigen binding; TAS.

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GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGG1; 2.
PROSITE; PS00835; IG LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; 3D-structure.

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|----|----------|---------|-----------|--------------------------------|
| FT | DOMAIN | 1 | 98 | HINGE. |
| FT | DOMAIN | 99 | 110 | CH2. |
| FT | DOMAIN | 111 | 223 | CH3. |
| FT | DOMAIN | 224 | 330 | |
| FT | DISULFID | 27 | 83 | |
| FT | DISULFID | 103 | 103 | |
| FT | DISULFID | 109 | 109 | INTERCHAIN (WITH LIGHT CHAIN). |
| FT | DISULFID | 112 | 112 | INTERCHAIN (WITH HEAVY CHAIN). |
| FT | DISULFID | 144 | 204 | INTERCHAIN (WITH HEAVY CHAIN). |
| FT | DISULFID | 250 | 308 | |
| FT | CARBOHYD | 180 | 180 | N-LINKED (GLCNAC. . .). |
| FT | MOD RES | 330 | 330 | REMOVED POST-TRANSLATIONALLY. |
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| FT | VARIANT | 239 | 239 | /FTid=VAR_003886. |
| FT | VARIANT | 241 | 241 | D -> E (IN G1M(NON-1) MARKER). |
| FT | VARIANT | 241 | 241 | L -> M (IN G1M(NON-1) MARKER). |
| FT | VARIANT | 241 | 241 | /FTid=VAR_003888. |
| FT | STRAND | 122 | 126 | |
| FT | HELIX | 130 | 134 | |
| FT | TURN | 136 | 137 | |
| FT | STRAND | 141 | 147 | |
| FT | STRAND | 157 | 162 | |
| FT | TURN | 163 | 164 | |
| FT | STRAND | 165 | 166 | |
| FT | TURN | 168 | 171 | |
| FT | STRAND | 176 | 179 | |
| FT | TURN | 180 | 181 | |
| FT | STRAND | 182 | 190 | |
| FT | HELIX | 193 | 197 | |
| FT | TURN | 198 | 199 | |
| FT | STRAND | 202 | 207 | |
| FT | TURN | 209 | 210 | |
| FT | STRAND | 215 | 219 | |
| FT | STRAND | 227 | 227 | |
| FT | STRAND | 230 | 234 | |
| FT | HELIX | 238 | 242 | |
| FT | STRAND | 245 | 256 | |
| FT | STRAND | 260 | 265 | |
| FT | STRAND | 270 | 270 | |
| FT | STRAND | 274 | 276 | |
| FT | STRAND | 280 | 281 | |
| FT | TURN | 283 | 284 | |
| FT | STRAND | 287 | 296 | |
| FT | HELIX | 297 | 301 | |
| FT | TURN | 302 | 303 | |
| FT | STRAND | 305 | 312 | |
| FT | TURN | 313 | 314 | |
| FT | TURN | 316 | 317 | |
| FT | STRAND | 320 | 325 | |
| SQ | SEQUENCE | 330 AA; | 36106 MW; | 3770EE106C2FA33D CRC64; |

Alignment Scores:

| Pred. No.: | 3,89e-100 | Length: | 330 |
|------------------------|-----------|---------------|-----|
| Score: | 1756.00 | Matches: | 328 |
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| Best Local Similarity: | 99.39% | Mismatches: | 2 |
| Query Match: | 73.01% | Indels: | 0 |
| DB: | 1 | Gaps: | 0 |

US-09-674-716b-18 (1-1335) x GCL_HUMAN (1-330)

QY 343 GCCTCCACCAAGGGCCCATCGTCTTCCCGCTGGCACCTCTCTCAAGACACCTCTGGG 402
 Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 20
 QY 403 GGCACAGGGCCCTGGCTGCTGCTCAAGCACTACTTCCCGAACCGGTGACGGTCTCG 462
 Db 21 GlyThrAlaLeuLeuGlyCysLeuValLysAspThrPheProGluProValThrValSer 40
 QY 463 TGGAACTCAGCGCCCTGACCAAGCGGGCTGCACACCTTCCCGGTCTCTACAGTCTCTCA 522
 Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
 QY 523 GGACTTACTCTCCACAGAGCGGTGGTACCGTGGCTCCAGCAGCTGGGGACCCAGACC 582
 Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80
 QY 593 TACATCTCAACGCTGAATCAAGCCCAAGCAACCAAGGTGGCAAGAGTGGAGCC 642
 Db 81 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100
 QY 643 AAATCTTGTCACAAACTCAACATGCCACCGTGGCCAGCACCTGAACCTGCGGGGCA 702
 Db 101 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuGlyGly 120
 QY 703 CCGTCAGTCTTCTCTCCCGCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCT 762
 Db 121 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 140
 QY 763 GAGTTCACATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 822
 Db 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 160
 QY 823 TACGTGGAGCGGTGGAGTGCATATCCAGACAAAGCCCGGGAGGACAGTACAC 882
 Db 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnThrAsn 180
 QY 893 AGCAGTACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 942
 Db 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200
 QY 943 GAGTCAAGTCAAGTCTCAACAAAGCCCTCCAGCCCGCCCAAGAGAAACCATCTCC 1002
 Db 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 220
 QY 1003 AAAGCCAAAGGACCCCGGAGAACACAGGTGTACACCTGCCCGCCATCCCGGATGAG 1062
 Db 221 LysAlaLysGlyGlnProArgGluProGlnValLysThrLeuProProSerArgAspGlu 240
 QY 1063 CTGACCAAGAACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1122
 Db 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260
 QY 1123 GCCGTGGAGTGGAGAGCAATGGGAGCGGAGAGCAACTACAGACCAAGCCCTCCCGTG 1182
 Db 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 280
 QY 1183 CTGGACTCCGAGGCT 1242
 Db 281 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300
 QY 1243 CAGCAGGGAAGCT 1302
 Db 301 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 320
 QY 1303 CAGAAGAGCT 1332
 Db 321 GlnLysSerLeuSerLeuSerProGlyLys 330
 RESULT 2
 ID GC2_HUMAN
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-2 chain C region.
 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 CX [1]
 RN SEQUENCE OF 2-326 FROM N.A.
 RP MEDLINE=82197521; PubMed=6804948;
 RA Ellison J.W., Hood L.E.;
 RX "Linkage and sequence homology of two human immunoglobulin gamma
 heavy chain constant region genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RN [2]
 RN SEQUENCE OF 88-115 FROM N.A.
 RP TISSUE=Fetal liver;
 RC MEDLINE=83001943; PubMed=6811139;
 RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;
 RX "Structure of human immunoglobulin gamma genes: implications for
 evolution of a gene family.";
 RL Cell 29:671-679(1982).
 RN [3]
 RN SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RP TISSUE=Fetal liver;
 RC MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rabbitts T.H.;
 RX "Comparison of the hinge-coding segments in human immunoglobulin gamma
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 genes.";
 RL EMBO J. 1:403-407(1982).
 RN [4]
 RN SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RP MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RX "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RN SEQUENCE OF 1-95 AND 132-325 (MYELOMA PROTEIN ZIE).
 RP MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Farr D.M., Hofmann T.;
 RX "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RN SEQUENCE OF 238-275 (ZIE).
 RP MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Farr D.M.;
 RX "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulins gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RN REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RP Hofmann T., Farr D.M.;
 RX Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RN SEQUENCE OF 1-121 (DOT).
 RP MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RX "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RN DISULFIDE BONDS.
 RP MEDLINE=72033500; PubMed=4940472;
 RX Milstein C., Frangione B.;
 RA "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RN DISULFIDE BONDS.
 RP MEDLINE=69064124; PubMed=5782707;
 RX

RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
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 CC -----
 CC EMBL; J00230; AAB59393.1; -.
 DR PIR; A93906; G2HU.
 DR HSP; P01857; 1FC1.
 DR Genev; HGNC:5526; IGHG2.
 DR MIM; 147110; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0005955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGH1; 2.
 DR PROSITE; PS00835; F-LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DOMAIN 1 98
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 FT HINGE.
 FT DOMAIN 99 110
 FT CH2.
 FT DOMAIN 111 219
 FT CH3.
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 FT INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 14 14
 FT DISULFID 27 83
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 FT DISULFID 140 200
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 FT SITE 156 156
 FT MOD_RES 326 326
 FT VARIANT 60 60
 FT AT OR NEAR THE COMPLEMENT-BINDING SITE
 FT REMOVED POST-TRANSLATIONALLY (PROBABLE).
 FT S-> A (IN MYELOMA PROTEINS TIL & ZIE).
 FT /FTIG=VAR 003889.
 FT C -> S (IN REF. 3).
 FT CONFLICT 109 109
 FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
 SQ

Alignment Scores:

Pred. No.: 4,25e-91 Length: 326
 Score: 1608.00 Matches: 302
 Percent Similarity: 95.1% Conservative: 12
 Best Local Similarity: 91.52% Mismatches: 12
 Query Match: 66.86% Indels: 4
 DB: 1 Gaps: 2

US-09-674-716B-18 (1-1335) x GC2_HUMAN (1-326)

QY 343 GCCTCACCAGGGCCCAFCGCTGTCCTCCCTGGACCTCTCTCAAGAGCAGCTCTGGG 402
 Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrGlu 20
 QY 403 GCACAGCGGCGCTGGCTGCTGCTCAAGACTACTTCCCGACCGGTACAGGTGTCG 462
 Db 21 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
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 Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
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 Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGlyThrGlnThr 80

QY 583 TACATCTGCACACGTGAATCAACAGCCCGACCAACAGAGGTGGACAAAGAGTGGAGCCC 642
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 QY 643 AAATCTTGTGACAAACTCACACATGCCCCACCTGGCCAGCAGCTCACTCGCGGGGCA 702
 Db 101 LysCysCysValGlu-----CysProCysProAlaProProValAlaGly--- 116
 QY 703 CCGTCACT 762
 Db 117 ProSerValPheLeuPheProLysProLysProLysAspThrLeuMetIleSerArgThrPro 136
 QY 763 GAGTCAATGCGTGGTGGAGCGTGGAGCGGACGACGACGACGACGACGACGACGACGAC 822
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RESULT 3

GC4_HUMAN

ID GC4_HUMAN STANDARD; PRT; 327 AA.

AC P01861;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE IG gamma-4 chain C region.

GN IGHG4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID:9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83157104; PubMed=6299662;

RA Ellison J.W., Buxbaum J.N., Hood L.E.;

RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";

RL DNA 1:11-18(1981).

RN [2]

RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RL Biochem. J. 117:33-47(1970).
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CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A90933; G4HU.
DR PDB; 1ADO; 16-SEP-98.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; --.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF0047; IG_3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON_TER 1 98
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Alignment Scores:
Pred. No.: 2,348-89 Length: 327
Score: 1579.50 Matches: 298
Percent Similarity: 93.94% Conservative: 12
Best Local Similarity: 90.30% Mismatches: 17
Query Match: 65.68% Indels: 3
DB: 1 Gaps: 1

US-09-674-716B-18 (1-1335) x GC4_HUMAN (1-327)

QY 343 GCCTCCACCAAGGGCCCATCGCTTCCCTGGCACCTCTCCACAGAGACCTCTGGG 402
Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 20
QY 403 GGCACAGCGCCCTGGGCTGCTGCTCAGGACTACTCCCGAACCGGTGACGGTGTG 462
Db 21 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 463 TGGAACTCAGGCGCCCTGACACCGCGGTGACACCTTCCCGGCTGTCTACAGTCTCTCA 522
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 523 GGACTTACTCTCCCTCAGCAGCGGTGTGACCGGTCCCTCCAGCAGTGTGGACCCAGACC 582
Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrLysThr 80
QY 583 TACATCTGCAAGCTGAATCACAGCCAGCAACCAAGGTGGACAAAGAAAGTGGAGGCC 642
Db 81 TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLysArgValGluSer 100

QY 643 AAATCTTGACAAAACCTCACATCCACCCACCGTGGCCAGCACCTGAATCTCGCGGGGCA 702
Db 101 Lys-----TyrGlyProProCysProSerCysProAlaProGluPheLeuGlyGly 117
QY 703 CGCTCAGTCTTCTCTTCCCCCAAAACCCAGGACACCTCATGATCTCCCGGAGCCCT 762
Db 118 ProSerValPheLeuPheProProLysProLysAspThrLeuMetLieserArgThrPro 137
QY 763 GAGTCCATCGCTGGTGGTGGACCTGAGCCAGCAAGACCTCAGGTCAAGTTCAAGTTG 822
Db 138 GluValThrCysValValValAspValSerGlnGluAspProGluValGlnPheAsnTrp 157
QY 823 TAGGTGACCGCTGAGGTGTCATATGCCAAGCAAAAGCCGGGAGGAGAGTACAAC 882
Db 158 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnPheAsn 177
QY 883 AGCAGGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 942
Db 178 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 197
QY 943 GAGTACAGTGCAGGTCTCCAAAGGCGCTCCAGCCCGCCCATCGAGAAACCATCTCC 1002
Db 198 GluTyrLysCysLysValSerAsnLysGlyLeuProSerSerSerileGluLysThrLieser 217
QY 1003 AAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACAGCTGCCCGCCCATCCCGGATGAG 1062
Db 218 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProSerGlnGluGlu 237
QY 1063 CTACCAAGAACAGGTGACCTGACCTGGTCAAGGCTTCTATCCAGCGACATC 1122
Db 238 MetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 257
QY 1123 GCGTGGAGTGGAGAGCAATGGGCGCGGAGAACAACTACAGACCCAGCTCCCGTG 1182
Db 258 AlaValGluTrpGluSerAsnGlyGlnProGluAsnTyrLysThrThrProVal 277
QY 1183 CTGACTCCGACGCTCTCTTCTCTCAGCAAGCTCACCGTGGCAAGAGCAGGTGG 1242
Db 278 LeuAspSerAspGlySerPhePheLeuTyrSerArgLeuThrValAspLysSerArgTrp 297
QY 1243 CAGCAGGGAAACGTCTTCTCATGCTCGTGTGATGATGAGCTCTGCAACACCTACAG 1302
Db 298 GlnGluGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 317

QY 1303 CAGAAGAGCTCTCCCTGCTCCCGGTAAA 1332
Db 318 GlnLysSerLeuSerLeuSerLeuGlyLys 327
RESULT 4
GC_RABIT STANDARD; PRT; 323 AA.
ID_PO1870; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-I haplotype."
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit

immunoglobulin G of different allotype.";

Biochem. J. 151:337-349(1975).

[3]

SEQUENCE OF 88-266 FROM N.A.

MEDLINE=8329917; PubMed=6193512;

RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;

RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma

RT heavy chain and identification of two genomic C gamma genes.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).

[4]

SEQUENCE OF 132-161.

MEDLINE=70110015; PubMed=5461106;

RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;

RT "Sequence studies of the Fd section of the heavy chain of rabbit

RT immunoglobulin G.";

RL Biochem. J. 116:249-259(1970).

[5]

SEQUENCE OF 129-131 AND 155-322.

RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;

RL (In) Killander J. (eds.);

RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,

RL Stockholm (1967).

CC -!- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker,

CC 104-Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15

CC markers and Ref.5 the E15 marker.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.

CC

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CC or send an email to license@isb-sib.ch).

CC

DR EMBL; M16426; AAA31289.1; -;

DR PIR; A91749; GHRB.

DR HSP; P01857; 1FC1.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 3.

DR SMART; SM00407; Igc1; 2.

DR PROSITE; PS00835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 1.

DR Immunoglobulin domain; Immunoglobulin C region; Repeat.

FT NON_TER 1 1

FT DOMAIN 6 96 IG-LIKE 1.

FT DOMAIN 114 213 IG-LIKE 2.

FT DOMAIN 222 318 IG-LIKE 3.

FT VARIANT 104 104 T -> M (IN D11 MARKER).

FT VARIANT 185 185 T -> A (IN E15 MARKER).

FT CONFLICT 48 48 N -> E (IN REF. 2).

FT CONFLICT 71 71 V -> VPV (IN REF. 2).

FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).

FT CONFLICT 173 173 N -> D (IN REF. 5).

FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).

FT CONFLICT 201 201 N -> D (IN REF. 5).

FT CONFLICT 218 218 Q -> E (IN REF. 5).

FT CONFLICT 233 233 E -> Q (IN REF. 5).

FT CONFLICT 246 246 N -> D (IN REF. 5).

FT CONFLICT 256 256 E -> G (IN REF. 5).

FT CONFLICT 260 260 N -> D (IN REF. 5).

FT CONFLICT 266 266 N -> D (IN REF. 5).

FT CONFLICT 280 280 Y -> W (IN REF. 5).

FT CONFLICT 284 284 N -> S (IN REF. 5).

SQ SEQUENCE 323 AA; 35404 MW; 69E9AA118D579A8B CRC64;

Alignment Scores:

Pred. No.: 2,28e-67 Length: 323

Score: 1219.50 Matches: 227

Percent Similarity: 79.82% Conservatives: 34

Best Local Similarity: 69.42% Mismatches: 59

Query Match: 50.71% Indels: 7

DB: 1 Gaps: 2

US-09-674-716B-18 (1-1335) x GC_RABIT (1-323)

QY 352 AAGGGCCATCGGTCTTCCCTGGCACCCCTCCCAAGAGCACCTCTCTGGGGCAGCG 411

DB 4 LysAlaProSerValPheProLeuAlaProCysCysGlyAspThrProSerThrVal 23

QY 412 GCCTGGGCTGCTGGTCAAGGACTACTCCCGAACCGGTGACGTCGTGGAACTCA 471

DB 24 ThrLeuGlyCysLeuValLysGlyThrLeuProGluProValThrValThrPheSer 43

QY 472 GGGCCCTGACCGCGCGTGACACCTCCCGGCTGCTCAGTCCTCAGTCCTCAGACTCTAC 531

DB 44 GlyThrLeuThrAsnGlyValArgThrPheProSerValArgGlnSerSerGlyLeuTy 63

QY 532 TCCTCAGAGCGGTGGTACCGTCCCTCCAGAGCTTGGGCACCCAGACCTACATCTGC 591

DB 64 SerLeuSerSerValValSerValThrSerSerSer-----GlnProValThrCys 80

QY 592 AAGGTGAATCACAAGCCACACCAAGGTGGACAAAGAGTGGAGCCCAATCTTGT 651

DB 81 AsnValAlaHisProAlaThrAsnThrLysValAspLysThrValAlaProSerThrCys 100

QY 652 GACAAACTCACACATGCCCGCCCGTCCAGCACCTGAATCGCGGGGACCGTCAGTC 711

DB 101 SerLys-----ProThrCysProProGluLeuLeuGlyGlyProSerVal 116

QY 712 TTCTCTTCCCCCAAAACCAAGGACACCTCATCTCCCGGACCCCTGAGGTACA 771

DB 117 PheIlePheProLysProLysAspThrLeuMetIleSerArgThrProGluValThr 136

QY 772 TGGTGTGTGTGACGTGAGCCACGACAGCCCTGAGGTCAAGTTCACCTGCTACGTGGAC 831

DB 137 CysValValValAspValSerGlnAspAspProGluValGlnPheThrTrpTyIleAsn 156

QY 832 GGGGTGAGGTGCATTAATGCCAAGACAAAGCCCGGAGAGAGAGTACACAGCAGTAC 891

DB 157 AsnGluGlnValArgThrAlaArgProProLeuArgGluGlnGlnPheAsnSerThrIle 176

QY 892 CGTGTGTGTGACGTCTCCACCGCTCGCACAGACTGGCTGAATGGCAAGAGTACAAG 951

DB 177 ArgValValSerThrLeuProIleThrHisGlnAspTrpLeuArgGlyLysGluPheLys 196

QY 952 TGCAAGGTCTCCAAGAACCCCTCCAGGCCCCCATCGAGAAACCATCTCCAAAGCCAA 1011

DB 197 CysLysValHisAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaArg 216

QY 1012 GGGCAGCCCCGAGNACACACAGGTGTACACCTCCCGGATCCCGGATGAGTGCACCAAG 1071

DB 217 GlyGlnProLeuGluProLysValThrMetGlyProProArgGluGluLeuSerSer 236

QY 1072 AACGAGTCACTGACCTCGCTGGTCAAGGGTCTTATCCAGCAGCATCGCGGTGGAG 1131

DB 237 ArgSerValSerLeuThrCysMetIleAsnGlyPheTy:ProSerAspIleSerValGlu 256

QY 1132 TGGGAGGCAATGGGACCGGAGAACACTACAGACCCAGCCCTCCCGTGGGACTCC 1191

DB 257 TrpGluLysAsnGlyLysAlaGluAspAsnTyLysThrProAlaValLeuAspSer 276

QY 1192 GACGGCTCTTCTCTCTACCAAGACTCACCGTGGACAAAGAGAGGTGGCAGCAGGGG 1251

DB 277 AspGlySerTyThrPheLeuTyAsnLysLeuSerValProThrSerGluTrpGlnArgGly 296

QY 1252 AAGTCTTCTCATGCTCCGCTGATGCTAGGCTCTGCACACCACTACAGCGAGAGAC 1311

DB 297 AspValPheThrCysSerValMetHisGluAlaLeuHisAsnHisTyThrGlnLysSer 316

QY 1312 CTCTCCCTGTCTCCGGGTAAA 1332

DB 317 IleSerArgSerProGlyLys 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birnstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -I- MISCELLANEOUS: This chain was isolated from pooled serum of strain
CC 13 inbred guinea pigs.
DR PIR; A94553; G2GP.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG-LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308

SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;
Alignment Scores:
Pred. No.: 1.64e-66 Length: 329
Score: 1205.50 Matches: 233
Percent Similarity: 78.14% Conservative: 64
Best Local Similarity: 69.76% Mismatches: 64
Query Match: 50.12% Indels: 9
DB: 1 Gaps: 4
US-09-674-716B-18 (1-1335) x GC2_CAVPO (1-329)
Qy 340 TCAGCTCCACCAAGGGCCCATCGTCTTCCCTCGCACCCCTCTCCAGACCACTCT 399
Db 1 SerAlaArgThrThrAlaProSerValPheProLeuAlaAlaSerCysValAspThrSer 20
Qy 400 GGGGGCACAGCGCCCTGGGCTGCTCAAGGACTTCTCCCGAACCGGTGACGGTG 459
Db 21 GlySerMetMetThrLeuGlyCysLeuValLysGlyTyPheProGluProValThrVal 40
Qy 460 TCGTGAACATCAGCGCCCTGACAGCGGGGTGCACACCTTCCCGCTGCTCTACAGTCC 519
Db 41 LysTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGln--- 59
Qy 520 TCAGGACTCTACTCCCTCAGCAGCGGTGGTACCGTCCCTCCAGCAGCTGGGCACCCAG 579
Db 60 SerGlyLeuTySerLeuThrSerMetValThrValProSerSerGlnLysAlaThr--- 78
Qy 580 ACCTATATCTGCAACGTGAATCAAGCCAGCACACCAAGGTGGACAGAAAGTGGAG 639
Db 79 -----CysAsnValAlaHisProAlaSerSerThrLysValAspLysThrValGlu 95
Qy 640 CCCAATCTTGTGACAAAACCTAC-----ACATGCCGCCCGTCCCGACCTGAACTC 693
Db 96 ProIleArgThrPro***ProCysThrCysProLysCysProProGluAsn 115
Qy 694 GCGGGGACCGTCAGTCTTCTTCCCTTCCCGCCCAAAACCAAGCACACCTCATGATCTCC 753
Db 116 LeuGlyGlyProSerValPheIlePheProProLysProLysAspThrLeuMetIleSer 135
Qy 754 CGGACCCCTGAGTCAATCGTGGTGGAGCGTGAGCCAGCAGACCTGAGGTCAAG 813
Db 136 LeuThrProArgValThrCysValValAspValSerGlnAspValProGluValGln 155
Qy 814 TTCAACTGGTACGTGGAGCGGTGGAGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 873
Db 156 PheThrTrpPheValAspAsnLysProValGlyAsnAlaGluThrLysProArgValGlu 175
Qy 874 CAGTACAACACAGCAGTACCGTGTGGTGGTCCCTCCTCCTCGCACCGACTCGCTG 933
Db 176 GlnTyAsnThrThrPheArgValGluSerValLeuProIleGlnHisGlnAspTrpLeu 195
Qy 934 AATGGCAGAGTACAGTCAAGTCCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAA 993
Db 196 ArgGlyLysGluPheLysCysLysValTyAsnLysAlaLeuProAlaProIleGluLys 215
Qy 994 ACCATCTCCAAAGCCAAAGGGCAGCCCGCAGAACACACAGGTGTACACCTGCCCCCATCC 1053
Db 216 ThrIleSerLysThrLysGlyAlaProArgMetProAspValTyThrLeuProProSer 235
Qy 1054 CGGATAGCTGACCAAGAACCGAGTCCAGCTGACCTGCTGCTGCTCAAGGCTTCTATCCC 1113
Db 236 ArgAspGluLeuSerLysSerLysValSerValThrCysLeuIleIleAsnPhePro 255
Qy 1114 AGGCACATCCCGTGGAGTGGAGAGCAATGGCAGCG-----GAGAACAACTACAAG 1167
Db 256 AlaAspIleHisValGluTrpAlaSerAsnArgValProValSerGluLysGluTyLys 275
Qy 1168 ACCACGCTCCCGTGGTGGACTCCGACGGCTCCTTCTTCTTCTACAGCAAGTCAACGGT 1227
Db 276 AsnThrProProIleGluAspAlaAspGlySerTyPheLeuTySerLysLeuThrVal 295
Qy 1228 GACAAGACAGGTGGCGAGCGGAGACGCTTCTCTCATGTCCGTGATGATGAGGCTCTG 1287

Db 296 AspLysSerAlaTrpAspGlnGlyThrValThrCysSerValMetHisGluAlaLeu 315
 QY 1288 CACAACACCTACACGACGAGAGCTCTCCCTGCTCCGGGT 1329
 Db 316 HisAsnHisValThrGlnLysAlaIleSerArgSerProGly 329

RESULT 6

GC3_RAT ID GC1_RAT STANDARD; PRT; 326 AA.
 AC P20759;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-1 chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232736; PubMed=3149946;
 RA Brueggemann M.;
 RT Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 DR PIR; PS0017; PS0017.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; Igcl; 2.
 DR PROSITE; PS50835; IG LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.

FT NON TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 112 HINGE.
 FT DOMAIN 113 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 105 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Alignment Scores:
 Pred. No.: 2,28e-63 Length: 326
 Score: 1154.00 Matches: 210
 Percent Similarity: 79.52% Conservative: 54
 Best Local Similarity: 63.25% Mismatches: 60
 Query Match: 47.98% Indels: 8
 DB: 1 Gaps: 4

US-09-674-716b-18 (1-1335) x GC1_RAT (1-326)

QY 343 GCCTCCACCAAGGGCCATCGGTCTTCCCTCCGACCCCTCCACAGACACCTCTGGG 402
 Db 1 AlaGluThrAlaProSerValThrProLeuAlaProGlyThrAlaLeuLysSerAsn 20
 QY 403 GGCACAGCGCCCTGGCTGCCTGTCAAGACTACTTCCCGAACCGGTGACGGTTCG 462
 Db 21 SerMetValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThrValThr 40
 QY 463 TGGAACTCAGGCGCCCTGACACGCGGTGACACCTTCCCGGCTGTCTACAGTCTCA 522
 Db 41 TrpAsnSerGlyAlaLeuSerSerGlyValHisThrPheProAlaValLeuGln---Ser 59
 QY 523 GGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCCACAGACTTGGGCACCCAGACC 582

Db 60 GlyLeuThrThrLeuThrSerSerValThrValProSerSerThrThrProSerGlnThr 79
 QY 583 TACATCTGCAACGTGAATCAAGCCGACCAACACCAAGGTGGCAAGAAAGTGGAGCCC 642
 Db 80 ValThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysLeuValPro 99
 QY 643 AAATCTTGTCACAAACTCACACATGCCACCG-----TGCCACGACCTGAACCTCGCG 696
 Db 100 ArgAsnCysGly-----GlyAspCysLysProCysIleCysThrGlySerGluValSer 117
 QY 697 GGGCACCGCTGAGTCTCTCTCCCTCCCAAAACCAAGACACACCTCAATCTCCCGG 756
 Db 118 -----SerValPheIlePheProLysProLysAspValLeuThrIleThrLeu 134
 QY 757 ACCCTGAGGTACATGCGGTGGTGGAGTGCATATGCCAAGACCAAGCCGCGGAGGACG 816
 Db 135 ThrProLysValThrCysValValValAspIleSerGlnAspAspProGluValHisPhe 154
 QY 817 AACTGTACGTGACGCGGTGGAGTGCATATGCCAAGACCAAGCCGCGGAGGACGAG 876
 Db 155 SerTrpPheValAspValGluValHisThrAlaGlnThrArgProGluGluGln 174
 QY 877 TACACAGCAGCTACGCTGCTGCTCAGGTCCTCACCCTGCTCCACGACGACTGGCTGAAT 936
 Db 175 PheAsnSerThrPheArgSerValSerGluLeuProIleLeuHisGlnAspTrpLeuAsn 194
 QY 937 GGCAAGGAGTACAAAGTCAAGGTCTCCAAACAGCCCTCCACGACCCCTCCAGAAAAC 996
 Db 195 GlyArgThrPheArgCysLysValThrSerAlaAlaPheProSerProIleGluLysThr 214
 QY 997 ATCTCCAAACCAAGGACGAGCCCGAGAACACACAGTGTACACCTGCCCTCCCGGAC 1056
 Db 215 IleSerLysProGluGlyArgThrGlnValProHisValThrMetSerProThrLys 234
 QY 1057 GATGAGTGCACCAAGACCAAGGTGACGCTGCTGCTCAAGGCTTCTATCCGAGC 1116
 Db 235 GluGluMetThrGlnAsnGluValSerIleThrCysMetValLysGlyPheThrProPro 254
 QY 1117 GACATCCCGCTGGAGTGGGAGCAATGGGACGCGGAGAACCAACACAGACACGCT 1176
 Db 255 AspiletyrValGluTrpGlnMetAsnGlyGlnProGlnGluAsnThrLysAsnThrPro 274
 QY 1177 CCGGTGCTGACCTCCGACGCTCTCTTCTCTACAGAGCTCACCCTGCGACAGAGC 1236
 Db 275 ProThrMetAspThrAspGlySerTyrPheLeuTyrSerLysLeuAsnValLysLysGlu 294
 QY 1237 AGGTGGCAGCAGGGGAACTCTTCTCATGCTCGGTGATCATGATGATGATGATGATGAT 1296
 Db 295 LysTrpGlnGlnGlyAsnThrPheThrCysSerValLeuHisGluGlyLeuHisAsnHis 314
 QY 1297 TACACGACGAGACCTCTCCCTGCTCCGGGTAAA 1332
 Db 315 HisThrGluLysSerLeuSerHisSerProGlyLys 326
 RESULT 7
 GC3_HUMAN STANDARD; PRT; 290 AA.
 AC P01860;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ig gamma-3 chain C region (heavy chain disease protein) (HDC).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (DISEASE PROTEIN WIS).
 RX MEDLINE=81021548; PubMed=6774747;
 RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
 RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:"

gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
[2]
RP REVISIONS TO 12-97 (PROTEIN WIS).
RX MEDLINE=77118561; PubMed=402363;
RA Michaelson T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
RT quadruplication of a 15-amino acid residue basic unit.";
RL J. Biol. Chem. 252:883-889(1977).
[3]
RP REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX MEDLINE=77021516; PubMed=823945;
RA Wolfenstein-Todel C., Frangione B., Prelli P., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT Structure of the Fc fragment of immunoglobulin G3.";
RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
[4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma Heavy Chain disease in man: cDNA sequence supports partial
RT gene deletion model.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC -!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra
CC interchain disulfide bond at position 7 in addition to the 11
CC normally present in the hinge region.
CC -!- MISCELLANEOUS: The heavy chain disease protein WIS is shown.
CC -!- MISCELLANEOUS: The sequence of residues 42-76 was taken from the
CC Ref.2.
CC -!- MISCELLANEOUS: Disease protein WIS is lacking most of the V region
CC and all of the CH1 region.
CC -!- MISCELLANEOUS: Disease protein ZUC lack most of the V region, all
CC of the CH1 region, and part of the hinge compared with normal
CC gamma-3 heavy chains.
CC -!- MISCELLANEOUS: Disease protein OMM may represent an allelic form
CC or another gamma chain subclass.
CC -!- MISCELLANEOUS: The hinge region in gamma-3 chains is about four
CC times as long as in other gamma chains and contains three
CC identical 15-residue segments preceded by a similar 17-residue
CC segment (12-28).
CC
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CC
CC EMBL; J00231; AAA52805.1; ALT_SEQ.
CC HSSP; P01857; 1FC1; IGHG3.
CC Genew; HGNC:5527; IGHG3.
CC MIM; 147120; -.
CC GO; GO:0005624; C:membrane fraction; NAS.
CC GO; GO:0003823; F:antigen binding; TAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003597; IG-cl.
CC InterPro; IPR003006; IG_MHC.
CC Pfam; PF00407; IG; 2.
CC SMART; SM00407; IGc1; 1.
CC PROSITE; PS50835; IG LIKE; 2.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
KW Pyrrolidone carboxylic acid.
FT DOMAIN 12 73 HINGE.
FT DOMAIN 74 183 CH2.
FT DOMAIN 184 289 CH3.
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .).
FT DISULFID 7 7 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 69 69 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 72 72 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .).
FT MOD_RES 290 290 REMOVED POST-TRANSLATIONALLY.
FT VARIANT 126 127 QV -> EB (IN ZUC).
FT VARIANT 134 134 /FTID=VAR 003890.
FT VARIANT 139 139 P -> L (IN OMM).
FT VARIANT 182 182 /FTID=VAR 003891.
FT VARIANT 227 227 F -> Y (IN OMM).
FT VARIANT 227 227 T -> A (IN OMM).
FT VARIANT 227 227 /FTID=VAR 003893.
FT VARIANT 227 227 S -> N (IN OMM).
FT VARIANT 227 227 /FTID=VAR 003894.
FT VARIANT 227 227 MISSING (IN ZUC).
FT VARIANT 279 279 /FTID=VAR 003895.
FT VARIANT 279 279 F -> Y (IN OMM).
FT VARIANT 290 290 /FTID=VAR 003896.
SQ SEQUENCE 290 AA; 32331 MW; B69CB95705B2F46 CRC64;

Alignment Scores:
Pred. No.: 2,42e-63 Length: 290
Score: 1153.50 Matches: 230
Percent Similarity: 78.16% Conservative: 17
Best Local Similarity: 72.78% Mismatches: 30
Query Match: 47.96% Indels: 39
DB: 1 Gaps: 8

US-09-674-716b-18 (1-1335) x GC3_HUMAN (1-290)

QY 389 AGAGCACTCTGGGGGACAGCGCGCTGGCTGCTCAAGGACTACTTCCCGAAC 448
Db 14 LysThrProLeuGlyAsp-----ThrThrHisThrCysPro--- 25
QY 449 CGGTGACGGTGTGCTGGAACCTAGGGCCCTGACGAGCGCGTGCACACTTCCGGCTG 508
Db 26 -----ArgCys-----ProGluProLysSerCys----- 33
QY 509 TCCTACAGTCTCAGGACTCTACTCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCT 568
Db 34 -----AspThrProPro-----ProCysProArg----- 41
QY 569 TGGGCACCCAGACTACATCTGCAAGCTGAATCACAAGCCAGCAGACACCAAGTGGACA 628
Db 42 ---CysProGluProLysSerCysAsp-----ThrProProCysProArgCys--P 58
QY 629 AGAAGTGGAGCCCAATCTTGTGACAAACTCACACATGCCCCACCGTCCCGACACCTG 688
Db 58 ro-----GluProLysSerCysAspThrProProCysProArgCysProAlaProG 76
QY 689 AACTCGCGGGGACCGCTCAGTCTTCTCTTCCCGGACCAAGGACCAAGGACCTCATGA 748
Db 76 luLeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetI 96
QY 749 TCTCCCGGACCTGAGGTACATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 808
Db 96 leSerArgThrProGluValThrCysValValValValValValValValValValVal 116
QY 809 TCAAGTTCACCTGCTAGTGGAGCGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAGGTGGAG 868
Db 116 alGlnPheLysTrpTyTrpValAspGlyValGlnValHisAlaLysThrLysProArg 136

QY 403 GGCACAGCGGCGCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTCTCG 462
Db 21 SerMetValThrLeuGlyCysLeuValGlyTyrPheProGluProValThrValThr 40
QY 463 TGGAACTCAGCGCGCTGACACAGCGGGTGCACACCTTCCCGGTGCTGTACAGTCTCTCA 522
Db 41 TrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGlnSerAsp 60
QY 523 GGACTCTACTCTCAGCAGCGGTGTGACCTGCTCCAGCAGCTTGGGCAACCCAGCC 582
Db 61 ---LeuTyrThrLeuSerSerValThrValProSerSerProAlaGProSerGluThr 79
QY 583 TACATCTCAACGCTGAATCAACAGCCAGCAACCAAGGTGGACAGAAAGTGGAGCC 642
Db 80 ValThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysValLeuValPro 99
QY 643 AAATCTTGTGACAAACTCACATGCCCCAGC-----TCCCGACACCTGACTCGCG 696
Db 100 ArgAspCysGly-----CysLysProCysLysCysThrValProGluValSer 115
QY 697 GGGGACCGCTAGTCTTCTTCCCGCCCAACCAAGGACACCTCATGCTCCCGG 756
Db 116 -----SerValPheIlePheProLysProLysAspValLeuThrIleThrLeu 132
QY 757 ACCCTGAGGTACATGCTGTGTGACGTGACGTGACGACGACGACGACGACGACGAC 816
Db 133 ThrProLysValThrCysValValAspLysSerLysAspAspProGluValGlnPhe 152
QY 817 AACTGTGACGTGGCGGTGGGTGATATGCAAGACCAAGACGCGGGAGGAGCAG 876
Db 153 SerTrpPheValAspValGluValHisThrAlaGlnThrGlnProArgGluGluGln 172
QY 877 TACACACAGCAGTACCGTGTGTGACGCTCTCCACGCTCTGACACGACGACGACGAC 936
Db 173 PheAsnSerThrPheArgSerValSerGluLeuProIleMetHisGlnAspTrpLeuAsn 192
QY 937 GCAAGGAGTCAAGTCAAGTCTCCACAAAGCCCTCCAGCCCGCATCGAAGAAC 996
Db 193 GlyLysGluPheLysCysArgValAsnSerAlaAlaPheProAlaProIleGluLysThr 212
QY 997 ATCTCCAAAGCCAGGCGCGCCGAGAACCAAGGTGTACACCTCCCGCCATCCCGG 1056
Db 213 IleSerLysThrLysGlyArgProLysAlaProGlnValThrIleProProLys 232
QY 1057 GATGAGTCAACAAAGCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1116
Db 233 GluGlnMetAlaLysAspLysValSerLeuThrCysMetIleThrAspPheProGlu 252
QY 1117 GACATCGCGGTGGAGGAGCAATGGGAGCGGAGACAACTACAAGACCAAGCGCT 1176
Db 253 AspIleThrValGluTrpGlnTrpAsnGlyGlnProAlaGluAsnTyrLysAsnThrGln 272
QY 1177 CCGGTGCTGGACTCCGAGCGCTCTTCTTCTCTACAGCAAGCTCACCGTGACAAAGC 1236
Db 273 ProIleMetAsnThrAsnGlySerTyrPheValTyrSerLysLeuAsnValGlnLysSer 292
QY 1237 AGGTGGCAGCGGAGCAAGCTCTCTCAGTCTCGGTGATGATGATGATGATGATGATGAT 1296
Db 293 AsnTrpGluAlaLysAsnThrPheThrCysSerValLeuHisGluGlyLeuHisAsnHis 312
QY 1297 TACAGCAGAGAGCTCTCCCTGCTCCCGGTA 1332
Db 313 HisThrGluLysSerLeuSerHisSerProGlyLys 324

RESULT 9
GCIM MOUSE
ID GCIM MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig-gamma-1 chain C region, membrane-bound form.

Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T.; Obata M.; Yamawaki-Kataoka Y.; Kataoka T.; Kawakami T.;
RA Takahashi N.; Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568 (1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M.; Cowman A.F.; Gerondakis S.D.; Adams J.M.; Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012 (1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J.; Choi E.; Souza L.; Carter C.; Word C.J.; Kuehl M.;
RA Eisenberg D.; Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
RL Cell 26:19-27 (1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-Kataoka Y.; Nakai S.; Miyata T.; Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627 (1982).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Membrane-bound;
CC IsoId=P01869-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoId=P01868-1; Sequence=External;
CC Note=May be the major isoform;
CC -----
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CC -----
DR EMBL; V00793; CAA24172.1; -;
DR EMBL; V00793; CAA24173.1; -;
DR EMBL; V00793; CAA24174.1; -;
DR PIR; B02159; GIMSM.
DR PDB; 15C8; 23-MAR-99.
DR PDB; 1AE6; 18-MAR-98.
DR PDB; 1CL7; 12-JAN-00.
DR PDB; 1FL1; 06-FEB-01.
DR PDB; 1F58; 29-DEC-99.
DR PDB; 1KCS; 24-JUL-02.
DR PDB; 1KCR; 11-MAY-02.
DR PDB; 25C8; 09-JUL-99.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane; 3D-structure.


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US-09-674-716b-18 (1-1335) x GCB_RAT (1-333)
QY 343 CCCTCCACCAAGGCCATCGCTCTTCCCTCGTCCAGCCCTCTCCACAGAGCACCTCTGGG 402
Db 1 AlaGlnThrThrAlaProSerValTyProLeuAlaProGlyCysGlyAspThrThrSer 20
QY 403 GGCACAGCGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 462
Db 21 SerThrValThrLeuGlyCysLeuValLysGlyTyPheProGluProValThrValThr 40
QY 463 TGGAACTCAGCGCGCTGACCAAGCGCGCTGACACACCTCTCCCGGTGCTCTACAGTCTCTCA 522
Db 41 TrpAsnSerGlyAlaLeuSerSerAspValHisThrPheProAlaValLeuGln--Ser 59
QY 523 GGACTCTACTCCCTCAGCAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582
Db 60 GlyLeuTyThrLeuThrSerSerValThr-----SerSerThrTrpProSerGlnThr 77
QY 583 TACATCTCAACGTAATCAACAGCCCAAGCAACCAAGGTTGGACAAAGAGTGGAGCC 642
Db 78 ValThrCysAsnValAlaHisProAsnSerThrLysValAspLysValGluArg 97
QY 643 AAATCT-----TGTGCAAAACTCACATGCCACCGTCCCGACCA 684
Db 98 ArgAsnGlyGlyIleGlyHisLysCysProThrCysProThrCysHisLysCysProVal 117
QY 685 CCTGAACCTCGGGGCGACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 744
Db 118 ProGluLeuLeuGlyGlyProSerValPheThrPheProLysProLysAspIleLeu 137
QY 745 ATGATCTCCGAGCCCTGAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 804
Db 138 LeuIleSerGlnAsnAlaLysValThrCysValValValAspValSerGluGluPro 157
QY 805 GAGTCAAGTCACTGCTAGTGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 864
Db 158 AspValGlnPheSerTrpPheValAsnValGluValHisThrAlaGlnThrGlnPro 177
QY 865 CGGGAGGAGCAGTCAACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 924
Db 178 ArgGluGluGlnTyPheSerThrPheArgValValSerAlaLeuProIleGlnHisGln 197
QY 925 GACTGGCTGAATGGCAAGGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 984
Db 198 AspTrpMetSerGlyLysGluPheLysCysLysValAsnValAsnLysAlaLeuProSerPro 217
QY 985 ATCGAAGAACCATCTCCAAAGCCCAAGGCGAGCCCGAGACACACAGGTGTACACCTG 1044
Db 218 IleGluLysThrIleSerLysProLysGlyLeuValArgLysProGlnValTyValMet 237
QY 1045 CCCCCATCCCGGATGAGTGCACCAAGAACCAAGGTGAGTGCACCTGCTGCTGCTCAAGGC 1104
Db 238 GlyProProThrGluGlnLeuThrGluGlnThrValSerLeuThrCysLeuThrSerGly 257
QY 1105 TTCTATCCAGCGCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1164
Db 258 PheLeuProAsnAspIleGlyValGluTrpThrSerAsnGlyHisIleGlyLysAsnTy 277
QY 1165 AAGACACGCCCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1224
Db 278 LysAsnThrGluProValMetAspSerAspGlySerPheMetTySerLysLeuAsn 297
QY 1225 GTGGACAAGAGCAGTGGCAGCGGGAACGCTTCTCTCATGCTCGTGCATGATGAGCT 1284
Db 298 ValGluArgSerArgTrpAspSerArgAlaProPheValCysSerValValHisGluGly 317
QY 1285 CTGGACACCACTACAGCAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
Db 318 LeuHisAsnHisHisValGluLysSerIleSerArgProProGlyLys 333
RESULT 11
GCB_MOUSE
ID GCB_MOUSE STANDARD; PRT; 329 AA.
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QY 646 TCTGTGACAAACTCACATGCCCA-----CGTGCCTCCAGCACCTGAATCTCGGGG 699
DB 100 ---IleProLysProSerThrProProGlySerSerCysProProGlyAsnIleuGly 118
QY 700 GCACCGTGTCTCTCTCTCCCAACCAAGGACACCTCATCATCTCCCGGACC 759
DB 119 GlyProSerValPheIlePheProLysProLysAspAlaLeuMetIleSerLeuThr 138
QY 760 CTGAGGTCACATGCTGTGTGTGTGAGCGTGCAGCAGACCTGAGGTCAAGTTCAAC 819
DB 139 ProLysValThrCysValValValAspValSerGluAspAspProAspValHisValSer 158
QY 820 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 879
DB 159 TrpPheValAspAsnLysGluValHisThrAlaTrpThrGlnProArgGluAlaGlnTrp 178
QY 880 AACAGCAGCTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 939
DB 179 AsnSerThrPheArgValValSerAlaLeuProlIleGlnHisGlnAspTrpMetArgGly 198
QY 940 AAGAGTACAAGTGAAGTCTCCAAAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAG 999
DB 199 LysGluPheLysCysLysValAsnAsnLysAlaLeuProAlaProIleGluArgThrIle 218
QY 1000 TCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCCCTCCCGGAT 1059
DB 219 SerLysProLysGlyArgAlaGlnThrProGlnValThrThrIleProProArgGlu 238
QY 1060 GAGCTGACCAAGAACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1119
DB 239 GlnMetSerLysLysLysValSerLeuThrCysLeuValThrAsnPheSerGluAla 258
QY 1120 ATCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1179
DB 259 IleSerValGluTrpGluArgGlnGlyGluLeuGluGlnAspTyrLysAsnThrProPro 278
QY 1180 GTGCTGAGCTCCGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1239
DB 279 IleLeuAspSerAspGlyThrThrPheLeuThrThrLeuThrValThrValAspSer 298
QY 1240 TGCAGCAGGGAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1299
DB 299 TrpLeuGlnGlyIlePheThrCysSerValValHisGluAlaLeuHisAsnHisHis 318
QY 1300 AGCAGAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
DB 319 ThrGlnLysAsnLeuSerArgSerProGlyLys 329

RESULT 12
GC3M MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
OS Ig gamma-3 chain C region, membrane-bound form.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine Ig3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041493; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;

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RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
RL segment.";
CC Nucleic Acids Res. 11:6775-6785(1983).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00451; AAB59655.1; --
DR EMBL; V01526; CAA24767.1; ALT_SEQ.
DR PIR; A01556; GSM5M.
DR HSP; P01857; IFCL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PSS0835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 F -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Alignment Scores:
Pred. No.: 3-22e-61 Length: 398
Score: 1119.00 Matches: 208
Percent Similarity: 77.51% Conservative: 47
Best Local Similarity: 63.22% Mismatches: 70
Query Match: 46.53% Indels: 4
DB: 1 Gaps: 3

US-09-674-716B-18 (1-1335) x GC3M_MOUSE (1-398)
QY 346 TCCACCAAGGCGCCATCGGTCTTCCCTCGGACACCTCTCCAGAGACCTCTGGGGG 405
DB 1 ThrThrAlaProSerValTyrProLeuValProGlyCysSerAspThrSerGlySer 20
QY 406 ACAGCGGCGCTGGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 465
DB 21 SerValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThrValLysTrp 40
QY 466 AACTAGGCGGCTGTACACGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 525
DB 41 AsnTyrGlyAlaLeuSerSerGlyValArgThrValSerSerValLeuGln---SerGly 59
QY 526 CTCTACTCTCTCAGCAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 585
DB 60 PheTyrSerLeuSerSerLeuValThrValProSerSerThrTrpProSerGlnThrVal 79
QY 586 ATCTGCAAGTGAATCAAGCCCAACACCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 645
DB 80 IleCysAsnValAlaHisProAlaSerLysThrGluLeuLeuLeuLeuLeuLeuLeuLeu 99
QY 646 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 699
DB 100 ---IleProLysProSerThrProProGlySerSerCysProProGlyAsnIleuGly 118
QY 700 GCACCGTGTCTCTCTCTCCCAACCAAGGACACCTCATCATCTCCCGGACC 759

```


QY 694 GCGGGGACCGTCAGTCTTCTCTCCCAAAACCCAGGACACCCCTCATGATCTCC 753
Db |||||
QY 117 LeuGluArgProSerValPheIlePheProProLysAspIleLeuMetIleThr 136
Db |||||
QY 754 CGGACCCCTGAGCTCACATGGCTGGTGGTGGACGACGACGACGACGACGACG 813
Db |||||
QY 137 LeuThrProLysValThrCysValValValValSerGluGluGluProAspValGln 156
Db |||||
QY 814 TTCAACTGGTACGTGGGCGGTGGAGGTGATATGCAAGACAAAGCCCGGGAGAG 873
Db |||||
QY 157 PheSerTrpPheValAspAsnValArgValPheThrAlaGlnThrGlnProHisGluGlu 176
Db |||||
QY 874 CAGTACACACGACGACGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 933
Db |||||
QY 177 GlnLeuAsnGlyThrPheArgValValSerThrLeuHisIleGlnHisGlnAspTrpMet 196
Db |||||
QY 934 AATGCAAGGAGTCAAGTCAAGTCTCCAAAGACCCCTCCAGCCGACGACGACGACG 993
Db |||||
QY 197 SerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProSerProIleGluLys 216
Db |||||
QY 994 ACCATCTCCAAAGCCAGGACGACGACGACGACGACGACGACGACGACGACGACG 1053
Db |||||
QY 217 ThrIleSerLysProArgGlyValArgValPheThrAlaGlnThrGlnProHisGluGlu 236
Db |||||
QY 1054 CGGATGAGTCAAGCAAGACGACGACGACGACGACGACGACGACGACGACGACG 1113
Db |||||
QY 237 ArgGluGlnMetSerLysAsnLysValSerLeuThrCysMetValThrSerPheTyPro 256
Db |||||
QY 1114 AGGACATCGCGTGGAGTGGAGCAATGGGACGCGGAGACAACTACAAACACG 1173
Db |||||
QY 257 AlaSerIleSerValGluTrpGluArgAsnGlyLeuGluGlnAspTyLysAsnThr 276
Db |||||
QY 1174 CTTCCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1233
Db |||||
QY 277 LeuProValLeuAspSerAspGluSerLysPheLeuTySerLysLeuSerValAspThr 296
Db |||||
QY 1234 AGCAGTGGGACGGGAAAGCTTCTTCATGCTCCGATGATGATGATGATGATGATG 1293
Db |||||
QY 297 AspSerTrpMetArgLysAspIleTyThrCysSerValValHisGluAlaLeuHisAsn 316
Db |||||
QY 1294 CACTACACGACGACGACGCTCCCTGCTCCGGGTAAA 1332
Db |||||
QY 317 HisHisThrGlnLysAsnLeuSerArgSerProGlyLys 329
Db |||||
RESULT 15
GCA_RAT
ID - GCA_RAT STANDARD; PRT; 322 AA.
AC P20760;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2A chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family";
RL Gene 74:473-482(1988).
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----

EMBL; M13804; AAA41376.1; ALT_INIT.
DR PIR; PS0019; PS0019.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT NON_TER 1 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 115 212 IG-LIKE 2.
FT DOMAIN 221 317 IG-LIKE 3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 136 196
FT DISULFID 242 300
FT CARBOHYD 172 172 N-LINKED (GLCNAC, ...) (POTENTIAL).
SQ SEQUENCE 322 AA; 35186 MW; E8EA136A9DE01EDB CRC64;

Alignment Scores:
Pred. No.: 6,33e-61 Length: 322
Score: 1114.00 Matches: 206
Percent Similarity: 77.27% Conservative: 49
Best Local Similarity: 62.42% Mismatches: 67
Query Match: 46.32% Indels: 8
DB: 1 Gaps: 4

US-09-674-716b-18 (1-1335) x GCA_RAT (1-322)
QY 343 GCCTCCACCAAGGGCCATCGGTCTTCCCTGGCACCCTCTCTCAAGACACCTCTGG 402
Db 1 AlaGluThrAlaProSerValTyProLeuAlaProGlyThrAlaLeuLysSerAsn 20
QY 403 GGCACACGGCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 462
Db 21 SerMetValThrLeuGlyCysLeuValLysGlyTyProLeuGluProValThrValThr 40
QY 463 TGGAACTCAGGCGCCCTGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 522
Db 41 TrpAsnSerGlyAlaLeuSerSerGlyValHisThrPheProAlaValLeuGln---Ser 59
QY 523 GGACTCTACTCTCCCTCAGCAGCGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
Db 60 GlyLeuTyThrLeuThrSerSerValThrValProSerSerThrTrpSerSerGlnAla 79
QY 593 TACATCTGCAAGCTGAATCACAAGCCCGACACACCAAGGTGGACAAAGAGTGGAGCCC 642
Db 80 ValThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysLysLysValPro 99
QY 643 AAATCTTGTGACAAAACCTCACACATGCCACCGTGGCCGACGACCTCAACTCGCGGGGCA 702
Db 100 ArgGluCys-----AsnProCys---GlyCysThrGlySerGluValSer----- 113
QY 703 CCTCAGTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 762
Db 114 ---SerValPheIlePheProLysThrLysAspValLeuThrIleThrLeuThrPro 132
QY 763 GAGTCCATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 822
Db 133 LysValThrCysValValValAspIleSerGlnAsnAspProGluValArgPheSerTrp 152
QY 823 TAGTGGAGGGGTGGAGGTGCATATGCAAGACAAAGCCCGGGAGGAGGAGCAGTACAAC 882
Db 153 PheIleAspAspValGluValHisThrAlaGlnThrHisAlaProGluLysGlnSerAsn 172
QY 883 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 942
Db 173 SerThrLeuArgSerValSerGluLeuProIleValHisArgAspTrpLeuAsnGlyLys 192

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QY 943 GAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCC 1002
Db ::::::::::::::::::::|
193 ThrPheLysCysLysValAsnSerGlyAlaPheProAlaProIleGluLysSerIleSer 212
QY 1003 AAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGGGATGAG 1062
Db ::::::::::::::::::::|
213 LysProGluGlyThrProArgGlyProGlnValTyrThrMetAlaProProLysGluGlu 232
QY 1063 CTGACCAAGAACAGGTACGCTGACCTGCTGGTCAAAAGGCTTCTATCCAGCGACATC 1122
Db ::::::::::::::::::::|
233 MetThrGlnSerGlnValSerIleThrCysMetValLysGlyPheTyrProProAspIle 252
QY 1123 GCCGTGGAGTGGGAGAGCAATGGGAGCGCGAGAACAACTACAGACCCACGCTCCCGTG 1182
Db ::::::::::::::::::::|
253 TyrThrGluTrpLysMetAsnGlyGlnProGlnGluAsnTyrLysAsnThrProProThr 272
QY 1183 CTGGACTCCGACGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGG 1242
Db ::::::::::::::::::::|
273 MetAspThrAspGlySerTyrPheLeuTyrSerLysLeuAsnValLysLysGluThrTrp 292
QY 1243 CAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAAACCACTACACG 1302
Db ::::::::::::::::::::|
293 GlnGlnGlyAsnThrPheThrCysSerValLeuHisGluGlyLeuHisAsnHisHisThr 312
QY 1303 CAGAGAGCGCTCTCCCTCTCTCCGGGTAAA 1332
Db ::::::::::::::::::::|
313 GluLysSerLeuSerHisSerProGlyLys 322
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Search completed: September 30, 2004, 08:43:02
Job time : 43.9645 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:27:18 ; Search time 169.047 Seconds
(without alignments)
4983.418 Million cell updates/sec

Title: US-09-674-716b-18

Perfect score: 2405

Sequence: 1 gaggtgacgtggaggatc.....ccctgtctcgggtaaatga 1335

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODBL=frame+n2p model -DEV=xlp
-Q=/sgn2_1/USPTC_spool_p/US09674716/runat_30092004_070258_25867/app_query.fasta_1.3164
-DB=SPTRMBL_25 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEX=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09674716 @CGN 1.1.499 @runat 30092004_070258_25867 -ICPU=3
-NO.MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=5
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_xvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | Score | Match | Length | DB | ID | Description |
|------------|--------|-------|-------|--------|--------|----|--------------------|
| 1 | 2139.5 | 89.0 | 470 | 4 | Q7Z5W1 | | Q7Z5W1 homo sapien |

RESULT 1

| ID | Q7Z5W1 | PRELIMINARY; | PRT; | 470 AA. |
|----|---|--------------|------|---------|
| AC | Q7Z5W1; | | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Created) | | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) | | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | | | |
| DE | Hypothetical protein. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Spleen; | | | |
| RX | MEDLINE=2238257; PubMed=12477932; | | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., | | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., | | | |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., | | | |
| RA | Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., | | | |
| RA | Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., | | | |
| RA | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., | | | |
| RA | Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | | | |

ALIGNMENTS

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Schmutz J., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC053984; AAH53984.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 470 AA, 51204 MW; 778CF34521483E1A CRC64;

Alignment Scores:

Pred. No.: 4,088-162 Length: 470
 Score: 2139.50 Matches: 407
 Percent Similarity: 91.85% Conservative: 10
 Best Local Similarity: 89.65% Mismatches: 24
 Query Match: 88.96% Indels: 13
 DB: 2 Gaps: 4

US-09-674-716b-18 (1-1335) x Q725W1 (1-470)

QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGCTGGTAAAGCCGGGGGCTCCCTTAGACTC 60
 DB 20 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
 QY 61 TCCTGTGAGCTAGCGGATTCATCTTCTAGTGGCTACTGGATGCTCGGGTCCGCGAGCT 120
 DB 40 SerCysValAlaSerGlyPheThrLeuAsnAspMetHisTrpValArgGlnGly 59
 QY 121 CCAGGGAGGGCTCGAGTGGTCTGCTGAAATAGATTGAAATCTGTAATATGCAACA 180
 DB 60 IleGlyGlyGlyLeuGlnTrpValSerLysIleGlyThrAlaGlyAspArgTrp 77
 QY 181 CATTTATCGGAGCTCTGTGAAGGGAAATTCACCAATCTCAAGAGATGATCAAAATCTAGA 240
 DB 78 ---TyrAlaGlySerValGlyArgPheThrIleSerArgGluAsnAlaLysAspSer 96
 QY 241 CTGTATCTGCAATGAACAGCTGTAACCGGACGACGCGGTGTTATCTGTACA--- 297
 DB 97 LeuTyrLeuGlnMetAsnSerLeuArgValGlyAspAlaAlaValTyrTyrCysAlaArg 116
 QY 298 -----GATTTTCATAGACTGGGCGCCAGGGAACACTAGTC 330
 DB 117 GlyAlaGlyArgTrpAlaProLeuGlyAlaPheAspIleTrpGlyGlnGlyThrMetVal 136
 QY 331 ACCGTCTCTCAGCTCCACCAAGGCGCATCGGTCTCCCTGGCACCTCTCCAG 390
 DB 137 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 156
 QY 391 AGCACCCTCTGGGGCACAGCGCCCTCGGCTGCTCGGTCAAGGACTACTTCCCGAACCG 450
 DB 157 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 176
 QY 451 GTGAGGTGCTGTGAATCTCAGCGCCCTGACGACGCGGTGCACACCTTCCCGGTGTC 510
 DB 177 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 196
 QY 511 CTACAGTCTCTCAGGACTCTACTCTCTCAGCAGCGGTGGACCGTCCCTCCAGAGCTTG 570
 DB 197 LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLys 216
 QY 571 GGCACCCAGACCTACATCTGCAACGTGAATCAAGCCGACCAACCAAGGTGGACAAG 630
 DB 217 GlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 236

QY 631 AAAGTCGACCCCAAAATCTTGTGCAAAAATCAACATGCCACCGTGGCCAGCACTGAA 690
 DB 237 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 256
 QY 691 CTCGCGGGGCGACCGTCAGTCTCTCTCTCCCCCAAAACCCCAAGGACACCTCATGTC 750
 DB 257 LeuLeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIle 276
 QY 751 TCCCGACCCCTGAGGTCAATCGGTGGTGGAGCTGAGCCACCAAGACCTCAGGTC 810
 DB 277 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 296
 QY 811 AGTTCAACTGGTACGTGACCGCGTGGAGTGCATATGCCAAGACAAAGCCGGGAG 870
 DB 297 LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 316
 QY 871 GAGCAGTCAACAGCAGCAGTACCGTGTGGTCAAGCTCCTCACCGTCTGACACGAGCTGG 930
 DB 317 GluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrp 336
 QY 931 CTGAATGGCAGGAGTACAAAGTGCAGGTCTCCAAAGACCTCCAGCCCTCCATCGAG 990
 DB 337 LeuAsnGlyLysGlnTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 356
 QY 991 AAAACCATCTCCAAAGCCAAAGCGGACCGCCCGAGAACCAACAGGTGTACACCTGCCCCA 1050
 DB 357 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProPro 376
 QY 1051 TCCCGGATGAGTACCAAGAACAGGTCAAGCTGACCTGCTGCTGCTCAAGGCTCTAT 1110
 DB 377 SerArgAspGluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr 396
 QY 1111 CCAGCGACATCGCGTGGAGTGGGAGCAGCAATGGCAGCGGAGAACAACTACAGAGCC 1170
 DB 397 ProSerAspIleAlaValGlnTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr 416
 QY 1171 ACCTCTCCGCTGTGACTCCGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230
 DB 417 ThrProProValLeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAsp 436
 QY 1231 AGACAGGTGGCAGCAGGAGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1290
 DB 437 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 456
 QY 1291 AACCACTACACGAGAGAGCCTCTCCCTGCTCTCCGGGTAAA 1332
 DB 457 AsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 470

RESULT 2

Q72351 PRELIMINARY; PRT; 482 AA.
 ID Q72351
 AC Q72351;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein DKFZP686N02209.
 GN DKFZP686N02209.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa;
 OC Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX538118; CAD98026.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 482 AA; 52852 MW; ED475F1901D1A034 CRC64;

Alignment Scores:

Pred. No.: 5,8e-158 Length: 482
 Score: 2087.50 Matches: 400
 Percent Similarity: 89.46% Conservative: 16
 Best Local Similarity: 86.02% Mismatches: 26
 Query Match: 86.80% Indels: 23
 DB: 4 Gaps: 4

US-09-674-716b-18 (1-1335) x Q72351 (1-482)

| | | | |
|----|-----|---|-----|
| QY | 1 | GAGTGCAGCTGGTGGAGCTTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC | 60 |
| DB | 20 | GlnAlaGlnValValGlnSerGlyGlySerValValGlnProGlyArgSerLeuArgLeu | 39 |
| QY | 61 | TCCTGTGAGCTAGCGGATTCACCTTTCAGTGGCTACTGGATGCTCTGGTCCGCCAGGCT | 120 |
| DB | 40 | SerCysIleAlaSerGlyPheSerPheSerGlySerAlaMetHisThrLeuArgGlnIle | 59 |
| QY | 121 | CCAGGAAAGGGCTCGAGTGGTGTCTGAAATAGATTGAATCTGATAATTATGCAACA | 180 |
| DB | 60 | ProGlyLysGlyLeuGluTrpValAlaValIle-----SerTyrAspGlyAsnHisLys | 77 |
| QY | 181 | CATTATGGGAGTCTGTGAAGGGNAATTCACCATCTCAAGAGATGATTCAAATCTAGA | 240 |
| DB | 78 | LeuTyrSerAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysSerLeu | 97 |
| QY | 241 | CTGTATCTGCAATGAACAGAGCTGAAAGCCGAGGACACAGCGCTGATTACTGTACA--- | 297 |
| DB | 98 | LeuPheLeuHisValAsnSerLeuThrSerAlaAspThrAlaIleTyrTyrCysAlaArg | 117 |
| QY | 298 | GATTC----- | 303 |
| DB | 118 | AspPheHisSerLysThrThrSerIlePheGlyLeuIleProLeuTyrPheTyrTyrSer | 137 |
| QY | 304 | ---ATAGAC---TGGGGCGGAGAACACTAGTACCGCTCTCTCAGCGCTCCACCAAGGGC | 357 |
| DB | 138 | AlaMetAspThrTrpGlyArgGlyThrThrValIleValSerSerAlaSerThrLysGly | 157 |
| QY | 358 | CCATCGGCTTCCCTGGCCCTCCCTCCAGAGACACTCTGGGGGACACGCGCCCTG | 417 |
| DB | 158 | ProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeu | 177 |
| QY | 418 | GGCTGCTGTCAGGACTACTTCCCGAAGCGGTGAGCGTGTCTGTGAACCTCAGGCGC | 477 |
| DB | 178 | GlyCysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAla | 197 |
| QY | 478 | CTGACGAGCGGCTGCACACCTTCCCGGCTGTCTCTACAGTCTCTCAGGACTCTACTCCCTC | 537 |
| DB | 198 | LeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeu | 217 |
| QY | 538 | AGCAGCGTGTGACCGTCCCTCCAGAGCTTGGGCACCCAGACCTACATCTGCAAGCTG | 597 |
| DB | 218 | SerSerValValThrValProSerSerLeuGlyThrGlnThrTyrIleCysAsnVal | 237 |
| QY | 598 | AATCAAGCCCGCAGCAACACCAAGCTGGACAAAGTGGAGCCCAATCTTGTGACAAA | 657 |
| DB | 238 | AsnHisLysProSerAsnThrLysValAspLysLysValGluProLysSerCysAspLys | 257 |
| QY | 658 | ACTCACATGCCCACCGTCCAGACCTGAACTCGCGGGGACACCGTCACTGCTTCTC | 717 |
| DB | 258 | ThrHisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSerValPheLeu | 277 |
| QY | 718 | TTCCCCCCTAAACCAAGCACCTCTGATCTCTCCCGGACCCCTGAGTGCATGCGTG | 777 |
| DB | 278 | PheProProLysProGlyAspThrLeuMetIleSerArgThrProGluValThrCysVal | 297 |
| QY | 778 | GTGGTGGAGCTGAGCCAGAACCCCTGAGTTCAGTTCAAGTTCAGTGGAGCGGCTG | 837 |
| DB | 298 | ValValAspValSerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyVal | 317 |
| QY | 838 | GAGTGCATATGCCAAGCAAGCCGGGGAGGAGGAGTACACAGCAGCTACCGTGTG | 897 |
| DB | 318 | GluValHisAlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyrArgVal | 337 |

| | | | |
|----|------|--|------|
| QY | 898 | GTCCAGGCTCTCACCGTCTGCACAGGACTGGCTGAATGGCGAGAGTACAGTGCAG | 957 |
| DB | 338 | ValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysLeuTyrLysCysLys | 357 |
| QY | 958 | GTCTCCAAACAAAGCCCTCCAGCCCTCCAGCCCTCCAGAGAAACCATCTCCAAAGCCAG | 1017 |
| DB | 358 | ValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaLysGlyGln | 377 |
| QY | 1018 | CCCCGAGAACCCAGGTGTACACCTGCCCTGCCCTCCCGGATGAGTGCACCAAGACCAG | 1077 |
| DB | 378 | ProArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThrLysAsnGln | 397 |
| QY | 1078 | GTCCAGCTCACCTCCCTGGTCAAGAGCTTCTATCCCGAGCAGCATCCCTGGAGTGGAG | 1137 |
| DB | 398 | ValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGlu | 417 |
| QY | 1138 | AGCAATGGGAGCCGAGAACCAACTCAAGACACACCGCTCCCGTGTGTGACTCCGACGGC | 1197 |
| DB | 418 | SerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProValLeuAspSerAspGly | 437 |
| QY | 1198 | TCCTCTTCTCTACAGCAGCTCACCGTGGCAAGAGCAGGTGGCAGAGGGAACGTC | 1257 |
| DB | 438 | SerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnVal | 457 |
| QY | 1258 | TTCTCATGCTCCGTGATGATGAGCTGTGCACCAACCATCACGAGAGACCTCTCTCC | 1317 |
| DB | 458 | PheSerCysSerValMetHisGlyLeuHisAsnHisTyrThrGlnLysSerLeuSer | 477 |
| QY | 1318 | CTGCTCTCCGGTAAA | 1332 |
| DB | 478 | LeuSerProGlyLys | 482 |

ID Q727P5 PRELIMINARY; PRT; 469 AA.
 AC Q727P5; 2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 MDLINE=22388257; PubMed=12477932;
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gnaratine P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
 RA Krzywinski M.I., Skalka U., Smalusz D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RV [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RA Srausberg R.;
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.

QY 1 GAGGTGACGCTGGTGGAGCTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
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 QY 20 GluValGlnLeuValAspSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
 Db
 QY 61 TCCTGTGACGTAGCGGATTACCTTTCAGTGGCTACTGGATGCTCCTGGGTCGGCAGGCT 120
 Db
 QY 40 SerCysAlaAlaSerGlyPheIleValSerAspHisTyrValGlnTyrPheValArgGlnAla 59
 Db
 QY 121 CCAGGGAAGGGGCTCGAGTGGTGTCTGCAAAATTAGATTGAATCTGATTAATTATTCACACA 180
 Db
 QY 60 ProGlyLysGlyProGluTyrValGlyCysPheArgSerLysAlaHisLysSerThrThr 79
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 QY 181 CATTAAGCGAGTCTGTGAAGGGGAATTCACATCTCAAGAGATGATTCAAAATCTAGA 240
 Db
 QY 80 GluTyrAlaAlaSerValLysGlyPheThrIleLeuArgAspSerLysAsnSer 99
 Db
 QY 241 CTGTATCTGCAAACTGAACAGCTGAAACCCAGAGACACAGCCGTGTTATTACTGTACAGAT 300
 Db
 QY 100 ValHisLeuGlnMetAsnSerLeuLysThrAspPheThrAlaValTyrTyrCysValArg 119
 Db
 QY 301 TTCATPAGAC-----TGGGGCCAGGGAACTA 327
 Db
 QY 120 AspLeuGluGlyAlaGlyLysTyrAspTyrPheAspIleTyrGlyArgGlyIleLeu 139
 Db
 QY 328 GTCACCGCTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCTCTCTCC 387
 Db
 QY 140 ValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaproCysSer 159
 Db
 QY 388 AAGACACACTCTGGGGGCACAGCGCCCTCGGCTGCTGCTGCTCAAGACTACTTCCCGGAA 447
 Db
 QY 160 ArgSerThrSerGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGlu 179
 Db
 QY 448 CCGGTGACGGTCTCTGGAACCTCAGCGCCCTGACAGCGGGGTGCACACTTCCCGCT 507
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 QY 180 ProValThrValSerTyrAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAla 199
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 QY 508 GTCCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGACCGTCCCTCCAGCAGC 567
 Db
 QY 200 ValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSer 219
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 QY 568 TTGGGACCCAGACTACACTGCAACGTGAATCAAGCCGAGCAACCAACAGGTGAC 627
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 QY 220 LeuGlyThrGlnThrTyrThrCysAsnValAsnHisLysProSerAsnThrLysValAsp 239
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 QY 628 AAGAAAGTG----- 636
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 QY 240 LysArgValGluLeuLysThrProLeuGlyAspThrThrHisThrCysProArgCysPro 259
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 QY 636 ----- 636
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 QY 260 GluProLysSerCysAspThrProProCysProArgCysProGluProLysSerCys 279
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 QY 637 -----GAGCCCAATCTGTGACAAACTCACACA 666
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 QY 280 AspThrProProCysProArgCysProGluProLysSerCysAspThrProProPro 299
 Db
 QY 667 TGCACACCGTCCAGCACCTCAACTCGCGGGGACCGTCACTGTCTCTTCCCGCCA 726
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 QY 300 CysProArgCysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPheProPro 319
 Db
 QY 727 AAACCCCAAGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGGGTGGTGTGAC 786
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 QY 320 LysProLysAspThrLeuMetIleSerArgThrProGluValThrCysValValValAsp 339
 Db
 QY 787 GTGAGCCAGAACCCCTCAGGTCAAGTTCAACTGTGACGGGTGGAGTGCAT 846
 Db
 QY 340 ValSerHisGluAspProGluValGlnPheLysTyrTyrValAspGlyValGluValHis 359
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 QY 847 AATGCCAAGACAAAGCCGGGAGGAGCAGTACAAACAGCACCTACCGTGTGTGACGCTC 906
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 QY 360 AsnAlaLysThrLysProArgGluGlnPheAsnSerThrPheArgValValSerVal 379
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QY 907 CTCACCGTCTCTGCACGAGCTGGCTGAATGGCAAGGAGTACAAAGTGCAGGCTCTCCAAC 966
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 QY 380 LeuThrValLeuHisGlnAspTyrLeuAsnGlyLysGluTyrLysCysLysValSerAsn 399
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 QY 967 AAAGCCCTCCCGCCCATCGAGAAACCACTCTCCAAAGCCAAAGCGGAGCCCGAGAA 1026
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 QY 400 LysAlaLeuProAlaProIleGluLysThrIleSerLysThrLysGlyGlnProArgGlu 419
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 QY 1027 CCACAGGTGTACACCTGCTCCCGCATCCCGGATGAGCTACCAAGAACAGGTCAGCTC 1086
 Db
 QY 420 ProGlnValTyrThrLeuProSerArgGluMetThrLysAsnGlnValSerLeu 439
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 QY 1087 ACCTGCTCTGCTCAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGG 1146
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 QY 440 ThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTyrGluSerSerGly 459
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 QY 1147 CAGCCCGGAGAACAACTACAGACCCAGCTCCCGTCTCGACTCCGACCGCTCTCTTCTTC 1206
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 QY 460 GlnProGluAsnAsnTyrAsnThrThrProProMetLeuAspSerAspGlySerPhePhe 479
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 QY 480 LeuTyrSerLysLeuThrValAspLysSerArgTyrGlnGlnGlyAsnIlePheSerCys 499
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 QY 1267 TCCGTGATGATGAGGCTCTGCACAACTACACAGCAGAGCGCTCTCCCTGTCTCCG 1326
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 Db
 QY 1327 GGTAAA 1332
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 QY 520 GlyLys 521
 Db
 RESULT 5
 Q8TC63 PRELIMINARY; PRT; 473 AA.
 ID Q8TC63
 AC Q8TC63; 01-JUN-2002 (TEMBLrel. 21, Created)
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025985; AAH25985.1; -.
 DR GO; GO:0005507; F:copper ion binding; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000923; BlueCu.1.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003008; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS00196; COPPER_BLUE; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
 Alignment Scores:
 Pred. No.: 2,24e-137 Length: 473
 Score: 1829.50 Matches: 351
 Percent Similarity: 84.51% Conservative: 31
 Best Local Similarity: 77.65% Mismatches: 55
 Query Match: 76.07% Indels: 15
 DB: 4 Gaps: 4

Db 103 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 122
Qy 520 TCAGGACTTACTCCCTCAGCAGCGTGGTGAACCGTGCCTCCAGCAGCTTGGGACACCCAG 579
Db 123 SerGlyLeuTySerLeuSerSerValValThrValProSerSerLeuGlyThrGln 142
Qy 580 ACCTACATCTGCAACGTTGATCAACAGCCAGCAGCAACCAACCAAGGTGGCAAGAAGTG--- 636
Db 143 ThrTyThrCysAsnValAsnHisCysProSerAsnThrLysValAspLysArgValGlu 162
Qy 636 ----- 636
Db 163 LeuLysThrProLeuGlyAspThrThrHisThrCysProArgCysProGluProLysSer 182
Qy 636 ----- 636
Db 183 CysAspThrProProProCysProArgCysProGluProLysSerCysAspThrProPro 202
Qy 637 -----GACCCCAATCTTGTGACAAATCTACACATCCACCATCCACCGCTGC 678
Db 203 ProCysProArgCysProGluProLysSerCysAspThrProProCysProArgCys 222
Qy 679 CCAGACCTGAACCTCGCGGGGGGCGCCGTCAGTCTTCTCTCTCCCTCCCAAAACCCCAAGAC 738
Db 223 ProAlaProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAsp 242
Qy 739 ACCCTCATGATCTCCGACCCCTGAGGTCAATCGGTGGTGGTGGACGTGAGCCACGAA 798
Db 243 ThrLeuMetIleSerArgThrProGluValThrCysValValAspValSerHisGlu 262
Qy 799 GACCTGAGGTCAAGTTCAACTGATGAGTGAACGGCGTGGAGGTGCATATATCCCAAGACA 859
Db 263 AspProGluValGlnPheLysTrpTyValAspGlyValGluValHisAsnAlaLysThr 282
Qy 859 AAGCCGCGGAGGAGCAGTCAACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 918
Db 283 LysProArgGluGluGlnPheAsnSerThrPheArgValValSerValLeuThrValLeu 302
Qy 919 CACCAGGACTGGCTGAATGGCAAGAGGTACAAAGTCAAGGTCTCCAAAGAGCCCTCCCA 978
Db 303 HisGlnAspTrpLeuAsnGlyLysGluTyLysCysLysValSerAsnLysAlaLeuPro 322
Qy 979 GCCCCCATCGAATAACCATCTCCAAAGCCAAAGGGAGCCCGAGCCAGACACAGGTGTAC 1038
Db 323 AlaProIleGluLysThrIleSerLysThrLysGlyGlnProArgGluProGlnValTy 342
Qy 1039 ACCCTGCCCATCCCGGATGAGTGAACCAAGACCAAGGTGCAGCTGACCTGCTGCTGC 1098
Db 343 ThrLeuProProSerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuVal 362
Qy 1099 AAAGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGCAGCCGAGAAC 1158
Db 363 LysGlyPheTyProSerAspIleAlaValGluTrpGluSerSerGlyGlnProGluAsn 382
Qy 1159 RACTCAAGACACCGCTCCCGTGGTGGACTCCGAGCGCTCTCTCTCTCTACAGCAAG 1218
Db 383 AsnTyAsnThrProProMetLeuAspSerAspGlySerPhePheLeuTySerLys 402
Qy 1219 CTCACCGTGGCAAGAGCAGGTGGCAGAGGGGAACTTCTCATGTCTCCGTGATGCAT 1278
Db 403 LeuThrValAspLysSerArgTrpGlnGlnGlyAsnIlePheSerCysSerValMetHis 422
Qy 1279 GAGGCTCTGCACACCACTACAGCAGAGACCTCTCCCTGCTCCG 1326
Db 423 GluAlaLeuHisAsnArgPheThrGlnLysSerLeuSerPro 438

RESULT 7
Q8R3V9 PRELIMINARY; PRT; 469 AA.
AC Q8R3V9
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Hypothetical protein.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024405; AAH24405.1; -.
DR PIR; B45837; B45837.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Igh-4.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_v.
DR Pfam; PF00047; Iq; 3.
DR SMART; SM00406; IqV; 1.
DR PROSITE; PS00835; Iq_LIKE; 4.
DR PROSITE; PS00290; Iq_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Alignment Scores:
Pred. No.: 2,41e-118 Length: 469
Score: 1591.00 Matches: 293
Percent Similarity: 78.82% Conservative: 68
Best Local Similarity: 63.97% Mismatches: 75
Query Match: 66.15% Indels: 22
DB: 5

US-09-674-716b-18 (1-1335) x Q8R3V9 (1-469)
Qy 1 GAGGTGACGTGTGGAGTCTGGGGAGCGTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 20 GluValAsnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
Qy 61 TCCTGTGACGTGACCGATTCACCTTCAGTGGCTACTGGATGTCCTGGTCCGCCAGGCT 120
Db 40 SerCysAlaAlaSerGlyPheThrAspTyTrpMetSerTrpValArgGlnPro 59
Qy 121 CCAGGGAAGGGCTCGAGTGGTGTGTAATAGATTGAAATCTGTAATATTCATCAACA 180
Db 60 ProGlyLysAlaLeuGluTrpLeuGlyPheIleArgAsnLysAlaAsnGlyTyThrThr 79
Qy 181 CATATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATCAAAATCTAGA 240
Db 80 GluTySerAlaSerValLysGlyArgPheThrIleSerArgAspAsnSerGlnSerIle 99
Qy 241 CTGTATCTGCAATGAACAGCCTGAAACCCGAGGACACAGCCGCTGTATTACTGT----- 294
Db 100 LeuTyIleGlnMetAsnAlaLeuArgAlaGluAspSerAlaThrTyTrpCysAlaArg 119
Qy 295 -----ACAGATTTCATAGACTGGGGCCAGGGAACA 324
Db 120 AspArgArgSerSerTyTrpTySerGlyThrSerPheAlaTyTrpGlyGlnGlyThr 139
Qy 325 CTAGTCACCGTCTCTCAGCTCCACAGGGCCCATCGTCTTCCCTCGGCACCTCC 384
Db 140 LeuValThrValSerAlaLysThrThrProSerValTyTrpProLeuAlaProGly 159
Qy 385 TCCAAAGACGACCTCTCGGGGCACAGCGCCCTGGGTGCTGCTCAAGGACTACTTCCCC 444
Db 160 SerAlaAlaGlnThrAsnSerMetValThrLeuGlyCysLeuValLysGlyTyTrpPhePro 179
Qy 445 GAACCGGTGACGGTGTGCTGGAACCTAGGCGCCCTGACAGCGCGCTGACACCTTCCCG 504
Db 180 GluProValThrValThrTrpAsnSerGlySerLeuSerSerGlyValHisThrPhePro 199
Qy 505 GCTGCTCTCAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGGCCGCTGCCCTCCAGC 564
Db 200 AlaValLeuGlnSerAsp---LeuTyThrLeuSerSerSerValThrValProSerSer 218


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QY 991 AAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTACACCCCTGCCCCCA 1050
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Db 241 LysThrIleSerLysThrLysGlyGlnProArgGluProGlnValThrLeuProPro 260
QY 1051 TCCCGGATGAGCTGACCAAGAACAGGTACAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 1110
Db
Db 261 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr 280
QY 1111 CCCAGCGATCGCGCTGAGTGGAGAGCAATGGCGAGCGGAGAGAACAACTACAAGACC 1170
Db
Db 281 ProSerAspIleAlaValGluTrpGluSerSerGlyGlnProGluAsnAsnTyrAsnThr 300
QY 1171 AGCCCTCCGCTGCTGAGATCCGACGGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230
Db
Db 301 ThrProProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAsp 320
QY 1231 AAGACAGGTGGCAGCAGGGAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1290
Db
Db 321 LysSerArgTrpGlnGlnGlyAsnIlePheSerCysSerValMetHisGluAlaLeuHis 340
QY 1291 AACCACTACGCGAAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
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Db 341 AsnArgPheThrGlnLysSerLeuSerLeuSerProGlyLys 354

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RESULT 9

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Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Gammat heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekrandodoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; RAD40243.1; -.
DR FIR; B45837.
DR PDB; 1COK; 11-SEP-99.
DR PDB; 1I91; 25-DEC-02.
DR PDB; 1KCU; 11-MAY-02.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EB7D697C CRC64;

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Alignment Scores:

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Pred. No.: 1.2e-111 Length: 437
Score: 1507.00 Matches: 281
Percent Similarity: 78.35% Conservative: 70
Best Local Similarity: 62.72% Mismatches: 81
Query Match: 62.66% Indels: 16
DB: 11 Gaps: 7

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US-09-674-716B-18 (1-1335) x Q9RIA4 (1-437)

QY 4 GTCACACTGGTGGAGTCTGGGGAGCGCTTGGTAAGACCCCGGGGGTCCCTTAGACTCTCC 63

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Db 1 ValGlnLeuGlnGluSerGlyGlyLeuValLysProGlyGlySerLeuLysLeuSer 20
QY 64 TGTGACAGCTAGCGGATTTCACTTTCACTGCTACTGATCTCTGGCTCCGCGAGGTCCA 123
Db
Db 21 CysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnThrPro 40
QY 124 GGGAGGGGCTGAGTGGGCTGCTGAAATAGATTGAAATCTGATAATTATGCAACACAT 183
Db
Db 41 GluLysArgLeuGluTrpValAlaSerPhe-----SerSerGlyGlyLeuIleTyr 57
QY 184 TATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGACTG 243
Db
Db 58 TyrThrAspSerValLysGlyArgPheThrIleTyrLysAspLysAspArgAsnIleLeu 77
QY 244 TATCTGCAATGAACAGCCTGAAACCGAGGACACAGCCGCTGATTACTGTACA-----297
Db
Db 78 SerLeuGlnMetSerSerLeuArgSerGluAspThrAlaMetTyrTyrCysAlaArgGly 97
QY 298 GATTTC---ATAGACTGGGCGAGGGAACACTAGTCACCGTCTCTCCAGCCTCCACCAAG 354
Db
Db 98 AspTyrSerAlaTyrTrpGlyProGlyThrLeuValThrValSerAlaAlaLysThrThr 117
QY 355 GGCCCATCGGTCTTCCCGCTGGCACCTCTCTCAAGAGCACCTCTCGGGGCACAGCGGCC 414
Db
Db 118 ProProSerValTyrProLeuAlaProGlySerAlaAlaGlnThrAsnSerMetValThr 137
QY 415 CTGGGTGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGGAATCAGGC 474
Db
Db 138 LeuGlyCysLeuValLysGlyTyrPheProGluProValThrValThrTrpAsnSerGly 157
QY 475 GCCTGACACAGCGCGCTGCACACCTTCCCGGTGTCTCTACAGTCTCTCAGACTCTCTACTCC 534
Db
Db 158 SerLeuSerSerGlyValHisThrPheProAlaValLeuGlnSerAsp---LeuTyrThr 176
QY 535 CTAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAAC 594
Db
Db 177 LeuSerSerSerValThrValProSerSerThrTrpProSerGluThrValThrCysAsn 196
QY 595 GTGAATCAACAAGCCAGCAACACAGGTGCAAGAAAGTGGAGCGGCCAAATCTTGTGAC 654
Db
Db 197 ValAlaHisProAlaSerSerThrLysValAspLysLysIleValProArgAspCysGly 216
QY 655 AAAACTCACACATGCCCAACCG-----TGCCAGCAGCTGAATCGCGGGGACCGTCA 708
Db
Db 217 -----CysLysProCysIleCysThrValProGluValSer-----Ser 229
QY 709 GTCTTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGAGCCCTCAGAGTC 768
Db
Db 230 ValPheIlePheProProLysProLysAspValLeuThrIleThrLeuThrProLysVal 249
QY 769 ACATGCGTGTGTGCTGACGCTGAGCCAGACACCTGAGGTCAAGTTCACTGCTAGCTG 828
Db
Db 250 ThrCysValValValAspIleSerLysAspAspProGluValGlnPheSerTrpPheVal 269
QY 829 GACGCGCTGGAGTGCATTAATGCAACAAAGCCCGGGAGGAGAGTACACAGCAGC 888
Db
Db 270 AspAspValGluValHisThrAlaGlnThrGlnProArgGluGluGlnPheAsnSerThr 289
QY 889 TACCGTGTGTGCTGACGCTCTCCAGCTCTCTGACCGAGGACTGGGTGAATGCAAGGAGTAC 948
Db
Db 290 PheArgSerValSerGluLeuProIleMetHisGlnAspTrpLeuAsnGlyLysGluPhe 309
QY 949 AAGTGCAGGTCTCCAACAAAGCCCTCCAGCCCGCCATCGAGAAACCATCTCCAAAGCC 1008
Db
Db 310 LysCysArgValAsnSerAlaAlaPheProAlaProIleGluLysThrIleSerLysThr 329
QY 1009 AAAGGCGAGCCCGAGAACACACAGGTGTACACCTCTGCCCCCATCCCGGGATGAGCTGACC 1068
Db
Db 330 LysGlyArgProLysAlaProGlnValTyrThrIleProProProLysGluGlnMetAla 349
QY 1069 AAGAACAGGTGTCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1128

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Q7TWK1
ID Q7TWK1 PRELIMINARY; PRT; 470 AA.
AC Q7TWK1.
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=CZECH II; TISSUE=Breast tumor;
RC MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
SEQUENCE FROM N.A.
RP STRAIN=CZECH II; TISSUE=Breast tumor;
RC Strausberg R.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055910; AAH55910.1; -.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;

Alignment Scores:
Pred. No.: 6,2e-106 Length: 470
Score: 1435.50 Matches: 272
Percent Similarity: 74.29% Conservative: 66
Best Local Similarity: 59.78% Mismatches: 102
Query Match: 59.69% Indels: 15
DB: 11 Gaps: 5

US-09-674-716b-18 (1-1335) x Q7TWK1 (1-470)

QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 20 GluValGlnLeuGlnSerGlyProGluLeuValValProGlyAlaSerVallylsile 39
QY 61 TCCTGTGACCTAGCGGATCACTTTCAGTCTGCTACTGCTGCTGGTCCGCCAGGCT 120
Db 40 SerCysLysAlaSerGlyThrPheThrGlyTyrThrMetHisTrpVallylsGlnSer 59
QY 121 CCAGGGAAGGGCTCGAGTGGGTGTGTAATAGATTGAAATCTGATAAATATGCAACA 180
Db 60 HisGlyLysSerLeuGluTrpIleGlyLeuVal-----AsnProSerAsnGlyAspThr 77
QY 181 CATTATGCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db 78 SerTyrAsnGlnLysPheLysGlyLysAlaThrLeuThrValAspLysSerSerThr 97
QY 241 CTGTATCTGCAATGAACGCTGAAACCGAGGACACAGCGCTGTATTACTGTACAGAT 300
Db 98 AlaTyrMetGluLeuAsnSerLeuThrSerGluAspSerAlaValTyrTyrCysalaarg 117

QY 301 -----TTCATAGACTGGGGCCAGGGAACACACTAGTCACC 333
Db 118 TyrTyrTyrSerGlySerTyrTrpTyrPheAspValTrpGlyAlaGlyThrThrValThr 137
QY 334 GTCTCTCAGCTCCACCAAGGCCCATCGTCTTCCCTCGCACCCTCTCCACAGAGC 393
Db 138 ValSerSerAlaThrThrAlaProSerValTyrProLeuValProGlyCysGlyAsp 157
QY 394 ACCTCTGGGGGCACAGCGCCCTGGCTCGCTGGTCAAGGACTACTTCCCGCAACCGGTG 453
Db 158 ThrSerGlySerSerValThrLeuGlyCysLeuValValysGlyTyrPheProGluProVal 177
QY 454 ACGGTGTCGTGAACTCAGGCGCCCTGACCAAGGGGGTGCACACTTCCCGGCTGCTTA 513
Db 178 ThrVallylsTrpAsnTyrGlyAlaLeuSerSerGlyValArgThrValSerSerValLeu 197
QY 514 CAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGCACCGTCCCTCCAGCAGCTGGGC 573
Db 198 Gln---SerGlyPheTyrSerLeuSerSerLeuValThrValProSerSerThrTrpPro 216
QY 574 ACCCAGACCTACATCTGCAACGTAATCAACGCCCAACCAACCAAGGFGGACAGAAA 633
Db 217 SerGlnThrValIleCysAsnValAlaHisProAlaSerLysThrGluLeuIleLysArg 236
QY 634 GTGAGGCCCAATCTGTGTGACAAACTCACACATGCCCA-----CGGTGCCAGCACCT 687
Db 237 IleGluProArg---IleProLysProSerThrProProGlySerSerCysProProGly 255
QY 688 GAATCTCGCGGGGCACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 747
Db 256 AsnIleLeuGlyGlyProSerValPheIlePheProLysProLysAspAlaLeuMet 275
QY 748 ATCTCCCGGACCCCTGAGGTGCATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 807
Db 276 IleSerLeuThrProLysValThrCysValValValValValValValValValVal 295
QY 808 GTCAAGTTCAACTGGTACGTGGACGGCGTGCAGTGCATATGCAAGCAACAAAGCCCGG 867
Db 296 ValHisValSerTrpPheValAspAsnLysGluValHisThrAlaTrpThrGlnProArg 315
QY 868 GAGGACGAGTACACACACGCTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 927
Db 316 GluAlaGlnTyrAsnSerThrPheArgValValSerAlaLeuProIleGlnHisGlnAsp 335
QY 928 TGGCTGATGCAAGGAGTACAGTCAAGTCTCCAACAAAGCCCTCCAGCCGCCCATC 987
Db 336 TrpMetArgGlyLysGluPheLysCysLysValAsnAsnLysAlaLeuProAlaProIle 355
QY 988 GAGAAAACCATCTCCAAAGCCAAAGGCGACGCCCGGAGAACACACAGTGTACACCTGCC 1047
Db 356 GluArgThrIleSerLysProLysGlyArgAlaGlnThrProGlnValTyrThrIlePro 375
QY 1048 CCATCCCGGATGAGTGCACCAAGACCGTGCAGCTGAGCTGCTGCTGCTGCTGCTGCTG 1107
Db 376 ProProArgGluGlnMetSerLysLysValSerLeuThrCysLeuValThrAsnPhe 395
QY 1108 TATCCAGCGACATCGCCGTGGAGTGGAGCAATGGGCGCGGAGAGAACAACTACAAG 1167
Db 396 PheSerGluAlaIleSerValGluTrpGluArgAsnGlyGluLeuGluGlnAspTyrLys 415
QY 1168 ACCACGCTCCCGTGTGAGCTCCGACGGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1227
Db 416 AsnThrProProIleLeuAspSerAspGlyThrTyrPheLeuTyrSerLysLeuThrVal 435
QY 1228 GACAAGACGAGGTGGCAGCGGGGAACGCTCTCTCATGCTCCGFGATGATGAGGCTCTG 1287
Db 436 AspThrAspSerTrpLeuGlnGlyGluIlePheThrCysSerValValHisGluAlaLeu 455
QY 1288 CACAACCACTACACGCAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
Db 456 HisAsnHisThrGlnLysAsnLeuSerArgSerProGlyLys 470

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RESULT 14
Q99L31      PRELIMINARY;      PRT;      468 AA.
ID   Q99L31
AC   Q99L31;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to RIKEN CDNA 1810060009 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR   EXBL: BC003878; AB03878.1; -.
DR   PDB: 2AP2; 24-NOV-99.
DR   InterPro: IPR007110; Ig-like.
DR   InterPro: IPR003006; Ig_MHC.
DR   InterPro: IPR003596; Ig_v.
DR   Pfam: PF00047; Ig_3.
DR   SMART: SM00406; IGV; 1.
DR   PROSITE: PS00835; IG_LIKE; 4.
DR   PROSITE: PS00290; IG_MHC; 1.
SQ   SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Alignment Scores:
Pred. No.:      4,2e-102      Length:      468
Score:          1387.50      Matches:      267
Percent Similarity: 72.63%      Conservative: 62
Best Local Similarity: 58.94%      Mismatches: 111
Query Match:      57.69%      Indels:      13
DB:              11          Gaps:         6

US-09-674-716B-18 (1-1335) x Q99L31 (1-468)
QY   1  GAGTGCACGTGCTGAGTCTGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGATC 60
DB   20  GluValGlnGlnGlnSerGlyAlaGluLeuValArgProGlyAlaSerValIysLeu 39
QY   61  TCCTGTGCAGCTAGCGGATTCACCTTTCAGTGGCTACTGGATGCTCTGGGTCGCCAGGCT 120
DB   40  SerCysThrAlaSerGlyPheAsnIleLysAspSerLeuMetHisTrpValIysGlnArg 59
QY   121  CAGGGAAGGGCTCAGTGGGTGCTGGAATAGATTGAATCTGATAATTATCAACA 180
DB   60  ProGluGlnGlyLeuGluTrpIleGlyTrpIle-----AspProGluAspGlyGluThr 77
QY   181  CATTATCGCGAGTCTGTGAAGGGGAATTCACATCTCAAGAGATGATTCAAAATCTAGA 240
DB   78  LysTyrAlaProLysPheGlnAspIysAlaThrIleThrAlaAspThrSerSerAsnThr 97
QY   241  CTGTATCTCAATGAATGAACAGCTGAAACCGAGGACACAGCGGTGATTAAGTACA--- 297
DB   98  AlaTyrLeuGlnLeuSerSerLeuThrSerGluAspThrAlaIleTyrTyrCysAlaArg 117
QY   298  -----GATTTCATAGAC---TGGGGCCAGGGAACACTAGTACCGCTTCC 339
DB   118  AsnLeuLeuTyrGlyGlyTyrTyrAspTyrTrpGlyGlnGlyThrIleThrValSer 137
QY   340  TCAGCTCCACCAAGGGCCATCGGTCTTCCCGCTGGCACCTCTCCCAAGAGCACTCT 399
DB   138  SerAlaLysThrThrAlaProSerValTyrProLeuAlaProValCysGlyAspThrThr 157
QY   400  GGGGGCACAGCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 459
DB   158  GlySerSerValThrLeuGlyCysLeuValIysGlyTyrPheProGluProValThrLeu 177
QY   460  TCGTGAATCTCAGGCGCCCTCAGCAGCGGCTGCACACTTCCCGGCTGTCTCAGAGTCC 519
DB   178  ThrTrpAsnSerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGlnSer 197

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QY   520  TCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTTCCAGCAGCTTGGCCACCCAG 579
DB   198  Asp---LeuTyrThrLeuSerSerSerValThrValThrSerSerThrTrpProSerGln 216
QY   580  ACCTACATCTGCAACGTAATCAAGCCAGCCAGCAACACCAAGGTGACAAAGTGGAG 639
DB   217  SerIleThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysIleGlu 236
QY   640  CCAGAACTTGTGCAAAACTCACACATGCCACCG-----TGCCAGCACCTGAATC 693
DB   237  ProArgGly--ProThrIleLysProCysProProCysLysCysProAlaProAsnLeu 255
QY   694  GCGGGGCACCGTCAGTCTTCTTCCCGCCCAAAACCCCAAGGACACCTCATGATCTCC 753
DB   256  LeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeuMetIleSer 275
QY   754  CGGACCCCTGAGTGCATCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 813
DB   276  LeuSerProMetValThrCysValValValValValValValValValValValVal 295
QY   814  TTCAACTGGTACGTGGACGCGGTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGAGG 873
DB   296  IleSerTrpPheValAsnAsnValGluValLeuThrAlaGlnThrGlnThrHisArgGlu 315
QY   874  CAGTACAAACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 933
DB   316  AspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMet 335
QY   934  AATGGCAAGGAGTCAAGTCAAGTCTCCAAAGCCCTCCAGCCCGCCCATCCGAGAAA 993
DB   336  SerGlyLysGluPheLysCysLysValAsnAsnLysAlaLeuProIleGluArg 355
QY   994  ACCATCTCAAAAGCAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCGCATCC 1053
DB   356  ThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeuProPro 375
QY   1054  CGGATGAGTGCACCAAGAACACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1113
DB   376  GluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetPro 395
QY   1114  AGCGACATCCCGTGGAGTGGGAGACAATGGCAGCCCGAGAACCACTACAGACCCAG 1173
DB   396  GluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThr 415
QY   1174  CTCCCGTGTGCACTCCGAGCGCTCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1233
DB   416  GluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLys 435
QY   1234  AGCAGTGGCAGCAGGGGACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1293
DB   436  LysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsn 455
QY   1294  CACTACCGCAGAGACCGCTCTCCCTGTCTCCGGGTAAA 1332
DB   456  HisHisThrThrLysSerPheSerArgThrProGlyLys 468

RESULT 15
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ID   Q8R3H6
AC   Q8R3H6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   AU04919.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

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Search completed: September 30, 2004, 08:54:03
Job time : 192.047 secs

QY 301 -----TTTCATAGACTGGGGCCAGGGAACACTAGTACCGTCTCC 339

Blank sheet

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:19:42 ; Search time 159.041 Seconds
(without alignments)
4743.430 Million cell updates/sec

Title: US-09-674-716B-19

Perfect score: 2405

Sequence: 1 gaggtgcagctgtggagtc.....ccctgtctccgggtaaatga 1335

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool.p/US09674716/runat.30092004.070257.25848/app_query.fasta.1.3164
-DB=A_Geneseq_29Jan04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -SPART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=oct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORV=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09674716@cgn.1.1.475@runat.30092004.070257.25848 -NCFU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------------|--------------------|
| 1 | 2367 | 98.4 | 444 | 3 AAY32263 | Aay32263 Humanised |
| 2 | 2199.5 | 91.5 | 461 | 2 AAR42162 | Aar42162 Anti-HIV- |
| 3 | 2191 | 91.1 | 447 | 6 AAE33524 | Aae33524 Human AQC |
| 4 | 2191 | 91.1 | 447 | 6 AAE33522 | Aae33522 Human AQC |
| 5 | 2188.5 | 91.0 | 449 | 6 ABP58273 | Abp58273 Humanised |
| 6 | 2188.5 | 91.0 | 468 | 6 ABP58275 | Abp58275 Humanised |
| 7 | 2187 | 90.9 | 444 | 6 AAE33537 | Aae33537 Humanised |
| 8 | 2187 | 90.9 | 444 | 6 AAE334876 | Aae34876 BIWA4/8 a |
| 9 | 2185 | 90.9 | 447 | 6 AAE33523 | Aae33523 Human AQC |
| 10 | 2183 | 90.8 | 442 | 6 ABR39465 | AbR39465 Humanised |

| | | | | | |
|----|--------|------|-----|-------------|---------------------|
| 11 | 2183 | 90.8 | 442 | 6 ABU08311 | Abu08311 Humanised |
| 12 | 2183 | 90.8 | 442 | 6 ABB80109 | Abb80109 Heavy cha |
| 13 | 2183 | 90.8 | 445 | 6 AAO31101 | Aao31101 Human A2- |
| 14 | 2183 | 90.8 | 461 | 4 AAU07745 | Aau07745 Humanised |
| 15 | 2183 | 90.8 | 461 | 6 ABR39844 | AbR39844 Hu266 N56 |
| 16 | 2183 | 90.8 | 461 | 6 ABR39847 | AbR39847 Hu266 N56 |
| 17 | 2183 | 90.8 | 461 | 6 ABR39843 | AbR39843 Hu266 N56 |
| 18 | 2183 | 90.8 | 461 | 6 ABR39848 | AbR39848 Hu266 N56 |
| 19 | 2183 | 90.8 | 442 | 6 ABR39474 | AbR39474 Humanised |
| 20 | 2178 | 90.6 | 442 | 6 ABU08320 | Abu08320 Humanised |
| 21 | 2178 | 90.6 | 442 | 6 ABR39793 | AbR39793 Humanised |
| 22 | 2178 | 90.6 | 442 | 6 ABB80113 | Abb80113 Deglycosy |
| 23 | 2173.5 | 90.4 | 449 | 3 AAY68810 | Aay68810 A rat hea |
| 24 | 2172.5 | 90.3 | 451 | 4 AAE12715 | Aae12715 Human rec |
| 25 | 2172.5 | 90.3 | 451 | 4 ABUS8807 | Abus8807 Mucin 1 (|
| 26 | 2172.5 | 90.3 | 474 | 5 AAO14065 | Aao14065 Heavy cha |
| 27 | 2172.5 | 90.3 | 474 | 5 AAO18400 | Aao18400 Mature hu |
| 28 | 2170 | 90.2 | 474 | 5 AABU08017 | Aabu08017 Human mon |
| 29 | 2166.5 | 90.1 | 582 | 4 AAB81987 | Aab81987 Ganglios |
| 30 | 2161.5 | 89.9 | 478 | 2 AAW63763 | Aaw63763 Macaque p |
| 31 | 2161.5 | 89.9 | 478 | 5 AAU11644 | Aau11644 Protein s |
| 32 | 2161 | 89.9 | 477 | 4 AAU14288 | Aau14288 Human nov |
| 33 | 2160 | 89.8 | 475 | 2 AAR20057 | Aar20057 Heavy cha |
| 34 | 2155.5 | 89.6 | 478 | 2 AAW01820 | Aaw01820 Primatise |
| 35 | 2151.5 | 89.5 | 453 | 3 AAR33311 | Aar33311 Humanised |
| 36 | 2151.5 | 89.5 | 453 | 3 AAY85199 | Aay85199 Heavy cha |
| 37 | 2151.5 | 89.5 | 464 | 5 ABG78151 | Abg78151 Human Fv |
| 38 | 2151.5 | 89.5 | 464 | 5 ABR91842 | AbR91842 Human ant |
| 39 | 2150.5 | 89.4 | 451 | 2 AAW95663 | Aaw95663 Mus muscu |
| 40 | 2150.5 | 89.4 | 451 | 2 AAY50031 | Aay50031 Human E27 |
| 41 | 2150.5 | 89.4 | 451 | 3 AAB07473 | Aab07473 Amino aci |
| 42 | 2150.5 | 89.4 | 451 | 4 AAB76952 | Abb76952 Full leng |
| 43 | 2150.5 | 89.4 | 451 | 4 AAB74212 | Abb74212 E27 anti- |
| 44 | 2150.5 | 89.4 | 451 | 6 ABU62798 | Abu62798 E27 anti- |
| 45 | 2150.5 | 89.4 | 478 | 6 AAE37362 | Aae37362 Monkey 7B |

ALIGNMENTS

RESULT 1

AAY32263

ID AAY32263 standard; protein; 444 AA.

XX

AC AAY32263;

DT 15-FEB-2000 (first entry)

XX

DE Humanised anti-CD23 Mab C11 heavy chain.

XX

KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;

KW monoclonal antibody; chimeric antibody; humanised antibody;

KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

KW urticaria; nephrotic syndrome; glomerulonephritis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinis;

KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

KW therapy.

XX

OS Homo sapiens.

OS Synthetic.

XX

Key

Region

Location/Qualifiers

1..30

/note= "framework region 1"

31..35

/note= "CDR 1"

36..49

/note= "framework region 2"

50..68

/note= "CDR 2"

69..100

FT Region /note= "framework region 3"
 FT 101..103
 FT /note= "CDR 3"
 FT Region 104..111
 FT /note= "framework region 4"
 FT Region 112..444
 FT /note= "constant region"

XX WC9958679-A1.

XX 18-NOV-1999.

PD 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX) GLAXO GROUP LTD.

XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

XX N-PSDB; AA234748.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 diabetes, multiple sclerosis and psoriasis.

XX Claim 9; Fig 4; 81pp; English.

XX This amino acid sequence represents the heavy chain of humanised anti-
 CD23 (FCER2) monoclonal antibody C11, composed of a human framework
 (HS10K171) and the heavy chain complementarity determining regions (see
 AAY32257-59) of murine antibody C11. The DNA was constructed by splice
 overlap PCR. The invention provides altered antibodies, such as chimeric
 or humanised antibodies, which comprise sufficient of the amino acid
 sequences of the C11 light and heavy chain complementarity determining
 regions to render them capable of binding to the CD23 type II molecule
 expressed on haematopoietic cells. The antibodies are used to block
 soluble CD23 formation in human therapy, for the treatment of arthritis,
 lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,
 glomerulonephritis, inflammatory bowel disease, ulcerative colitis,
 Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 malignancies (claimed). They are also useful for studying interactions
 between CD23 and various ligands and determining the binding agents

XX Sequence 444 AA;

XX Alignment Scores:

Pred. No.: 3,43e-141 Length: 444
 Score: 2367.00 Matches: 444
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.42% Indels: 0
 DB: 3 Gaps: 0

US-09-674-716B-18 (1-1335) x AAY32263 (1-444)

QY 1 GAGGTGACGCTGGTGGGAGCTGGTAAAGCCGGGGGTCTCTAGACTC 60

DB 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlyGlySerLeuArgLeu 20

QY 61 TCCTGTGACGTAGCGGATTCATCTTTCAGTGCGTACTGGATGCTCGGTCGGCAGGCT 120

DB 21 SerCysAlaAlaSerGlyPheThrPheSerGlyTyrTrpMetSerTrpValArgGlnAla 40

QY 121 CCAGGGAAGGGGCTCGAGTGGGTTCCTGAAATTAGATTGAATCTGATAATTATGCAACA 180

DB 41 ProGlyLysGlyLeuGluTrpValAlaGluLeuLeuArgLeuLysSerAspAsnTyrAlaThr 60

QY 181 CATTATGCGGAGTCTGTGAGGGGAAATTCACCACTCAAGAGATGATTCAAAATCTAGA 240

DB 61 HistyrAlaGluSerValLysGlyLysPheThrIleSerArgAspSerLysSerArg 80

QY 241 CTGTATCTGCAAAATGAACAGCCTCAAAAACCCAGAGACACAGCCCGTATTACTGTACAGAT 300

DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrAsp 100

QY 301 TTATAGACTGGGGCCAGGAAACACATAGTACACCGTCTCTCTACGCTCCACCAAGGGCCCA 360

DB 101 PheIleAspTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro 120

QY 361 TCGGTCTTCCCTGGCAGCCCTCTCCAGAGCACCTCTGGGGGACAGCGGCGCTGGGC 420

DB 121 SerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGly 140

QY 421 TGCTGTGTCAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGCGCCCTG 480

DB 141 CysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu 160

QY 481 ACCAGCGGCTGCACACCTTCCCGGCTGCTCTACAGTCTCTCAGGACTCTACTCCCTCAG 540

DB 161 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSer 180

QY 541 AGCGTGTGACCGTGCCTCTCAGCAGCTTGGGACCCAGACCTTACATCTGCAACGTGAAT 600

DB 181 SerValValThrValProSerSerLeuGlyThrGlnThrTyrIleCysAsnValAsn 200

QY 601 CACAAGCCGACCAACCAAGGTGGGACAAAGTGGAGCCCAATCTTGTGACAAACT 560

DB 201 HisLysProSerAsnThrLysValAspLysLysValGluProLysSerCysAspLysThr 220

QY 661 CACACATGCCACCGTGGCCAGCACCTGAACTCGCGGGGACCCGCTCAGTCTTCTCTCTC 720

DB 221 HisThrCysProCysProAlaProGluLeuAlaGlyAlaProSerValPheLeuPhe 240

QY 721 CCCCCAAACCCAAAGACACCCCTCATGATCTCCCGAACCCCTGAGTGCATCGGTGGTG 780

DB 241 ProProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCysValVal 260

QY 781 GTGAGTGTGAGCCACCAAGACCCCTGAGTCAAGTTCAGTGTGAGTGGACGCGCTGGAG 840

DB 261 ValAspValSerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGlu 280

QY 841 GTCATATAATGCCAAGACAAAGCCGGGAGGAGCAGTACACAGCAGCAGTACCGTGTGGTC 900

DB 281 ValHisAsnAlaLysThrLysProArgGluGlnTyrAsnSerThrTyrArgValVal 300

QY 901 AGCGTCTCTCAGCTGCTGTCAGCAGGACTGGCTCATGTCAGTGGCAGGAGTACAGTGCAGGTC 960

DB 301 SerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGlnTyrLysCysVal 320

QY 961 TCCAAACAAAGCCCTCCAGCCCGCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGGCC 1020

DB 321 SerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnPro 340

QY 1021 CGAGAACCAAGGTGTACACCCCTGCCCCCATCCCGGATGAGTCAACCAAGAACAGGTC 1080

DB 341 ArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnVal 360

QY 1081 AGCTGACCTGCTGTGTCAAAGCTTCTATCCAGCGCATCCCGTGGAGTGGGAGAGC 1140

DB 361 SerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSer 380

QY 1141 AATGGCAGCCGGAGAACAACTACAGACCAACGCTCCGCTCGCTGGACTCCGACCGCTCC 1200

DB 381 AsnGlyGlnProGluAsnAsnTyrLysThrThrProValLeuAspSerAspGlySer 400

QY 1201 TTCTTCTCTCAGCAAGCTCAACCGTGGACAGAGCAGGTGGCAGCAGGGGAACCTCTTC 1260

DB 401 PhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPhe 420

QY 1261 TCATGCTCGTGTGATGATGAGGCTCTGCACAAACCTACACGACGAGAGGCTCTCCCTG 1320

Db 421 SerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu 440
 QY 1321 TCTCCGGTAAA 1332
 Db 441 SerProGlyLys 444

RESULT 2
 AAR42162
 ID AAR42162 standard; protein; 461 AA.
 XX
 AC AAR42162;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-APR-1994 (first entry)
 XX
 DE Anti-HIV-1 recombinant antibody 447-52D heavy chain.
 XX
 KW Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
 KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
 KW acquired immune deficiency syndrome; chimeric antibody;
 KW surface glycoprotein gp120; V3 loop.
 XX
 OS Homo sapiens.
 XX
 FN WO9319785-A1.
 XX
 PD 14-OCT-1993.
 XX
 DF 23-MAR-1993; 93WO-US002629.
 XX
 PR 01-APR-1992; 92US-00861701.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Emimi EA, Conley AJ, Mark GE, Johnson LS, Pfarr DS;
 XX
 DR WPI; 1993-336600/42.
 DR N-PSDB; AAQ49834.
 XX
 PT New recombinant human antibody - with HIV neutralising activity against
 PT at least two isolates, useful for preventing or treating infection in
 PT diagnosis, etc.
 XX
 PS Example 9; Fig 2A; 154pp; English.
 XX
 CC EBV-transformed cell lines and mouse-human heterohybridomas producing
 CC human MAbs specific for the gp120 V3 loop of HIV-1 MN isolate were
 CC obtained. Mab 447-52D was found to recognise the tetrapeptide motif GPGR,
 CC i.e. the Principal Neutralising Determinant common to the V3 loop of
 CC different HIV isolates. A recombinant Ab was produced in which the H
 CC chain V region was derived from 447-52D and to which a signal sequence
 CC and a H chain intronic sequence are appended, fused to a fragment contg.
 CC a short intronic segment of the human gamma 1 C region and the human
 CC gamma 1 encoding domain in its genomic form. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 461 AA;

Alignment Scores:
 Pred. No.: 1,266-130 Length: 461
 Score: 2199.50 Matches: 416
 Percent Similarity: 92.62% Conservative: 11
 Best Local Similarity: 90.24% Mismatches: 17
 Query Match: 91.46% Indels: 17
 DB: 2 Gaps: 2

US-09-674-716B-18 (1-1335) x AAR42162 (1-461)

QY 1 GAGGTGCACCTGGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTC 60
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
 QY 61 TCCTGTGCAGTACGGGATTCATTCTAGTGGCTACTGGATGCTCTGGGTCCGCCAGGCT 120

Db 21 ThrCysValAlaSerGlyPheThrPheSerAspValTrpLeuAsnTrpValArgGlnAla 40
 QY 121 CCAGGGAAGGGCTCGAGTGGTCTCTGAAATAGATTGAATCTGATAATTATCAACA 180
 Db 41 ProGlyLysGlyLeuGluTrpValGlyArgLeuLysSerArgThrPheGlyThrThr 60
 QY 181 CATTATGGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATCAAAATCTAGA 240
 Db 61 AspTyrAlaAlaSerValLysGlyArgPheThrIleSerArgAspSerLysAsnThr 80
 QY 241 CTGTATCTGCAAAATGAACAGCCTGAAACCCAGGACACAGCCGCTGATTACTGTACAGAT 300
 Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrSerCysThrThr 100
 QY 301 -----TTCATAGAC--- 309
 Db 101 AspGlyPheIleMetIleArgGlyValSerGluAspTyrTyrTyrMetAspVal 120
 QY 310 TGGGGCCAGGGAACACTAGTCAACGCTTCCTCAGCTCTCACCAAGGGCCCATCGGTCTTC 369
 Db 121 TrpGlyLysGlyThrThrValThrValSerAlaSerThrLysGlyProSerValPhe 140
 QY 370 CCCCTGGCACCTCTCTCCAAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGGCTGCTC 429
 Db 141 ProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuVal 160
 QY 430 AAGGACTACTTCCCGAACCCGGTGCAGGTCGTCGGAACCTCAGGCGCCCTGACCGCGGC 489
 Db 161 LysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGly 180
 QY 490 GTGCACACCTTCCCGCTGCTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGG 549
 Db 181 ValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSerValVal 200
 QY 550 ACCGTGCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAGCCC 609
 Db 201 ThrValProSerSerSerLeuGlyThrGlnThrTyrIleCysAsnValAsnHisLysPro 220
 QY 610 AGCAACACAGGTGACAGAAAGTGGAGCCCAATCTTGACAAAACACTCACATGC 669
 Db 221 SerAsnThrLysValAspLysValGluProLysSerCysAspLysThrHisThrCys 240
 QY 670 CCACCTGGCCAGCACCTGAACTCGCGGGGACCCCTCAGTCTTCTCTTCCCCCAAAA 729
 Db 241 ProProCysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPheProLys 260
 QY 730 CCCAAGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGGACGTG 789
 Db 261 ProLysAspThrLeuMetIleSerArgThrProGluValThrCysValValValAspVal 280
 QY 790 AGCCACGACACCTCAGGTCAAGTTCAACTGCTAGTGGAGCGCGCTGGAGGTGCATAAT 849
 Db 281 SerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGluValHisAsn 300
 QY 850 GCCAAGACAAAGCCCGGGAGGACAGTACAAACAGCACCTGCTGGTGGTCAAGTCTCCTC 909
 Db 301 AlaLysThrLysProArgGluGlnTyrAsnSerThrTyrArgValValSerValLeu 320
 QY 910 ACCGTCTGCACAGGACTGGCTGAATGCAAGAGTACAGTCAAGTCTCCACACAAA 969
 Db 321 ThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLys 340
 QY 970 GCCTCCCGACCCCATCGGAAAAACCATCTCCAAAGCCAAAGCGGACGCCCGGAGAACCA 1029
 Db 341 AlaLeuProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnProArgGluPro 360
 QY 1030 CAGGTGTACACCTGCCCCCATCCCGGATGACTGACCAAGAACCAAGTCAAGTCAAGTCAAC 1089
 Db 361 GlnValTyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnValSerLeuThr 380
 QY 1090 TGCCGTGCTCAAAGCTTCTATCCAGCGACATCCCGTGGAGTGGGAGAGCAATGGGCAG 1149

Db 381 CysLeuVallysGlyPheTyProSerAspIleAlaValGluTrpGluSerAsnGlyGln 400
 QY 1150 CCGAGAACAACTACAGACCCGCTCCGCTGGACTCCGAGCGGCTCCTTCTTCCTC 1209
 Db |||||
 Db 401 ProGluAsnAsnTyrlsYthrThrProProValLeuAspSerAspGlySerPhePheLeu 420
 QY 1210 TACAGCAAGTCCACCGTGGCAAGACAGTGGCAGCGGGAAGCTTCTTCATGCTCC 1269
 Db 421 TySerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSer 440
 QY 1270 GTGATCATGAGCTCTGCACACCACTACAGCAGAGAGCTCTCCCTGTCTCCGGGT 1329
 Db 441 ValMetHisGluAlaLeuHisAsnHisTyThrGlnLysSerLeuSerLeuSerProGly 460
 QY 1330 AAA 1332
 Db |||||
 Db 461 Lys 461
 RESULT 3
 AAE33524
 ID AAE33524 standard; protein; 447 AA.
 XX
 AC AAE33524;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human AOC2 heavy chain mutant protein, hsAQC2.

XX Human; very late activation antigen; VLA-1; beta1 containing integrin;
 KW immunological disorder; inflammatory disorder; skin related condition;
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
 KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;
 KW irritable bowel syndrome; colitis; colorectal cancer; perianteritis nodosa;
 KW atherosclerosis; thyroiditis; aplastic anaemia; rheumatoid arthritis;
 KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
 KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
 KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
 KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
 KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
 KW graft versus host disease; myocardial ischaemia; mutant; mutein.
 XX
 OS Homo sapiens.
 XX
 WO200283854-A2.
 XX
 PD 24-OCT-2002.

PF 12-APR-2002; 2002WO-US011521.
 XX
 PR 13-APR-2001; 2001US-0283794P.
 PR 06-JUL-2001; 2001US-0303689P.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Lyne PD, Garber EA, Saldanha JW, Karpusas M;
 XX
 DR WPI; 2003-093009/08.

PT New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
 PT burns, dermatitis, and abnormal proliferation of hair follicle cells or
 PT fibrosis.

XX Example 23; Page 92; 248pp; English.
 PS
 CC The present invention relates to novel antibodies that specifically bind
 CC to very late activation (VLA-1; beta1 containing integrins) antigens and
 CC methods of using these antibodies to treat immunological disorders. The
 CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 CC mediated immunological or inflammatory disorders such as skin related
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung

CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),
 CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
 CC perianteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 CC immediate hypersensitivity), graft and transplant rejections, graft
 CC versus host disease, conjunctivitis, swelling occurring after injury,
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 CC human AOC2 heavy chain mutant protein, hsAQC2
 XX
 SQ Sequence 447 AA;

Alignment Scores:
 Pred. No.: 4.33e-130 Length: 447
 Score: 2191.00 Matches: 418
 Percent Similarity: 94.44% Conservative: 7
 Best Local Similarity: 92.89% Mismatches: 15
 Query Match: 91.10% Indels: 10
 DB: 6 Gaps: 2

US-09-674-716b-18 (1-1335) x AAE33524 (1-447)
 QY 1 GAGTGTCAGTGTGGAGTCTGGGGAGGCTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuValGln 20
 QY 61 TCTGTGACGACGAGGATGCTTTCAGTGGCTACTGATGCTCTGGTGGCGCAGGCT 120
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyThrMetSerTrpValArgGlnAla 40
 QY 121 CCAGGGAAGGGGCTCGAGTGGGTTGCTGAAATAGATTGAAATCTGATAATATGCAACA 180
 Db 41 ProGlyValGlyLeuGlnTrpValAlaThrIle-----SerGlyGlyGlyHisThr 57
 QY 181 CATTATGCGGAGTCTGTGAAGGGAATTCACATCTCAAGAGATGATTCAAAATCTAGA 240
 Db 58 TyrTyLeuAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 77
 QY 241 CTGTATCTGCAATGAACAGCCTGAAACCGAGGACACAGCCGTGTATTACTGTACAGAT 300
 Db 78 LeuTyLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyTyCysThrArg 97
 QY 301 -----TTCATAGACTGGGCGCAGGGAACACTAGTACCGTCTCC 339
 Db 98 GlyPheGlyAspGlyGlyTyPheAspValTrpGlyGlnGlyThrLeuValThrValSer 117
 QY 340 TCAGCCTCCACCAAGCGCCATCGGCTTCCCGCTGGGACCCCTCTCCAGAGACCTCT 399
 Db 118 SerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSer 137
 QY 400 GGGGGCACAGCGCCCTGGGCTCGCTTGTCAAGGACTACTTCCCGGAACCGGTGACGGTG 459
 Db 138 GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyPheProGluProValThrVal 157
 QY 460 TCGTGAACCTCAGGCGCCCTGACACAGCGGTGACACCTTCCCGCTGTCTCAGTCC 519
 Db 158 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 177
 QY 520 TCAGGACTCTACTCCCTCAGCAGCGGTGGTGCACCGTCCCTCCAGCAGCTTGGGACCCAG 579
 Db 178 SerGlyLeuTySerLeuSerSerValValThrValProSerSerSerLeuGlyThrGln 197
 QY 580 ACTTACATCTGCAAGTGTGAATCACAAGCCAGCAACACAGGTGGACAGAAAGTGAG 639
 Db 198 ThrTyIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGlu 217
 QY 640 CCAATATCTGTGACAAACTCACAATGCCACCGTCCCGAGCAGCTGAACTCCGCGGG 699

| | | |
|----------|---|------|
| 218 | ProLysSerCysAspLysThrHisThrCysProCysProAlaProGluAlaIaGly | 237 |
| 700 | GCACCGTCAGTCTCTCTTCCCGCCAAAACCAAGGACACCCCTCATGATCTCCCGGACC | 759 |
| 238 | GlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThr | 257 |
| 760 | CCTGAGTGCATCGCTGGTGGAGCTGAGCCACGAGACCCCTGAGTCAAGTTCAC | 819 |
| 258 | ProGluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsn | 277 |
| 820 | TGTCAGCTGCAGCGCGCTGGAGGTGCATAATGCCAACAAAGCGCGGAGGACGAGTAC | 879 |
| 278 | TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyr | 297 |
| 880 | AACAGCACGATCACGCTGGTGGTGCAGCTCTCCACCGTCTCGCACGAGCTGCTGAATGCC | 939 |
| 298 | AsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly | 317 |
| 940 | AAGGAGTACAAGTGCAGAGGTCTCCAAACAAAGCCCTCCACGCCCCATCGAGAAAAACCATC | 999 |
| 318 | LysGluTyrLysCysLysValSerAsnLysAlaLeuProIleGluLysThrIle | 337 |
| 1000 | TCCAAAGCCAAAGGCGAGCCCGAGAACCCACAGGTGTACACCTGCCCCCATCCCGGAT | 1059 |
| 338 | SerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAsp | 357 |
| 1060 | GAGCTGACCAAGAACACAGGTGACGCTGACCTGCTCAAAGCGCTTCTATCCAGCGAC | 1119 |
| 358 | GluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAsp | 377 |
| 1120 | ATCCCGCTGGAGTGGGAGACCAATGGGACCGGAGAACAACTACAAGACCAAGCTCCC | 1179 |
| 378 | IleAlaValGluTrpGluSerAsnGlyGlnProGluAsnTyrLysThrThrProPro | 397 |
| 1180 | GTGCTGAGTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAGG | 1239 |
| 398 | ValLeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArg | 417 |
| 1240 | TGGCAGCAGGGGAAACGCTTCTCTCATGCTCCGTCATGCATGAGGCTCTGCACAAACCATC | 1299 |
| 418 | TrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyr | 437 |
| 1300 | ACGCAAGAGCGCTCTCCCTGTCTCCGGT | 1329 |
| 438 | ThrGlnLysSerLeuSerLeuSerProGly | 447 |
| RESULT 4 | | |
| AAE33522 | | |
| ID | AAE33522 standard; protein; 447 AA. | |
| XX | AAE33522; | |
| XX | | |
| DT | 02-APR-2003 (first entry) | |
| XX | | |
| DE | Human AQC2 heavy chain protein. | |
| XX | | |
| KW | Human; very late activation antigen; VIA-1; betal containing integrin; | |
| KW | immunological disorder; inflammatory disorder; skin related condition; | |
| KW | psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; | |
| KW | fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; | |
| KW | fever; migraine headache; inflammatory bowel disease; Crohn's disease; | |
| KW | irritable bowel syndrome; colitis; colorectal cancer; periarthritis nodosa; | |
| KW | atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa; | |
| KW | gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; | |
| KW | osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis; | |
| KW | systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; | |
| KW | renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis; | |
| KW | hypersensitivity; graft rejection; transplant rejection; conjunctivitis; | |
| KW | graft versus host disease; myocardial ischaemia. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | WO200283854-A2. | |

Db 78 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysThrArg 97
 QY 301 -----TTCATAGACTGGGGCAGGAACTAGTACCGCTCTCC 339
 Db 98 GlyPheGlyAspGlyTyrPheAspValTrpGlyGlnGlyThrLeuValThrValSer 117
 QY 340 TCAGCTCCACCAAGGCGCATCGGTCTCCCTGGCACCTCTCTCCAGAGACCTCT 399
 Db 118 SerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSer 137
 QY 400 GGGGGCACAGCGCGCTGGCTGCTGGTCAAGGACTCTCCCGACCGGTGACGGTG 459
 Db 138 GlyGlyThrAlaAlaLeuGlyCysLeuValHisAspTyrPheProGluProValThrVal 157
 QY 460 TCGTGAACCTCAGGCGCTGACAGCGCGGTGCACACCTCTCCGGCTGTCTACAGTCC 519
 Db 158 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 177
 QY 520 TCAGGACTCTACTCCCTCAGCAGCGGTGGTGGTGGCTCCCTCCAGCAGCTTGGGACCCAG 579
 Db 178 SerGlyLeuTyrSerLeuSerValValThrValProSerSerSerLeuGlyThrGln 197
 QY 580 ACTTACATCTGCAACGTGAATCACAGCCCGACCAACCAAGCTGGACAAAGAGTGGAG 639
 Db 198 ThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGlu 217
 QY 640 CCCAACTCTGTGACAAACTCACACATGCGCCACCGTGGCCAGCACCTGAACTCGCGGG 699
 Db 218 ProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGly 237
 QY 700 GCACCGTCACT 759
 Db 238 GlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThr 257
 QY 760 CTGAGGTCAATGCGT 819
 Db 258 ProGluValThrCysValValValValValValValValValValValValValValVal 277
 QY 820 TGGTACGTGAGCGGTGAGTGCATATGCAAGACCAAGACCAAGACCAAGACCAAGACCA 879
 Db 278 TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyr 297
 QY 880 AACAGCAGCTACCGT 939
 Db 298 AsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly 317
 QY 940 AAGGAGTACAGTGCAGGTCTCCACAAAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCC 999
 Db 318 LysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIle 337
 QY 1000 TCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTGCCCGCCATCCCGGAT 1059
 Db 338 SerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAsp 357
 QY 1060 GAGCTGACCAAGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1119
 Db 358 GluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAsp 377
 QY 1120 ATCCGCTGGAGTGGAGAGCAATGGGAGCGGAGAGCAACTACAGACCAAGCCCTCC 1179
 Db 378 IleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProPro 397
 QY 1180 GTGCTGAGCTCCGAGCGCT 1239
 Db 398 ValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArg 417
 QY 1240 TGGCAGCAGGGAAGCT 1299
 Db 418 TrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyr 437
 QY 1300 AGCAGAAAGAGCT 1329
 Db 438 ThrGlnLysSerLeuSerLeuSerProGly 447

RESULT 5
 ID ABP58273 standard; protein; 449 AA.
 AC ABP58273;
 DT 23-OCT-2003 (revised)
 DT 31-MAR-2003 (first entry)
 XX Humanised 3D6 antibody heavy chain.
 XX Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;
 KW human; humanised antibody; antibody; Alzheimer's disease;
 KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 FH Key Location/Qualifiers
 FT Region 1..119
 FT /note= "heavy chain variable region"
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 50..66
 FT /note= "CDR2"
 FT Region 99..108
 FT /note= "CDR3"
 XX WO200288306-A2.
 DD 07-NOV-2002.
 XX 26-APR-2002; 2002WO-US011853.
 XX 30-APR-2001; 2001US-0287539P.
 XX (ELIL) LILLY & CO ELI.
 XX Tsurushita N, Vasquez M;
 XX WPI; 2003-183835/18.
 XX New humanized forms of mouse 3D6 antibodies, useful for treating Down's
 syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral
 amyloid angiopathy, or for inhibiting formation of or reducing Abeta
 plaque in the brain.
 PS Claim 5; Page 10-11; 54pp; English.
 CC The present sequence is that of a preferred heavy chain of a humanised
 antibody of the present invention. In the variable region of this
 sequence, the complementarity determining regions (CDRs) originate from
 murine monoclonal antibody 3D6 and the framework region originates from
 human germline VH segment DP-45 and J segment JH4. Novel humanised
 antibodies of the invention have CDRs from 3D6 and human framework
 sequences. These humanised antibodies have binding affinities (affinity
 and epitope location) approximately the same as those of the mouse 3D6
 antibody. The invention includes antibodies, single chain antibodies, and
 their fragments, as well as nucleotide sequences, vectors, transformed
 host cells, and methods of using the humanised antibody to treat,
 prevent, alleviate, reverse or otherwise ameliorate symptoms and/or
 pathology associated with Down's syndrome, (pre-)clinical Alzheimer's
 disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit
 formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to
 standardise OS field)
 XX Sequence 449 AA;
 SQ
 Alignment Scores: 6.23e-130 Length: 449
 Pred. No.: 2188.50 Matches: 415
 Score:

Percent Similarity: 94.48% Conservative: 13
 Best Local Similarity: 91.61% Mismatches: 12
 Query Match: 91.00% Indels: 13
 DB: 6 Gaps: 3

US-09-674-716b-18 (1-1335) x ABP58273 (1-449)

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QY 1 GAGGTGAGCTGCTGGAGTCTGGGGAGGCTGTGTAAGCCCGGGGGTCCCTAGACTC 60
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCCTGTGAGCTAGCGGATTACATTTTCAGTGGCTACTGCATGTCTCTGGTCCGCGAGGCT 120
DB 21 SerCysAlaGlySerGlyPheThrPheSerAsnTyrGlyMetSerTrpValArgGlnAla 40
QY 121 CGAGGAAGGGCTCGAGTGGTCTGCAAAATGAAATGAAATCTGATATATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValAlaSerIleArg-----SerGlyGlyArgThr 58
QY 181 CATTATGGGAGTCTGTCAAGGGGAATTCAACATCTCAAGAGATGATTCAAATCTAGA 240
DB 59 TyrTyrSerAspAsnValGlyArgPheThrIleSerArgGluAsnAlaLeuAsnSer 78
QY 241 CTGTATCTGCAAAATGAACAGCTGAAACCGAGACACAGCCGTGTATTACTGT----- 294
DB 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysValArg 98
QY 295 -----ACAGATTCTAGACTGGGCGCAGGGAACACTAGTCACC 333
DB 99 TyrAspHisTyrSerGlySerAspTyr-----TrpGlyGlnGlyThrLeuValThr 116
QY 334 GTCTCTCAGCTCCACCAAGGGGCCATCGGTCTTCCCTCGGACACCTCTCCCAAGAGC 393
DB 117 ValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSer 136
QY 394 ACCTCTGGGGCACAGCGCCCTGGCTGCTGTCTCAAGACTACTTCCCGAACCGGTG 453
DB 137 ThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProVal 156
QY 454 ACGGTGTCTGGAATCTAGCGCGCTGACACAGCGGTGACACCTTCCCGGTGTCTCTA 513
DB 157 ThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeu 176
QY 514 CAGTCTCAGGACTTACTCTCAGCAGCTGTGACCGTGTGACCGTCCCTCAGCAGCTGGC 573
DB 177 GlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGly 196
QY 574 ACCCAGACTCATCTGCAAGTGAATCACAGCCCGACACACCAAGGTGGACAGAA 633
DB 197 ThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLys 216
QY 634 GTGGAGCCCCAAATCTGTGACAAACTCACATGCCCCACCGTCCCGCAGCACCTGAATC 693
DB 217 ValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeu 236
QY 694 GCGGGGACCGTCACTGCTTCTCTCTTCCCGGCAAAACCCAGGACACCTCATGATCTCC 753
DB 237 LeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIleSer 256
QY 754 CGGACCCCTGAGGTGCATGCTGTGTGTGGAGCTGAGCCACGAGACCCCTGAGGTCAAG 813
DB 257 ArgThrProGluValThrCysValValValAspValSerHisGluAspProGluValLys 276
QY 814 TTCAACTGGTACGTGGACGGCGTGGAGGTGATATGCAAGACAAAGCCCGGGAGGAG 873
DB 277 PheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu 296
QY 874 CAGTCAACAGCAGCTACGTGTGTGTGCTGCTCTCCCGTCCCTGACCGAGCTGGCTG 933
DB 297 GlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeu 316
QY 934 AATGCAAGAGTACAAGTCAAGTCTCCAAAGAGCTCCAGAGCCCTCCAGCCCTCCAGAAA 993

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DB 317 AsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLys 336
QY 994 ACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAACAGGTGTACACCTGCCCCATCC 1053
DB 337 ThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSer 356
QY 1054 CGGGATGAGCTGACCAAGAACAGGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1113
DB 357 ArgAspGluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrPro 376
QY 1114 AGCAGCATCCCGTGGAGTGGAGAGCAATGGCGAGCCGAGAACCACTACAGAACACAG 1173
DB 377 SerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThr 396
QY 1174 CTCCCGTGTGAGTCCGACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1233
DB 397 ProProValLeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLys 416
QY 1234 AGCAGTGGCAGCAGGGAACGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1293
DB 417 SerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsn 436
QY 1294 CACTACGACGAGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
DB 437 HisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 449
RESULT 6
ABP58275
ID ABP58275 standard; protein; 468 AA.
XX
AC ABP58275;
XX
XX 23-OCT-2003 (revised)
DT 31-MAR-2003 (first entry)
XX
DE Humanised 3D6 antibody heavy chain.
XX
KW Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;
KW human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nontropic.
XX
OS Mus sp.
OS Homo sapiens.
XX
XX Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Signal_peptide
FT /label= Mature_peptide
FT /note= "the mature heavy chain is claimed in Claim 5"
FT Region 20..138
FT /note= "heavy chain variable region, claimed in Claim 4"
FT Region 50..54
FT /note= "CDR1"
FT Region 69..85
FT /note= "CDR2"
FT Region 118..127
FT /note= "CDR3"
XX
PN WO200288306-A2.
XX
PD 07-NOV-2002.
XX
XX 26-APR-2002; 2002WO-US011853.
XX
XX 30-APR-2001; 2001US-0287539P.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Tsurushita N, Vasquez M;
XX
XX WPI; 2003-183835/18.
DR

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DR N-PSDB; AB224633, AB224635.
 XX New humanized forms of mouse 3D6 antibodies, useful for treating Down's
 PT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral
 PT amyloid angiopathy, or for inhibiting formation of or reducing Abeta
 PT plaque in the brain.
 XX Disclosure; Page 13-14; 54pp; English.
 XX
 XX The present sequence is that of a preferred heavy chain of a humanised
 CC antibody of the present invention. In the variable region of this
 CC sequence, the complementarity determining regions (CDRs) originate from
 CC murine monoclonal antibody 3D6 and the framework region from human
 CC germline VH segment DP-45 and J segment JH4. Novel humanised antibodies
 CC of the invention have CDRs from 3D6 and human framework sequences. These
 CC humanised antibodies have binding affinities (affinity and epitope
 CC location) approximately the same as those of the mouse 3D6 antibody. The
 CC invention includes antibodies, single chain antibodies, and their
 CC fragments, as well as nucleotide sequences, vectors, transformed host
 CC cells, and methods of using the humanised antibody to treat, prevent,
 CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
 CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
 CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation of
 CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
 CC OS field)
 XX
 XX Sequence 468 AA;
 SQ

Alignment Scores:
 Pred. No.: 6,266-130 Length: 468
 Score: 2188.50 Matches: 415
 Percent Similarity: 94.48% Conservative: 13
 Best Local Similarity: 91.61% Mismatches: 12
 Query Match: 91.00% Indels: 13
 DB: Gaps: 3

US-09-674-716B-18 (1-1335) x ABP58275 (1-468)

QY 1 GAGGTGACGTCTGGAGTCTGGGGAGGCTTGTAAAGCCGGGGGTCTCTAGACTC 60
 DB 20 GluValGlnLeuValGlnSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
 QY 61 TCTGTGACGTAGCGATTCCTTCAAGTGGCTACTGGATGCTCTGGTCCGCGAGCT 120
 DB 40 SerCysAlaGlySerGlyPheThrPheSerAsnTyrGlyMetSerTrpValArgGlnAla 59
 QY 121 CCAGGAGGGGCTGAGTGGTCTGCTGAATAGATTGAATCTGAATATTCACACA 180
 DB 60 ProGlyLysGlyLeuGlnTrpValAlaSerIleArg-----SerGlyGlyArgThr 77
 QY 181 CATTATCGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
 DB 78 TyrTyrSerAspAsnValLysGlyArgPheThrIleSerArgGluAsnAlaLysAsnSer 97
 QY 241 CTGTATCTCAAATGACAGCTGTAACACCGAGGACACAGCGCTGTTACTGT----- 294
 DB 98 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysValArg 117
 QY 295 -----ACAGATTTCATAGACTGGGGCCAGGGAACTAGTCACCTAC 333
 DB 118 TyrAspHisTyrSerGlySerSerAspTyr-----TrpGlyGlnGlyThrLeuValThr 135
 QY 334 GTCTCTCAGCTCCACCAAGGGCCATCGGTCTTCCCGCTGGGACCTCTCTCAAGAGC 393
 DB 136 ValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSer 155
 QY 394 ACCTCTGGGGCAGACGCGCTGGCTGCTGGTCAAGGACTACTTCCCGAACCGGTG 453
 DB 156 ThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProVal 175
 QY 454 ACGGTGCTGTGAATCTAGCGCCCTGACACGCGGCTGCACACCTTCCCGGTGTCTTA 513
 DB 176 ThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeu 195

QY 514 CAGTCTCAGGACTCTTACTCTCCCTCAGCAGCGTGGTGAACGCTGCTCCAGCAGCTTGGGC 573
 DB 196 GlnSerSerGlyLeuTyrSerLeuSerValValThrValProSerSerSerLeuGly 215
 QY 574 ACCCAGACCTCATCTGCAACGCTGAATCAACAGCCAGCAACCAACCAAGGTGACAAAGAA 633
 DB 216 ThrGlnThrTrpIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 235
 QY 634 GTGAGCCCAAAATCTTGTGCACAAACTCACATGCCCAACCGTGCAGCAGCTGAATCTC 693
 DB 236 ValGluProLysSerCysAspLysThrHisThrCysProCysProAlaProGluLeu 255
 QY 694 GCGGGGGACCGCTCAGTCTTCTCTCCCAAAACCAACCAAGCAGCAGCTCATGATCTCC 753
 DB 256 LeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIleSer 275
 QY 754 CGGACCCCTGAGTCAATGCTGCTGGTGGTGGACGCGAGCCAGCAAGACCTGAGGTCAAG 813
 DB 276 ArgThrProGluValThrCysValValValAspValSerHisGluAspProGluValLys 295
 QY 814 TTCAACTGTGATGAGCGGCTGAGGTGATGATGATGATGATGATGATGATGATGATGATG 873
 DB 296 PheAsnTrpTrpValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu 315
 QY 874 CAGTACCAACAGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 933
 DB 316 GlnTyrAsnSerThrTrpArgValValSerValLeuThrValLeuHisGlnAspTrpLeu 335
 QY 934 ATGGCAAGAGTACAAAGTGCAGGTCTCCAAACAGCCCTCCAGCCCGCCATCCAGAAA 993
 DB 336 AsnGlyLysGlnTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLys 355
 QY 994 ACCATCTCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCGCCATCC 1053
 DB 356 ThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSer 375
 QY 1054 CGGGATGAGTGCACCAAGAACAGGTGTACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113
 DB 376 ArgAspGluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrPro 395
 QY 1114 AGCAGATGCGCGTGGAGTGGGAGACATGGCGAGGAGCACTACAGCAAGTCTACAGACCG 1173
 DB 396 SerAspIleAlaValGlnTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThr 415
 QY 1174 CTTCCCGTGTGAGTCCGACCTCCGACCGCTCTTCTTCTCTCTACAGCAAGTCTACAGCAAG 1233
 DB 416 ProProValLeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLys 435
 QY 1234 AGCAGTGGCAGCAGGGGAAACGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1293
 DB 436 SerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsn 455
 QY 1294 CACTACACGAGCAAGAGCTCTCCCTGTCTCCGGGTAAA 1332
 DB 456 HisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 468

RESULT 7
 AAE35327
 ID AAE35327 standard; protein; 444 AA.
 XX AC AAE35327;
 XX 17-JUN-2003 (first entry)
 XX Humanised murine antibody BIWA4 heavy chain protein.
 DE CD44; cytotoxic drug; therapy; cancer; tumour; minimal residual disease;
 KW antigen; cytostatic; BIWA4 antibody; murine.
 XX Homo sapiens.
 OS Homo sapiens.
 PN EP1258255-A1.

XX 20-NOV-2002.
 XX 18-MAY-2001; 2001EP-00112227.
 XX 18-MAY-2001; 2001EP-00112227.
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX Adolf G, Heider K, Patzelt E, Sproll M;
 XX WPI; 2003-177273/18.
 XX N-PSDB; AAD53977.
 XX New compound useful for treatment of cancer comprises CD44 specific
 PT antibody molecule conjugated to a highly cytotoxic drug, which cleaves
 PT under intracellular conditions.
 XX Claim 7; Page 15-16; 31pp; English.
 XX The invention relates to a compound comprising CD44 specific antibody
 CC molecule conjugated to a highly cytotoxic drug, which cleaves under
 CC intracellular conditions. The compound is used in pharmaceutical
 CC composition for the treatment of cancer, solid tumours, and as an
 CC adjuvant to surgical intervention to treat minimal residual disease. The
 CC present sequence is humanised murine antibody BIWA4 heavy chain protein
 CC used in the invention
 XX SQ Sequence 444 AA;
 Alignment Scores:
 Pred. No.: 7,74e-130 Length: 444
 Score: 2187.00 Matches: 415
 Percent Similarity: 95.09% Conservative: 11
 Best Local Similarity: 92.63% Mismatches: 14
 Query Match: 90.94% Indels: 8
 DB: 6 Gaps: 3
 US-09-674-716B-18 (1-1335) x AAE35327 (1-444)
 QY 1 GAGGTGCACTGCTGAGCTCTGGGGAGGCTTGGTAAGCCGGGGTCCCTTAGACTC 60
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu 20
 QY 61 TCCTGTGCACTAGCGGATTCACATTTACGTGCTACTGCTGCTGCTGCTGCTGCTGCT 120
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyxAspMetSerTrpValArgGlnAla 40
 QY 121 CCAGGAGGGGCTCGAGTGGTTCCTGAATAGATTGAATCTGATAATTATGCAACA 180
 Db 41 ProGlyLysGlyLeuGluTrpValSerThrIle-----SerSerGlyGlySerTyxThr 58
 QY 181 CATTATGGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
 Db 59 TyrTyxLeuAspSerIleGlyGlyArgPheThrIleSerArgAspAsnAlaLysAsnSer 78
 QY 241 CTGTATCTGAAATGAACAGCTGAAACCCGAGACACAGCGGTGTATTACTGTACA--- 297
 Db 79 LeuTyxLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyxTrpCysAlaArg 98
 QY 298 -----GATTTTCATAGCTGGGCGCAGGAGACACTAGTCACCGTCTCTCAGCTCC 348
 Db 99 GlnGlyLeuAspTyx-----TrpGlyArgGlyThrLeuValThrValSerSerAlaSer 116
 QY 349 ACCAAGGGCCCATCGGTCTTCCCTCGCACCTCTCCCAAGAGACACCTCTGGGGGACCA 408
 Db 117 ThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThr 136
 QY 409 GCGGCGCTGGGCTGCTGGTCAAGACTACTTCCCGAACCAGGTGACGGTGTCTGTGAAC 468
 Db 137 AlaAlaLeuGlyCysLeuValLysAspTyxPheProGluProValThrValSerTrpAsn 156
 QY 469 TCAGGCGCCTGACAGCGGGGTGACACACCTTCCCGGCTGCTCCTACAGTCTCAGGACTC 528

Db 157 SerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeu 176
 QY 529 TACTCCTCAGCAGCGTGTGACCGCTCCCTCAGCAGCTTGGGCACCCAGACCTACATC 588
 Db 177 TyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThrTyxIle 196
 QY 589 TGCACGTGAATCACAAGCCCAAGCAACACCAAGGTGGCAAGAAAGTGGAGCCCAATCT 648
 Db 197 CysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluProLysSer 216
 QY 649 TGTGACAAAACACACATGCCACCGTCCCAAGCACCTGAACCTCGCGGGGACCGTCA 708
 Db 217 CysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGlyProSer 236
 QY 709 GTCTTCTCTTCCCCCAAAACCAAGGACACCTCATCATCTCCCGGACCCCTGAGGTC 768
 Db 237 ValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrProGluVal 256
 QY 769 ACATGCGTGGTGGTGGACGTGAGCCAGGACCCCTGAGTCAAGTTCAGTCAACTCGTACG 828
 Db 257 ThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrpTyxVal 276
 QY 829 GACGGGTGGAGGTGCATATATGCCAAGACAAAGCCCGGGAGGAGCAGTACACACGACG 888
 Db 277 AspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyxAsnSerThr 296
 QY 889 TACCGTGTGGTGGTGGTCTCCTCAGCTGCTGACACGAGTGGTGAATGGCAGGAGTAC 948
 Db 297 TyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyx 316
 QY 949 AAGTGAAGGTCTCCCAAGGCCCTCCAGGCCCATCGAGAAAACCATCTCCAAAGCC 1008
 Db 317 LysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAla 336
 QY 1009 AAGGGCAGCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACC 1068
 Db 337 LysGlyGlnProArgGluProGlnValTyxThrLeuProProSerArgAspGluLeuThr 356
 QY 1069 AACAACACGTACGTGACCTGACCTGCTGGTCAAGGCTTCTATCCAGCGACATCGCCGTG 1128
 Db 357 LysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyxProSerAspIleAlaVal 376
 QY 1129 GAGTGGAGAGCAATGGGAGCCGGAGAACAACTCAAGACCAACGCTCCCGTCTGGAC 1188
 Db 377 GluTrpGluSerAsnGlyGlnProGluAsnAsnTyxLysThrThrProValLeuAsp 396
 QY 1189 TCCGACGGCTCTCTTCTCTCTACACAGCTCACCGTGGACAGAGCAGGTGGCAGCAG 1248
 Db 397 SerAspGlySerPhePheLeuTyxSerLysLeuThrValAspLysSerArgTrpGlnGln 416
 QY 1249 GGAACGCTCTTCTCATGCTCCGTCATGATGAGCTCTGCACAAACCATACACGCAAG 1308
 Db 417 GlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyxThrGlnLys 436
 QY 1309 AGCTCTCTCTGCTCTCCGGGTAAA 1332
 Db 437 SerLeuSerLeuSerProGlyLys 444
 RESULT 8
 AAE34876
 ID AAE34876 standard; protein; 444 AA.
 XX AAE34876;
 XX 28-MAY-2003 (first entry)
 XX BIWA4/8 antibody heavy chain mature protein.
 XX BIWA8 antibody; heavy chain variable region; light chain variable region;
 KW VH; VL; CD44v6; medicament; cancer; antibody therapy.
 XX Unidentified.
 OS

XX WO200294879-A1.
 XX 28-NOV-2002.
 XX 17-MAY-2002; 2002WO-BP005467.
 XX 18-MAY-2001; 2001EP-00112237.
 XX 26-SEP-2001; 2001US-0325147P.
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX Adolf G, Ostermann E, Patzelt E, Sproll M, Heider K;
 XX Miglietta JJ, Van Dongen AAMS;
 XX N-PSDB; AAD53212, AAD53215.
 XX WPI; 2003-129413/12.
 XX New antibodies specific for an epitope coded by the variant exon of the
 XX CD44 gene, useful for treating cancer, including non-small cell lung,
 XX breast, head and neck, ovarian and lung cancer.
 XX Claim 24; Col 44; 78pp; English.
 XX The present invention relates to novel antibody molecules comprising a
 XX variable region of the heavy (VH) and/or light chain (VL) of CD44v6
 XX specific humanised antibody called Biw48 and Biw44. Sequences of the
 XX invention are useful for manufacturing a medicament and for treating
 XX cancer including colorectum, non-small cell lung, breast, head and neck,
 XX ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the
 XX brain. They are also useful in antibody therapy. The present sequence is
 XX Biw44/8 antibody heavy chain mature protein. This sequence is used in the
 XX exemplification of the invention
 XX
 XX Sequence 444 AA;
 Alignment Scores:
 Pred. No.: 7-74e-130 Length: 444
 Score: 2187.00 Matches: 415
 Percent Similarity: 95.09% Conservative: 11
 Best Local Similarity: 92.63% Mismatches: 14
 Query Match: 90.94% Indels: 8
 DB: 6 Gaps: 3
 US-09-674-716B-18 (1-1335) x AAE34876 (1-444)
 QY 1 GAGTGCACCTGGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTC 60
 DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
 QY 61 TCTGTGACGTAGCGGATCTCTTTCAGTGGCTACTGGATCTCTGGGTCCGCCAGGCT 120
 DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAspMetSerTyrValArgGlnAla 40
 QY 121 CAGGGAAGGGCTGAGTGGGTCTGTAATAGATTGAATCAATCTGTAATATTCACACA 180
 DB 41 ProGlyLysGlyLeuGluTrpValSerThrIle-----SerSerGlyGlySerTyrThr 58
 QY 181 CATTATCGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
 DB 59 TyrTyrLeuAspSerIleLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSer 78
 QY 241 CTGTATCTGCAATGAACAGCTGTAACACCGAGGACACAGCGGTGTATTACTGTACA--- 297
 DB 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98
 QY 298 -----GATTTCATAGCTGGGGCCAGGGAACACTAGTCACCGTCTCTCAGCTCC 348
 DB 99 GlnGlyLeuAspTyr-----TrpGlyArgGlyThrLeuValThrValSerSerAlaSer 116
 QY 349 ACCAAGGGCCCATCGGTCTTCCCTTGGCACCCCTCTCCAGAGACCTCTTGGGGGACACA 408

DB 117 ThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThr 136
 QY 409 GCGGCCCTGGGTGCTGCTCAAGGACTACTTCCCGCAACCGGTGACGGTGTCTGGGAAC 468
 DB 137 AlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSerTrpAsn 156
 QY 469 TCAGGCGCTGACACGCGGTGACACCTTCCGGGTGTCTACAGTCTCAGTCTCAGACTC 528
 DB 157 SerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeu 176
 QY 529 TACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTCCGGCACCCAGACCTACATC 588
 DB 177 TyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThrTyrIle 196
 QY 589 TGAACGTGAATCACAAGCCCGACACACAGGTGGACAAAGAAAGTGGAGCCCAAACTCT 648
 DB 197 CysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluProLysSer 216
 QY 649 TGTGACAAAACACTCACACATGCCCGTCCCGACGACCTGAACTCGCGGGGACCCGCTCA 708
 DB 217 CysAspLysThrHisThrCysProCysProAlaProGluLeuGlyGlyProSer 236
 QY 709 GTCTTCTCTTCCCGCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGTCT 768
 DB 237 ValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrProGluVal 256
 QY 769 ACATGCGTGTGTGGTGGACGTGAGCCACGAGACCTCCAGGTCAAGTCAACTGGTACGTC 828
 DB 257 ThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrpTyrVal 276
 QY 829 GACGGCTGTGAGTGTGATTAATCCAAAGACAAAGCCCGGAGGAGCAGTACAAACAGCAG 889
 DB 277 AspGlyValGluValHisAlaLysThrLysProArgGluGluGlnTyrAsnSerThr 296
 QY 889 TACCGTGTGTGTCAGCTCTCCCGTCCAGGACCTGCTGAATCGCAAGGAGTAC 948
 DB 297 TyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyr 316
 QY 949 AAGTGAAGGTCTTCCAAACAAAGCCCTCCAGCCCGCCCATCGAGAAACCATCTCCAAAGCC 1008
 DB 317 LysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAla 336
 QY 1009 AAAGGCGCCCGCCGAGAACACAGGTGTACACCTCCCGCCCATCCCGGATGAGTGCACC 1068
 DB 337 LysGlyGlnProArgGluProGlnValTyrThrLeuProSerArgAspGluLeuThr 356
 QY 1069 AAGAACCCAGGTCTGACCTGACCTCCCTGGTCAAGGCTTCTATCCAGCCGACATCGCCGTG 1128
 DB 357 LysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal 376
 QY 1129 GAGTGGGAGAGCAATGGCGAGCGGAGAGAACACTACAGACCCGCTCCCGTGTGGAC 1188
 DB 377 GluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProValLeuAsp 396
 QY 1189 TCCGACCGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAAGACGAGGTGGCAGCAG 1248
 DB 397 SerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGln 416
 QY 1249 GGAAGCTCTTCTATGCTCCCGTGTGATGATGAGCTCTGCACACCCACTACAGCGAGAG 1308
 DB 417 GlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLys 436
 QY 1309 AGCTCTCCCTGCTCCGGGTAAA 1332
 DB 437 SerLeuSerLeuSerProGlyLys 444
 RESULT 9
 AAE33523
 ID AAE33523 standard; protein; 447 AA.
 XX
 AC AAE33523;
 XX
 DT 02-APR-2003 (first entry)

XX DE Human AOC2 heavy chain mutant protein, hAAQC2.
 XX KW Human; very late activation antigen; VLA-1; betal containing integrin;
 KW immunological disorder; inflammatory disorder; skin related condition;
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
 KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;
 KW irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
 KW atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa;
 KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
 KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
 KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
 KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
 KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
 KW graft versus host disease; myocardial ischaemia; mutant; mutein.
 XX OS Homo sapiens.
 XX WO200203854-A2.
 XX PD 24-OCT-2002.
 XX PF 12-APR-2002; 2002WO-US011521.
 XX PR 13-APR-2001; 2001US-0283794P.
 XX PR 06-JUL-2001; 2001US-0303689P.
 XX PA (BIOJ) BIOGEN INC.
 XX PI Lyne PD, Garber EA, Saldanha JW, Karpusas M;
 XX WPI; 2003-093009/08.
 XX New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
 burns, dermatitis, and abnormal proliferation of hair follicle cells or
 fibrosis.
 XX Example 23; Page 91-92; 248pp; English.
 XX The present invention relates to novel antibodies that specifically bind
 to very late activation (VLA-1; betal containing integrins) antigens and
 methods of using these antibodies to treat immunological disorders. The
 anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 mediated immunological or inflammatory disorders such as skin related
 conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
 proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
 fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
 bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
 intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
 gastritis, irritable bowel syndrome, colitis and colorectal cancer),
 vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
 periarthritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
 arthritis, systemic lupus erythematosus and multiple sclerosis), renal
 failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 immediate hypersensitivity), graft and transplant rejections, graft
 versus host disease, conjunctivitis, swelling occurring after injury,
 myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 human AOC2 heavy chain mutant protein, hAAQC2

US-09-674-716B-18 (1-1335) x AAE33523 (1-447)
 QY 1 GAGGTGAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
 QY 61 TCTGTGACAGTACGGGATTCATTTTCAGTGGCTACTGGATGTCCTGGGTCCCGCAGGCT 120
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrThrMetSerTrpValArgGlnAla 40
 QY 121 CCAGGGAAGGGCTCCAGTGGTGTGTAATAGATGAAATCTGATAATTATGCAACA 180
 Db 41 ProGlyLysGlyLeuGluTrpValAlaThrIle-----SerGlyGlyGlyHisThr 57
 QY 181 CATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240
 Db 58 TyrTyrLeuAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 77
 QY 241 CTGTATCTGCATAATGAACAGCTGAAACCGAGACACAGCCGCTGTATTACTCTACAGAT 300
 Db 78 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysThrArg 97
 QY 301 -----TTCATAGACTGGGGCCAGGGAAACACTAGTACACCGCTCTCC 339
 Db 98 GlyPheGlyAspGlyGlyTyrPheAspValTrpGlyGlnGlyThrLeuValThrValSer 117
 QY 340 TCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCGCACCCTCTCTCCAAGACACCTCT 399
 Db 118 SerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSer 137
 QY 400 GGGGGCACAGCGGCTCGGTGGCTCAAGGACTACTTCCCGAACCGGTGACGGTG 459
 Db 138 GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrVal 157
 QY 460 TCGTGGAACTCAGGGCCCTGACAGCGGCTGCACACCTTCCCGGCTGTCCTACAGTCC 519
 Db 158 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 177
 QY 520 TCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTCCCTCCAGCAGCTGGGCACCCAG 579
 Db 178 SerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGln 197
 QY 580 ACCTACATCTGCAACGTGAATCAAGCCCGACCAACCAAGGTGGACAAAGATGGAG 639
 Db 198 ThrTyrIleCysAsnValAlaHisLysProSerAsnThrLysValAspLysValGlu 217
 QY 640 CCCAAATCTTGTACAAAATTCACATGCCCCACCGTCCACACACTGACTGACTCGCGGG 699
 Db 218 ProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuGly 237
 QY 700 GCACCGTCACTCTCTCTCTTCCCGCCCAAAACCAAGACACCCCTCATGATCTCCCGACC 759
 Db 238 GlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThr 257
 QY 760 CTGAGGTACATGGTGGTGGTGGAGCCGAGCCAGAACCCCTGAGTCAAGTTCAC 819
 Db 258 ProGluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsn 277
 QY 820 TGGTACGTGACGCGGTGGAGGTGCATATGCAACAAAGCCCGGGAGGAGCAGTAC 879
 Db 278 TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyr 297
 QY 880 AACAGACGTACCGTGTGGTCAACCGTCTCCACCGTCTCCACCGAGTGGCTGAATGGC 939
 Db 298 GlnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly 317
 QY 940 AAGAGGTACAGTCAAGGTCTCCCAAGAGCCCTCCCGCCCGCCCTCCGAGAAACCATC 999
 Db 318 LysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIle 337
 QY 1000 TCCAAAGCCCAAGGCGAGCCCGGAGAACCCACAGGTGTACACCTGCCCGCCCATCCCGGAT 1059
 Db 338 SerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAsp 357

Alignment Scores:
 Pred. No.: 1,048-129 Length: 447
 Score: 2185.00 Matches: 417
 Percent Similarity: 94.22% Conservative: 7
 Best Local Similarity: 92.67% Mismatches: 16
 Query Match: 90.85% Indels: 10
 DB: 6 Gaps: 2

QY 1060 GAGCTGACCAAGACAGCTGAGCTGAGCTGCTGGTCAAGGCTTCTATCCAGCGAC 1119
 Db 358 GluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAsp 377
 QY 1120 ATCGCGCTGGAGTGGAGAGCAATGGGAGCGCGGAGAACAACTACAAGACACGCTCC 1179
 Db 378 IleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProPro 397
 QY 1180 GTGCTGACTCCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGGCAAGACGAGG 1239
 Db 398 ValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArg 417
 QY 1240 TGGCAGCAGGGAAGCTCTCTCATCTCCGTCGATGCGATGAGGCTCTGCACACCACTAC 1299
 Db 418 TrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyr 437
 QY 1300 AGCAGAGAGGCTCTCCCTGCTCCGGGT 1329
 Db 438 ThrGlnLysSerLeuSerLeuSerProGly 447

RESULT 10

ABR39465
 ID ABR39465 standard; protein; 442 AA.

XX AC ABR39465;

DT 12-JUN-2003 (first entry)

XX DE Humanised anti-Abeta antibody 266 heavy chain.

XX KW Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;

XX KW immunostimulant.

XX OS Homo sapiens.

XX PN WO2003016467-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US021324.

XX PR 17-AUG-2001; 2001US-0313576P.

XX PR 28-WAY-2002; 2002US-0383851P.

XX PA (ELIL) LILLY & CO ELI.

XX PI Bales KR, Paul SM;

XX PI WPI; 2003-289975/28.

XX DR Treating or reducing the progression of diseases associated with amyloid-

XX PT beta peptide, e.g. Alzheimer's disease, vascular dementia or mild

XX PT cognitive impairment, comprises administering an anti-amyloid-beta

XX PT peptide antibody.

XX PS Disclosure; Page 20-22; 84pp; English.

XX CC The invention relates to treating cognitive symptoms or reducing disease

XX CC progression in a subject having a condition or disease associated with

XX CC amyloid-beta peptide (Abeta). The method involves administering an amount

XX CC of an anti-Abeta antibody that has greater affinity for soluble Abeta

XX CC than 10⁻⁹ M, that has affinity (KD) for soluble Abeta1-40 or Abeta1-42

XX CC higher than 10⁻⁹ M, or that has greater affinity for soluble Abeta than

XX CC antibody 266 has. The method or the anti-Abeta antibody is useful in

XX CC preparing a medication for treating cognitive symptoms or reducing

XX CC disease progression in a subject having a condition or disease associated

XX CC with Abeta. The condition or disease is Alzheimer's disease, Down's

XX CC syndrome, cerebral amyloid angiopathy, vascular dementia, or mild

XX CC cognitive impairment. The present sequence represents a humanised anti-

XX CC Abeta antibody 266 heavy chain

XX CC Sequence 442 AA;

Alignment Scores:
 Pred. No.: 1,38e-129 Length: 442
 Score: 2183.00 Matches: 414
 Percent Similarity: 95.72% Conservative: 11
 Best Local Similarity: 93.24% Mismatches: 17
 Query Match: 90.77% Indels: 2
 Gaps: 1

US-09-674-716b-18 (1-1335) x ABR39465 (1-442)

QY 1 GAGGTGAGTGTGGAGTCTGGGGAGGCTGGTAAAGCCCGGGGGTCCCTTACACTC 60
 Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
 QY 61 TCCTGTGCAGCTAGCGGATTCATCTTCAGTGGCTACTGATGCTCTGGGTCCGCGAGGCT 120
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerA-gTyrSerMetSerTrpValArgGlnAla 40
 QY 121 CCAGGGAAGGGGCTCGAGTGGGTGCTGAAATTCAGATTGAAATCTGATAAATTATGCAACA 180
 Db 41 ProGlyLysGlyLeuGluLeuValAlaGlnIle-----AsnSerValGlyAsnSerThr 58
 QY 181 CATTATCGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
 Db 59 TyrTyrProAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThr 78
 QY 241 CTGTATCTGCAATGAACAGCCCTGAAACCGAGGACACAGCCGCTGTATTACTGTACAGAT 300
 Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaSer 98
 QY 301 TTATAGACTGGGGCCAGGGAACACTAGTACACGCTCTCTCAGCTCCACCAAGGGCCCA 360
 Db 99 GlyAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro 118
 QY 361 TCGGTCTTCCCTCCCTGGCACCTCTCCAGAGGACACCTCTGGGGGACACGCGCCCTGGGC 420
 Db 119 SerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGly 138
 QY 421 TGCTGTGTCAGGAGTACTTCCCGGAACCGGTGACGCTGCTGTGGAACTCAGCGCCCTG 480
 Db 139 CysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu 158
 QY 481 ACCAGGGCGGTGCACACCTTCCCGGCTGCTCAGTCTCAGTCTCAGTCTCAGTCTCAGC 540
 Db 159 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSer 178
 QY 541 AGCGTGTGACCGTGCCTCCAGCAGCTGGGACCCAGACCTACATCTGCAACCGTGAAT 600
 Db 179 SerValValThrValProSerSerSerLeuGlyThrGlnThrTyrIleCysAsnValAsn 198
 QY 601 CACAAGCCCAAGCAACCAAGGTGGACAGAAAGTGGAGCCCAATCTTGTGACAAAAC 660
 Db 199 HisLysProSerAsnThrLysValAspLysLysValGluProLysSerCysAspLysThr 218
 QY 661 CACACATGCCCGTCCCGGACACCTGAACTCCGCGGGGACCCGTCAGTCTTCTCTCTTC 720
 Db 219 HisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPhe 238
 QY 721 CCCCCAAAACCCCAAGGACACCTCATGATCTCCCGACCCCTGAGTCACTACGCTGGT 780
 Db 239 ProProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCysValVal 258
 QY 781 GTGAGTGTAGCCACCAAGACCTGAGGTCAAGTCACTTCACTGGTACGTGACCGCGTGGAG 840
 Db 259 ValAspValSerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGlu 278
 QY 841 GTGCATAATGCCAAGCAAAAGCCCGGGAGGAGCAGTACACAGCAGCAGTACCGTGTGGTC 900
 Db 279 ValHisAsnAlaLysThrLysProArgGluGlnTyrAsnSerThrTyrArgValVal 298
 QY 901 AGCGTCTCTACCGTCTCTGACACGAGGCTGGTGAATGGCAAGGAGTACAAAGTCCAGGTC 960

Db 299 SerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysVal 318
QY 961 TCCAAAGAGCCCTCCAGAGCCCATCGAGAAACCATCTCCAAAGCCAAAGAGGACGCC 1020
Db 319 SerAsnLysAlaLeuProAlaProIleGluLysThrLysLysAlaLysGlyGlnPro 338
QY 1021 CGAGAACACAGGTGTACACCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 1080
Db 339 ArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnVal 358
QY 1081 AGCTGACCTCGCTGCTCAAGGCTTCTATCCAGCAGCATCGCGTGGAGTGGAGAGC 1140
Db 359 SerLeuThrCysLeuValGlyGlyPheYrProSerAspIleAlaValGluTrpGluSer 378
QY 1141 AATGGGACGCGGAGAACCAACTACAGACCAAGCCTCCCTCCCTCCCTCCCTCCCTCC 1200
Db 379 AsnGlyGlnProGluAsnAsnTyrLysThrProProValLeuAspSerAspGlySer 398
QY 1201 TTCCTCTCTACAGCAAGCTCACCGTGCACAGAGCAGGTGGCAGCAGGAAAGTCTTC 1260
Db 399 PhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPhe 418
QY 1261 TCATGCTCGGTGATGATGAGGCTCTGCACCAACCACTACAGCAGAGAGGCTCTCCCTG 1320
Db 419 SerCysSerValMetHisGluAlaLeuHisHisTyrThrGlnLysSerLeuSerLeu 438
QY 1321 TCTCCGGTAAA 1332
Db 439 SerProGlyLys 442
RESULT 11
ID ABU08311 standard; protein; 442 AA.
AC ABU08311;
DT 22-MAY-2003 (first entry)
XX Humanised 266 antibody heavy chain.
DE Mouse; cognition; Abeta peptide associated disorder; anti-Abeta antibody;
KW cognitive impairment; Alzheimer's disease; Down's syndrome;
KW cerebral amyloid angiopathy; vascular dementia; noctropic; neurotropic;
KW mild cognitive impairment; antibody 266; heavy chain; humanised; mutant;
KW mutin.
XX Mus sp.
OS Synthetic.
XX WO2003015691-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US021323.
XX 17-AUG-2001; 2001US-0313222P.
XX 28-MAY-2002; 2002US-0383846P.
XX (ELIL) LILLY & CO ELI.
XX PA Bales KR, Dodart JF, Paul SM;
PI WPI; 2003-268234/26.
XX Effecting rapid improvement of cognition in a subject having Alzheimer's
PT disease, Down's syndrome, cerebral amyloid angiopathy, or mild cognitive
PT impairment, comprises administering anti-A beta antibody.
XX Disclosure; Page 21-23; 85pp; English.
XX The present invention relates to a method for effecting rapid improvement
CC of cognition in a subject having a condition or disease related to the
CC Abeta peptide. The method comprises administering an anti-Abeta antibody.

CC The method is useful for treating cognitive impairments associated with
CC Abeta peptide including those involved in Alzheimer's disease, Down's
CC syndrome, cerebral amyloid angiopathy, certain vascular dementia, and
CC certain forms of mild cognitive impairment. The anti-Abeta antibody is
CC useful for preparing a medicament for effecting rapid improvement in
CC cognition in a subject having Alzheimer's disease, Down's syndrome,
CC cerebral amyloid angiopathy, or mild cognitive impairment. The present
CC sequence represents a preferred heavy chain for a humanised 266 antibody
XX Sequence 442 AA;
SQ Alignment Scores: Length: 442
Pred. No.: 1.38e-129 Matches: 414
Score: 2183.00
Percent Similarity: 95.72% Conservative: 11
Best Local Similarity: 93.24% Mismatches: 17
Query Match: 90.77% Indels: 2
DB: Gaps: 1
US-09-674-716B-18 (1-1335) x ABU08311 (1-442)
QY 1 GAGTGCAGCTGTGTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTACATC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCCTGTCCAGCTAGCGGATTCCTTTCAGTGGTACTGCTGATGCTGCTGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrSerMetSerTrpValArgGlnAla 40
QY 121 CCAGGAAGGGGCTCGAGTGGTGTGTAATAGATTTGAAATCTGATATTAATATGCAACA 180
Db 41 ProGlyLysGlyLeuGluLeuValAlaGlnIle-----AsnSerValGlyAsnSerThr 58
QY 181 CATATGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCATAATCTAGA 240
Db 59 TyrTyrProAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThr 78
QY 241 CTGTATCTGCAATGAACAGCCTGAAACCGAGGACACAGCCGCTGTATTACTGTACAGAT 300
Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaSer 98
QY 301 TTCATGAGTGGGGGAGGAGAACATGATGACCGTCTCTTCCAGCTCCACCAAGGCGCCA 360
Db 99 GlyAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro 118
QY 361 TCGGTCTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 420
Db 119 SerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGly 138
QY 421 TGCTGTCTCAAGGACTACTTCCCGAACCGGTGACCGTGTCTGGAACCTCAGCGCCCTG 480
Db 139 CysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu 158
QY 481 ACCAGCGGCTGCACACCTTCCCGGCTGCTCCTACAGTCTCCTCAGACTCTACTCCCTCAGC 540
Db 159 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSer 178
QY 541 AGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAAT 600
Db 179 SerValValThrValProSerSerSerLeuGlyThrGlnThrThrIleCysAsnValAsn 198
QY 601 CACAGCCCAAGAACACCAAGGTGGACAGAAAGTGGAGCCCAAACTCTGTGACAAACT 660
Db 199 HisLysProSerAsnThrLysValAspLysLysValGluProLysSerCysAspLysThr 218
QY 661 CACATATGCCCGTCCCGGACCACTGAACTCCCGGGGACCCGTCAGTCTTCTCTCTTC 720
Db 219 HisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPhe 238
QY 721 CCCCCAAAACCCAGGACACCTCATGATCTCCCGACCCCTCAGGTCATCGGTGGTGT 780
Db 239 ProProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCysValVal 258

QY 781 GTGAGCTGAGCAGACAGACCTGAGGTCAAGTTCAACTGCTGAGCGGTGAG 840
 Db |||||
 QY 259 ValAspValSerHisGluAspProGluValLysPheAsnTrpValAspGlyValGlu 278
 Db |||||
 QY 841 GTGCATAATGCCAAGCAAGCGGGAGAGAGTACAAACAGCACGTACCGTGTGTC 900
 Db |||||
 QY 279 ValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValVal 298
 Db |||||
 QY 901 AGCGTCTCACGCTGCTGACAGAGAGTGGCTGAATGCCAAGAGTACAGTGCAGTGC 960
 Db |||||
 QY 299 SerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysVal 318
 Db |||||
 QY 961 TCCAAACAAAGCCCTCCAGCCCTCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCC 1020
 Db |||||
 QY 319 SerAsnLysAlaLeuProAlaProLleGluLysThrLysLysAlaLysGlyGlnPro 338
 Db |||||
 QY 1021 CGAGAACCAACAGGTGTACACCTGCTGCCCTCCATCCCGGATGAGCTGACCAAGAACAGTGC 1080
 Db |||||
 QY 339 ArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnVal 358
 Db |||||
 QY 1081 AGCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGC 1140
 Db |||||
 QY 359 SerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSer 378
 Db |||||
 QY 1141 AATGGCAGCCGAGAACAACTACAGACACCGCTCCCGTCTCGACTCCGACGGTCC 1200
 Db |||||
 QY 379 AsnGlyGlnProGluAsnAsnTyrLysThrThrProProValLeuAspSerAspGlySer 398
 Db |||||
 QY 1201 TTCTTCTCTACAGCAAGCTCACCTGGACAGAGCAGTGGCAGCGGAGAGCTCTTC 1260
 Db |||||
 QY 399 PhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPhe 418
 Db |||||
 QY 1261 TCATGCTCCGTCATGATGAGGCTCTGCACACACCTACAGCAGAGAGGCTCTCCCTG 1320
 Db |||||
 QY 419 SerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu 438
 Db |||||
 QY 1321 TCTCCGGTAAA 1332
 Db |||||
 QY 439 SerProGlyLys 442
 Db |||||

RESULT 12

ABB80109
 ID ABB80109 standard; protein; 442 AA.

XX AC ABB80109;
 XX AC ABB80109;

DT 13-JUN-2003 (first entry)
 XX DT 13-JUN-2003 (first entry)

DE Heavy chain.

XX Complementarity determining region; CDR; humanised; mouse; 266; light;
 KW heavy; variable; domain; antibody; preclinical; clinical;
 KW Alzheimer's disease; epitope; amyloid beta peptide; Abeta;
 KW central nervous system; plasma.

XX Homo sapiens.
 OS Mus musculus.

XX WO2003015617-A2.

XX 27-FEB-2003.

XX 16-AUG-2002; 2002WO-US026321.

XX 17-AUG-2001; 2001US-0313221P.

XX 17-AUG-2001; 2001US-0313224P.

XX 23-OCT-2001; 2001US-0334987P.

XX (UNIW) UNIV WASHINGTON.
 PA (ELIL) LILLY & CO ELI.

PI Holtzman DM, Demattos R, Bales KR, Cummins DJ, Paul SM;

DR WPI; 2003-278505/27.
 XX Diagnosing preclinical or clinical Alzheimer's disease in a subject by
 Pt administering an antibody which specifically binds an epitope.
 XX Disclosure; Page 15-16; 64pp; English.

XX The sequences given in AAG80104-09 represent preferred antibodies of the
 CC invention. This sequence represents the preferred heavy chain. The
 CC humanised antibody of the invention may be used for diagnosing
 CC preclinical or clinical Alzheimer's disease. The antibody specifically
 CC binds an epitope, preferably the amyloid beta peptide (Abeta). The
 CC antibodies sequester Abeta from its bound, circulating form in blood and
 CC alter clearance of soluble and bound forms of Abeta in central nervous
 CC system and plasma. The antibodies specifically bind an epitope
 CC representing amino acids 13-28 of the Abeta molecule

XX Sequence 442 AA;
 SQ

Alignment Scores:

Pred. No.: 1-38e-129 Length: 442
 Score: 2183.00 Matches: 414
 Percent Similarity: 95.72% Conservative: 11
 Best Local Similarity: 93.24% Mismatches: 17
 Query Match: 90.77% Indels: 2
 DB: 6 Gaps: 1

US-09-674-716B-18 (1-1335) x ABB80109 (1-442)

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 Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrSerMetSerTrpValArgGlnAla 40
 QY 121 CAGGGAAGGGCTCGAGTGGTGTGCTGAAGGGAAATTCACCATCTCAAGAGATGATCAAAATCTAGA 180
 Db 41 ProGlyLysGlyLeuGluLeuValAlaGlnIle-----AsnSerValGlyAsnSerThr 58
 QY 181 CATTATGCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATCAAAATCTAGA 240
 Db 59 TyrTrpProAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysThr 78
 QY 241 CTGTATCTGCAATGAACAGCTGAAACCGAGGACACAGCGGTGTATTACTGTACAGAT 300
 Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaSer 98
 QY 301 TTCATAGACTGGGCGCAGGGAACACATAGTCACCGCTCCCTCAGCTCCACCAAGGCCCA 360
 Db 99 GlyAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro 118
 QY 361 TCGGTCTTCCCGCTGGCACCCCTCTCCAAAGAGCACCTCTGGGGGCACAGCGCCCTGGGC 420
 Db 119 SerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGly 138
 QY 421 TGCTGTGTCAGGACTACTTCCCGNACCGGTGACGGTGTCTGGAACTCAGCGCCCTG 480
 Db 139 CysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu 158
 QY 481 ACCAGCGGCTGCACACCTTCCCGGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGC 540
 Db 159 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSer 178
 QY 541 AGCGTGTGACCGTGCCTCCAGCTTGGGACCCAGACCTACATCTGCACGTAAT 600
 Db 179 SerValValThrValProSerSerLeuGlyThrGlnThrTyrIleCysAsnValAsn 198
 QY 601 CACAAGCCAGCAACACCAAGGTGGACAGAAGTGGAGCCCAAAATCTGTGACAAAAC 660
 Db 199 HisLysProSerAsnThrLysValAspLysLysValGluProLysSerCysAspLysThr 218


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Db      219  AspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGlyProSerVal 238
QY      712  TTCTCTTCCCTCCCAACCCAGGACACCTCATGATCTCCGGACCCCTGAGTCA 771
Db      239  PheLeuPheProLysProLysAspThrLeuMetIleSerArgThrProGluValThr 258
QY      772  TGGCTGGTGTGACGTGACGACCAAGACCCCTGAGCTCAAGTTCAAGTTGAGTGGAC 831
Db      259  CysValValValAspValSerHisGluAspProGluValValPheAsnTrpTyrValAsp 278
QY      832  GGGGTGAGGTGATATATGTCAGACAAAGCCCGGGAGGAGAGTACACAGCAGTAC 891
Db      279  GlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyr 298
QY      892  CGTGTGCTGAGCTCTCACCGTCCCTGACACAGGACTGCTGAATGGCAAGGAGTACAG 951
Db      299  ArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLys 318
QY      952  TGCAAGGTCTCCAAAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAA 1011
Db      319  CysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaLys 338
QY      1012  GGGCAGCCCGAGAACACAGAGTGTACACCCCTGCCCCATCCCGGATGAGTGCACAG 1071
Db      339  GlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThrLys 358
QY      1072  AACAGGTGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1131
Db      359  AsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGlu 378
QY      1132  TGGAGAGCAATGGGAGCGGAGGAGACACTACAGACACCCCTCCCGTGTGACTCC 1191
Db      379  TrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProValLeuAspSer 398
QY      1192  GACGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCAGGG 1251
Db      399  AspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGly 418
QY      1252  AACGTTCTCTATGCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 1311
Db      419  AsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSer 438
QY      1312  CTCTCCCTCTCTCCGGGTAAA 1332
Db      439  LeuSerLeuSerProGlyLys 445

```

RESULT 14

AAU07745

ID AAU07745 standard; protein; 461 AA.

XX

AC AAU07745;

XX

DT 04-DEC-2001 (first entry)

XX

DE Humanised monoclonal antibody Hu266, heavy chain.

XX

KW Monoclonal antibody; Hu266; neotropic; neuroprotective; Abeta peptide;
 KW Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
 KW gene therapy.

XX

OS Mus sp.

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT 1..19

FT /label= Signal peptide

FT 20..461

FT /label= Mature Hu266 heavy chain

FT /note= "This sequence is specifically claimed in claim

FT 17"

XX

PN WO200162801-A2.
 PD 30-AUG-2001.
 XX 26-FEB-2001; 2001WO-US006191.
 XX 24-FEB-2000; 2000US-0184601P.
 PR 08-DEC-2000; 2000US-0254465P.
 PR 08-DEC-2000; 2000US-0254498P.
 XX (UNIV) UNIV WASHINGTON.
 PA (EJIL) LILLY & CO ELI.
 XX Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;
 PI Vasquez M;
 XX WPI; 2001-550087/61.
 DR New humanized antibody for the treatment of Alzheimer's comprises the
 XX inhibition and reduction of the formation of amyloid plaques.
 PT Example 13; Fig 5; 63pp; English.
 PS
 XX The invention relates a humanised antibody that specifically binds an
 CC epitope contained within positions 13-28 of amyloid beta peptide, Abeta.
 CC The antibody is useful to inhibit and reduce the formation of amyloid
 CC plaques or the effects of toxic soluble Abeta species in humans their
 CC fragments are used for the manufacture of a medicament. This includes the
 CC prolonged expression of recombinant sequences of them in human tissues
 CC for the treatment of clinical/pre-clinical Alzheimer's disease, Down's
 CC syndrome or pre clinical cerebral amyloid angiopathy. Specifically, the
 CC antibody is used to sequester Abeta into plasma, brain or cerebrospinal
 CC fluid to prevent/reverse accumulation of the Abeta peptide within the
 CC brain thereby improving cognition. The present sequence is the heavy
 CC chain of a humanised monoclonal antibody, Hu266, based on the mouse
 CC antibody 266
 XX
 SQ Sequence 461 AA;

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 1,39e-129 | Length: | 461 |
| Score: | 2183.00 | Matches: | 414 |
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| Best Local Similarity: | 93.24% | Mismatches: | 17 |
| Query Match: | 90.77% | Indels: | 2 |
| DB: | 4 | Gaps: | 1 |

US-09-674-716B-18 (1-1335) x AAU07745 (1-461)

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 Db 20 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
 QY 61 TCCTGTGACGCTAGCGGATTCACCTTTCAGTGGCTACTGCGATGCTCGGCTCGCAGGCT 120
 Db 40 SerCysAlaAlaSerGlyPheThrPheSerArgTyrSerMetSerTrpValArgGlnAla 59
 QY 121 CCAGGGAAGGGCTCGAGTGGTGGTAAATAGATTCAAAATCTCATATATTCACACA 180
 Db 60 ProGlyLysGlyLeuGluLeuValAlaGlnIle-----AsnSerValGlyAsnSerThr 77
 QY 181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACATCTCAAGAGATGATTCAAAATCTAGA 240
 Db 78 TyrTrpProAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThr 97
 QY 241 CTGTATCTCAATGAACAGCTGAAACCCAGGAGACACAGCCGTGTATCTGTACAGAT 300
 Db 98 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaSer 117
 QY 301 TTCATAGACTGGGGCCAGGGAACACTAGTACCGCTCTCTCTAGCCCTCCACCAAGGCCCA 360
 Db 118 GlyAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro 137

| | | | |
|-----|---|---|------------------|
| XX | | 18-AUG-2003 | (first entry) |
| XX | | Hu266 N56T heavy chain. | |
| XX | | Amyloid-beta; Abeta; antibody 266; neurotropic; neuroprotective; CDR; | |
| XX | | immunostimulant. | |
| KW | | Homo sapiens. | |
| XX | | WO2003016466-A2. | |
| XX | | 27-FEB-2003. | |
| PPD | | 14-AUG-2002; 2002WO-US021322. | |
| PF | | 17-AUG-2001; 2001US-0313224P. | |
| PER | | (ELIL) LILLY & CO ELI. | |
| XX | | Jia AY, Tsurushita N, Vasquez MJ, | |
| XX | | WPI; 2003-278557/27. | |
| XX | | N-PSDB; ACC47228. | |
| DRR | | New antibodies comprising a heavy chain and a light chain complementarity | |
| DRR | | determining regions from antibody 266, for treating and preventing | |
| DRR | | conditions associated with the A beta peptide, e.g. Alzheimer's disease | |
| DRR | | or Down syndrome. | |
| PT | | Disclosure; Fig 3; 82pp; English. | |
| XX | | The invention relates to an anti-Beta (amyloid-beta peptide) antibody | |
| XX | | 266. The antibodies are useful for treating and preventing conditions | |
| CC | | associated with the Beta peptide, such as Alzheimer's disease, Down | |
| CC | | syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in | |
| CC | | humans; for determining whether a human subject will respond to treatment | |
| CC | | using humanized antibodies against Abeta; for treating, preventing and | |
| CC | | reversing cognitive decline in clinical or pre-clinical Alzheimer's | |
| CC | | disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting | |
| CC | | formation of amyloid plaques of the effects of toxic soluble Abeta / | |
| CC | | species in humans. Treatment of the patients with antibody will inhibit | |
| CC | | or prevent cognitive decline typically associated with disease | |
| CC | | progression and reverses it. The present sequence represents a humanised | |
| CC | | anti-Beta antibody 266 N56T heavy chain | |
| XX | | Sequence 461 AA; | |
| SQ | | Alignment Scores: | |
| | Pred. No.: | 1.39e-129 | Length: 461 |
| | Score: | 2193.00 | Matches: 414 |
| | Percent Similarity: | 95.72% | Conservative: 11 |
| | Best Local Similarity: | 93.24% | Mismatches: 17 |
| | Query Match: | 90.77% | Indels: 2 |
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| Db | 20 | GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu | 39 |
| QY | 61 | TCCCTGTGCAGTACCGGATTCACCTTTTCAGTGGCTACTGGATGCTCGGTCCGCCAGGCT | 120 |
| Db | 40 | SerCysAlaAlaSerGlyPheThrPheSerArgTyTyrSerMetSerTrpValArgGlnAla | 59 |
| QY | 121 | CCAGGAAGGGGCTCGAGTGGTGTCTGTAATTAGATTGAATTCATTAATCATTAATTCACA | 180 |
| Db | 60 | ProGlyLysGlyLeuGluLeuValAlaGlnIle-----AsnSerValGlyThrSerThr | 77 |
| QY | 181 | CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGACATGATTCAAATCTAGA | 240 |
| Db | 78 | IrryIrrProAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThr | 97 |

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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:54:09 ; Search time 175.104 Seconds
(without alignments)
4906.833 Million cell updates/sec

Title: US-09-674-716b-18

Perfect score: 2405

Sequence: 1 gaggtgcagctggtggagtc.....ccctgtctccgggtaaatga 1335

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Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 2702124

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40 cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
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-FCAPOP=6 -FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
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RESULT 1
US-10-474-832-4
; Sequence 4, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-10-474-832-4

ALIGNMENTS

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| 2 | 2191 | 91.1 | 447 | 16 | US-10-474-832-6 | Sequence 6, Appli |
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| 4 | 2187 | 90.9 | 444 | 16 | US-10-704-522-6 | Sequence 6, Appli |
| 5 | 2187 | 90.9 | 444 | 16 | US-10-645-215-6 | Sequence 6, Appli |
| 6 | 2185 | 90.9 | 447 | 16 | US-10-474-832-5 | Sequence 5, Appli |
| 7 | 2183 | 90.8 | 442 | 12 | US-10-226-435A-12 | Sequence 12, Appli |
| 8 | 2183 | 90.8 | 445 | 14 | US-10-320-231A-79 | Sequence 79, Appli |
| 9 | 2173.5 | 90.4 | 449 | 9 | US-09-736-371B-21 | Sequence 21, Appli |
| 10 | 2173.5 | 90.4 | 449 | 15 | US-10-463-442-21 | Sequence 21, Appli |
| 11 | 2172.5 | 90.3 | 451 | 9 | US-09-822-698A-26 | Sequence 26, Appli |
| 12 | 2172.5 | 90.3 | 474 | 14 | US-09-848-832-3 | Sequence 3, Appli |
| 13 | 2172.5 | 90.3 | 474 | 14 | US-10-225-108A-3 | Sequence 3, Appli |
| 14 | 2172.5 | 90.3 | 474 | 15 | US-10-461-148-1 | Sequence 1, Appli |
| 15 | 2170 | 90.2 | 663 | 12 | US-10-412-406-33 | Sequence 33, Appli |
| 16 | 2170 | 90.2 | 4852 | 12 | US-10-412-406-33 | Sequence 33, Appli |
| 17 | 2169 | 90.1 | 446 | 16 | US-10-408-901-46 | Sequence 46, Appli |
| 18 | 2167 | 90.1 | 446 | 16 | US-10-408-901-38 | Sequence 38, Appli |
| 19 | 2166 | 90.1 | 469 | 16 | US-10-656-769-26 | Sequence 26, Appli |
| 20 | 2161.5 | 89.9 | 478 | 9 | US-09-948-429B-8 | Sequence 8, Appli |
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| 22 | 2161.5 | 89.9 | 478 | 13 | US-10-124-905-8 | Sequence 8, Appli |
| 23 | 2161.5 | 89.9 | 478 | 14 | US-10-124-807-8 | Sequence 8, Appli |
| 24 | 2161.5 | 89.9 | 478 | 15 | US-10-291-532-8 | Sequence 8, Appli |
| 25 | 2161 | 89.9 | 477 | 15 | US-10-291-265-395 | Sequence 395, App |
| 26 | 2159.5 | 89.8 | 451 | 15 | US-10-423-293-4 | Sequence 4, Appli |
| 27 | 2158 | 89.7 | 489 | 16 | US-10-656-769-20 | Sequence 20, Appli |
| 28 | 2156.5 | 89.7 | 445 | 16 | US-10-408-901-42 | Sequence 42, Appli |
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| 30 | 2151.5 | 89.5 | 453 | 9 | US-09-802-096-8 | Sequence 8, Appli |
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| 38 | 2150.5 | 89.4 | 451 | 14 | US-10-113-996-18 | Sequence 18, Appli |
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US-09-674-716B-18 (1-1335) x US-10-474-832-4 (1-447)

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QY 241 CTGTATCTGCAATGAACAGCCTGAAACCGAGGACACAGCCGCTGTATTACTGTACAGAT 300
Db 78 LeuTyrLeuGlnValMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysThrArg 97
QY 301 -----TTCATAGACTGGGCGCAGGGAACACTAGTCAACCGCTCTCC 339
Db 98 GlyPheGlyAspGlyGlyTyrPheAspValTyrGlyGlnGlyThrLeuValThrValSer 117
QY 340 TCAGCTCTCACCAAGGGCCATCGCTTCCCTCGGACCTCTCCCAAGAGCACTCT 399
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QY 400 GGGGGCACAGCGCCCTCGGCTGCTGTCAAGGACTACTTCCCGGAACCGGTGACGGTG 459
Db 138 GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrVal 157
QY 460 TCGTGAATCAGGCGCCTGACAGCGCGTGCACACTTCCCGGCTGTCTACAGTCC 519
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Db 198 ThrTyrIleCysAsnValAlaAsnHisLysProSerAsnThrLysValAspLysValGlu 217
QY 640 CCCAAATCTGTGACAAACTCACATGCCCCACCGTCCAGCAGCTTGGGCGGG 699
Db 218 ProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGly 237
QY 700 GCACCGTCACTTCTCTTCCCTCCCAACCAAGGACACCTCATGATCTCCGGACC 759
Db 238 GlyProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThr 257
QY 760 CTGAGGTCACTGCTGTGTGTGGTGGCTGACCGACGAGACCTGAGTCAAGTTCAC 819
Db 258 ProGluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsn 277
QY 820 TGGTACGTGGAGCGGTGAGGTGTCATATGCAAGACAAAGCCCGGGAGGAGCAGTAC 879
Db 278 TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyr 297
QY 880 AACAGCACGTACGCTGTGTGTGCTGACGCTCTCACCCTGCTGCACCGACTGCTGAATGC 939

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Db 298 AsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly 317

QY 940 AAGGAGTACAAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCCCGGCTCGAGAAAACCAATC 999

Db 318 LysGluTyrIysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIle 337

QY 1000 TCCAAAGCCAAAGGCGAGCCCGGAGAACCAACAGTGTACACCTGCTCCCGCATCCCGGAT 1059

Db 338 SerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAsp 357

QY 1060 GAGTGTACCAAGAACCAAGGTCAACCTGACCTGCTGCTCAAGGCTTCTATCCACGAC 1119

Db 358 GluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAsp 377

QY 1120 ATCGCGTGGAGTGGGAGCAATGGCAGCCGAGAACCAACTACAGACCAAGCAGCTCC 1179

Db 378 IleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProPro 397

QY 1180 GTGTGTGACTCCGACGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAG 1239

Db 398 ValLeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArg 417

QY 1240 TGGCAGCAGGGGACGCTTCTCTCATGCTCCGTGATGCATGAGCTCTGCACACCACTAC 1299

Db 418 TrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyr 437

QY 1300 ACGCAGAGAGCCCTCTCCCTGTCTCCGGGT 1329

Db 438 ThrGlnLysSerLeuSerLeuSerProGly 447

RESULT 2

US-10-474-832-6

; Sequence 6, Application US/10474832

; Publication No. US20040081651A1

; GENERAL INFORMATION:

; APPLICANT: BIOGEN, INC.

; TITLE OF INVENTION: ANTIBODIES TO VLA-1

; FILE REFERENCES: A101 PCT

; CURRENT APPLICATION NUMBER: US/10/474,832

; PRIOR FILING DATE: 2003-10-14

; PRIOR APPLICATION NUMBER: 60/283,794

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/303,689

; PRIOR FILING DATE: 2001-07-06

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 447

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: polypeptide

US-10-474-832-6

Alignment Scores:

Pred. No.: 6,93e-134 Length: 447

Score: 2191.00 Matches: 418

Percent Similarity: 94.44% Conservatives: 7

Best Local Similarity: 92.89% Mismatches: 15

Query Match: 91.10% Indels: 10

DB: 16 Gaps: 2

US-09-674-716B-18 (1-1335) x US-10-474-832-6 (1-447)

QY 1 GAGGTGACGTGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60

Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlySerLeuArgLeu 20

QY 61 TCCTGTGCAGTACGCGATTCACTTTCAGTGGCTACTGATGCTCTGGGTCCGCCAGCT 120

Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrThrMetSerTrpValArgGlnAla 40

QY 121 CCAGGGAAGGGGCTCGAGTGGGTGCTGAAATAGATTGAAATCTGATAATTATGCAACA 180

Db 41 ProGlyValGlyLeuGluTrpValAlaThrIle-----SerGlyGlyGlyHisThr 57

QY 181 CATTATCGGAGTCTGTGAAGGGAAATTCACATCTCAAGAGATGATTCAAAATCTAGA 240

Db 58 TyrTyrLeuAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 77

QY 241 CTGTATCTGCAATGAACAGCCTGAAACCGAGGACACAGCCGCTGTATTACTGTACAGAT 300

Db 78 LeuTyrLeuGlnValMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysThrArg 97

QY 301 -----TTCATAGACTGGGCGCAGGGAACACTAGTCAACCGCTCTCC 339

Db 98 GlyPheGlyAspGlyGlyTyrPheAspValTyrGlyGlnGlyThrLeuValThrValSer 117

QY 340 TCAGCTCTCACCAAGGGCCATCGCTTCCCTCGGACCTCTCCCAAGAGCACTCT 399

Db 118 SerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysThrSer 137

QY 400 GGGGGCACAGCGCCCTCGGCTGCTGTCAAGGACTACTTCCCGGAACCGGTGACGGTG 459

Db 138 GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrVal 157

QY 460 TCGTGAATCAGGCGCCTGACAGCGCGTGCACACTTCCCGGCTGTCTACAGTCC 519

Db 158 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 177

QY 520 TCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAG 579

Db 178 SerGlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGln 197

QY 580 ACTATCATCTGAACCTGAATCACAAGCCCAACACCAAGTGGACAAAGAAAGTGGAG 639

Db 198 ThrTyrIleCysAsnValAlaAsnHisLysProSerAsnThrLysValAspLysValGlu 217

QY 640 CCCAAATCTGTGACAAACTCACATGCCCCACCGTCCAGCAGCTTGGGCGGG 699

Db 218 ProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGly 237

QY 700 GCACCGTCACTTCTCTTCCCTCCCAACCAAGGACACCTCATGATCTCCGGACC 759

Db 238 GlyProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThr 257

QY 760 CTGAGGTCACTGCTGTGTGTGGTGGCTGACCGACGAGACCTGAGTCAAGTTCAC 819

Db 258 ProGluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsn 277

QY 820 TGGTACGTGGAGCGGTGAGGTGTCATATGCAAGACAAAGCCCGGGAGGAGCAGTAC 879

Db 278 TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyr 297

QY 880 AACAGCACGTACGCTGTGTGTGCTGACGCTCTCACCCTGCTGCACCGACTGCTGAATGC 939

QY 121 CCAGGAGGGCTCGAGTGGTTCCTCAATAGATTGAATCTGATAATTATGCAACA 180
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QY 181 CATTATCGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATCAAAATCTAGA 240
Db 58 TyTrpLeuAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 77
QY 241 CTGTATCTGCAATGAACAGCTGAACACCGAGACACAGCCGCTGATTACTGTACAGAT 300
Db 78 LeuTyLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyTrpCysThrArg 97
QY 301 -----TTGATAGCTGGGGCCAGGGAACACTAGTCAACCTCTCC 339
Db 98 GlyPheGlyAspGlyGlyTyTrpPheAspValTrpGlyGlnGlyThrLeuValThrValSer 117
QY 340 TCAGCTCCACAGAGGCCCATCGGTCTTCCCTCCCTCGCACCTCTCTCAAGAGACCTCT 399
Db 118 SerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSer 137
QY 400 GGGGACAGCGCCCTGGCTGGCTGCTCAAGACTACTTCCCGCAACCGGTGACCGGTG 459
Db 138 GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyPheProGluProValThrVal 157
QY 460 TCGTGGAACTCAGCGCCCTCACCAGCGCGGTGCACACCTTCCCGGTCTCTACAGTCC 519
Db 158 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 177
QY 520 TCAGGACTCTACTCCCTCAGAGGGTGTGACCTGCGCTCCAGCAGCTGGGACCCAG 579
Db 178 SerGlyLeuTySerLeuSerSerValValThrValProSerSerSerLeuGlyThrGln 197
QY 580 ACCTACATCTGCAACCTGAAATCAAGCCAGCACCAAGGTGGACAAAGAGTGGAG 639
Db 198 ThrTyIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGlu 217
QY 640 CCCAAATCTGTGACAAACTCACATGCCACCGTCCCGACACCTGAACCTCGCGGG 699
Db 218 ProLysSerCysAspLysThrHisThrCysProCysProAlaProGluAlaGly 237
QY 700 GCACCGTCTGCTCTCTCCCGCAAAACCAAGGACACCTCATGATCTCCCGGACC 759
Db 238 GlyProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThr 257
QY 760 CTGAGGTGCATGCGTGGTGGTGCAGCCAGACACCTGAGTCAAGTCAAC 819
Db 258 ProGluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsn 277
QY 820 TCGTACGTGGAGCGGTGGAGTGCATTAATCCAGACAAAGCCGCGGAGGACCTAC 879
Db 278 TrpTyValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyTr 297
QY 880 AACAGCAGTACCGTGTGCTCAGCGTCTCTCCCTGACCCAGGACTGGCTGAATGGC 939
Db 298 AsnSerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly 317
QY 940 AAGAGTACAGTCAAGTCTCCAAAGCCCTCCAGCCCGCATCGAGAAACCATC 999
Db 318 LysGluTyLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIle 337
QY 1000 TCCAAAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTCGCCCGCATCCCGGAT 1059
Db 338 SerLysAlaLysGlyLysProArgGluProGlnValTyThrLeuProProSerArgAsp 357
QY 1060 GAGCTGACAAAGAACAGGTCAAGTCAAGTCCCTGGTCAAGGCTTCTATCCAGCGAC 1119
Db 358 GluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAsp 377
QY 1120 ATCCGCGGTGGAGGAGCAATGGGAGCGGAGACACTACAAGACACCGCTCC 1179
Db 378 IleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyTrpLysThrProPro 397
QY 1180 GTGCTGGACTCCGAGCGGTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAGGACAGG 1239

Db 398 ValLeuAspSerAspGlySerPhePheLeuTySerLysLeuThrValAspLysSerArg 417
QY 1240 TGGCAGCAGGGAAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACACCACTAC 1299
Db 418 TrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyTr 437
QY 1300 ACGCAGAACAGCGCTCTCCCTGTCTCCGGGT 1329
Db 438 ThrGlnLysSerLeuSerLeuSerProGly 447
RESULT 3
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: AGOLF, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
US-10-150-475A-6
Alignment Scores:
Pred. No.: 1,26e-133 Length: 444
Score: 2187.00 Matches: 415
Percent Similarity: 95.09% Conservative: 11
Best Local Similarity: 92.63% Mismatches: 14
Query Match: 90.94% Indels: 8
DB: 14 Gaps: 3
US-09-674-716B-18 (1-1335) x US-10-150-475A-6 (1-444)
QY 1 GAGTGCAGCTGTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu 20
QY 61 TCCTGTGCAGTACGCGATTTCATTTTCAGTGGCTACTGGATGCTCCGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyAspMetSerTrpValArgGlnAla 40
QY 121 CCAGGGAAGGGCTCGAGTGGTTCGTAATTTAGATTGAATCTGATAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValSerThrIle-----SerSerGlyGlySerTyThr 58
QY 181 CATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATCAAAATCTAGA 240
Db 59 TyTrpLeuAspSerLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSer 78
QY 241 CTGTATCTGCAATGAACAGCTGAACACCGAGACACAGCCGCTGATTACTCTACA--- 297
Db 79 LeuTyLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyTrpCysAlaArg 98
QY 298 -----GATTTTCATAGACTGGGGCCAGGGAACACTAGTCAACCTCTCTCAGCTCC 348
Db 99 GlnGlyLeuAspTyTrp-----TrpGlyArgGlyThrLeuValThrValSerSerAlaSer 116
QY 349 ACCAAGGGCCCATCGGTCTTCCCGTGGCACCTCTCCCAAGAGACCTCTCGGGGACACA 408
Db 117 ThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThr 136
QY 409 GCGGCCCTGGGTGCTCTGTCAGAGACTACTTCCCGCAACCGGTGACGGTGTCTGTGAAC 468

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Db 137 AlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSerTrpAsn 156
QY 469 TCAGGGCGCCTCAGCAGCGCGTGCACACCTCCCGGCTGTCTCCTACAGTCTCCTCAGGACTC 528
Db 157 SerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerGlyLeu 176
QY 529 TACTCCTCAGCAGCGTGTGACCGTCCCTCAGCAGCTTGGGACCCAGCAGCTACATC 588
Db 177 TyrSerLeuSerSerValValThrValProSerSerLeuGlyThrGlnThrTyrIle 196
QY 589 TGCAGCTGAATCAGACCGCCAGCACACACAGGTGGACAGAGTGGAGCCCAATCT 648
Db 197 CysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluProLysSer 216
QY 649 TGTGACAAAACCTCACACATGCCCGCTGCCAGCAGCTGAACTCCGGGGGCGACCGTCA 708
Db 217 CysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGlyProSer 236
QY 709 GCTCTCCTCTCCCGCCAAAACCGAGACACCTCATGATCTCCGACCCCTGAGTGC 768
Db 237 ValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrProGluVal 256
QY 769 ACATGCGTGTGTCAGCTGAGCAGCAGAACCTGAGGTCAAGTTCAACTTCACTGGTACGTG 828
Db 257 ThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrpTyrVal 276
QY 829 GACGGGTGAGGTGATTAATCCCAAGACAAAGCCCGGAGGAGCAGTACAACAGCAG 888
Db 277 AspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnLysPheAsnSerThr 296
QY 389 TACCCTGTGTCAGCGTCTCCTCCTGACAGGAGTCTGCTCAATGGCAAGAGTAC 948
Db 297 TyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyr 316
QY 949 AAGTGCAAGGTCTCAACAAAGCCCTCCAGCCCGCCATCGAGAAACCATCTCAAAAGCC 1008
Db 317 LysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSerLysAla 336
QY 1009 AAGGGCAGCCCGAGAACCAAGTGTACACCTGCCCGCCATCCCGGATGAGCTGACC 1068
Db 337 LysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThr 356
QY 1069 AAGAACCAAGTCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATCGCCGTG 1128
Db 357 LysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal 376
QY 1129 GAGTGGAGAGCAATGGGAGCGGAGAACAACTACAAGACAGCCCTCCCGTCTGGAC 1188
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QY 1189 TCCGAGCGTCTCTCTCTCTACAGCAGCTCACCGTGGCAAGAGCAGGTGGCAGCAG 1248
Db 397 SerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGln 416
QY 1249 GGGAGCTTCTCTATGCTCCGTGATGATGAGGTCTGCAACACCACTACACGAGAG 1308
Db 417 GlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisThrGlnLys 436
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RESULT 4

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US-10-704-522-6
; Sequence 6, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
; APPLICANT: Adol, Gunther
; APPLICANT: Baumann, Michael
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and methods for treating cancer using
; TITLE OF INVENTION: cytotoxic CD44 Antibody Immunocjugates

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; FILE REFERENCE: 1/1414
; CURRENT APPLICATION NUMBER: US/10/704,522
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/429,516
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP 02024881
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-704-522-6
Alignment Scores: 1,26e-133 Length: 444
Pred. No.: 2187.00 Matches: 415
Score: 95.09% Conservative: 11
Best Local Similarity: 92.63% Mismatches: 14
Query Match: 90.94% Indels: 8
DB: 16 Gaps: 3
US-09-674-716B-18 (1-1335) X US-10-704-522-6 (1-444)
QY 1 GAGTGCAGCTGTGTGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTTAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCCTGTGCGAGCTAGCGGATTCACCTTCAGTGGCTACTGTGATGCTCTGGGTCCGCGAGGT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAspMetSerTrpValArgGlnAla 40
QY 121 CCAGGAAGGGCTCGAGTGGGTGCTGAAATTTAGATTGAAATCTGTAATATATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValSerThrIle-----SerSerGlyGlySerTyrThr 58
QY 181 CATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAGAGAGATGATTCAAATCTAGA 240
Db 59 TyrTyrLeuAspSerIleLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSer 78
QY 241 CTCTATCTGCAAAATGAACACCTCTGAAACCCAGGACACAGCGGTGTATTACTGTACA --- 297
Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98
QY 298 -----GATTTCTAGACTGGGGCCAGGGAACACTAGTACCGTCTCCTCAGCCTCC 348
Db 99 GlnGlyLeuAspTyr-----TrpGlyArgGlyThrLeuValThrValSerSerAlaSer 116
QY 349 ACCAAGGGCCCATCGGTCTTCCCGTGGCACCTCTCCCAAGAGACACCTCTCGGGGCACA 408
Db 117 ThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThr 136
QY 409 GCGGCGCTGGGTGCTGTGTCAGGACTACTTCCCGGAAACCGGTGACGGTGTGGGAAAC 468
Db 137 AlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSerTrpAsn 156
QY 469 TCAGGCGCCTGACAGCGCGTGCACACCTTCCCGGCTGTCTCAGTCCCTCAGGACTC 528
Db 157 SerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeu 176
QY 529 TACTCCTCAGCAGCGTGTGACCGGTGCCCTCCAGCAGCTTGGGACCCAGCAGCTACATC 588
Db 177 TyrSerLeuSerSerValValThrValProSerSerLeuGlyThrGlnThrTyrIle 196
QY 589 TGCAGCTGAATCAGACCGCCAGCACACAGGTGGACAGAGTGGAGCCCAATCT 648
Db 197 CysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluProLysSer 216
QY 649 TGTGACAAAACCTCACACATGCCCGCTGCCAGCAGCTGAACTCCGGGGGCGACCGTCA 708

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Db 297 TyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyr 316
QY 949 AAGTGCAGAGTCTCCAAACAAAGCCCTCCAGAGCCCTCCAGAGCCCTCCAGAGAAACCATCTCCAAAGCC 1008
Db 317 LysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAla 336
QY 1009 AAGGACGAGCCCGAGAACACAGGTGTACACCTGCGCCCATCCCGGAGTACAGCTGACC 1068
Db 337 LysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThr 356
QY 1069 AAGAACCAGGTACAGCTGAGCTGCTGGTCAAGGCTTCTATCCAGAGGACATCCCGGTG 1128
Db 357 LysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal 376
QY 1129 GAGTGGAGAGCAATGGGAGCCGAGAACAACTACAGACACACCCCTCCCGTGTGGAC 1188
Db 377 GluTrpGluSerAsnGlyGlnProGluAsnAspTyrLysThrThrProProValLeuAsp 396
QY 1189 TCCGAGCGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAGAGGAGTGGCAGAG 1248
Db 397 SerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGln 416
QY 1249 GGAACAGCTCTCTCATGCTCCCGTGTGATGATGAGGCTCTGCACAACTACAGCAGAG 1308
Db 417 GlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLys 436
QY 1309 AGCTCTCCCTGCTCCCGGTA 1332
Db 437 SerLeuSerLeuSerProGlyLys 444

RESULT 6

US-10-474-832-5

; Sequence 5, Application US/10474832

; Publication No. US20040081651A1

; GENERAL INFORMATION:

; APPLICANT: BIOGEN, INC.

; TITLE OF INVENTION: ANTIBODIES TO VLA-1

; FILE REFERENCE: A101 PCT

; CURRENT APPLICATION NUMBER: US/10/474,832

; CURRENT FILING DATE: 2003-10-14

; PRIOR APPLICATION NUMBER: 60/283,794

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/303,689

; PRIOR FILING DATE: 2001-07-06

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 447

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: polypeptide

US-10-474-832-5

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 1,7e-133 | Length: | 447 |
| Score: | 2185.00 | Matches: | 417 |
| Percent Similarity: | 94.22% | Conservative: | 7 |
| Best Local Similarity: | 92.67% | Mismatches: | 16 |
| Query Match: | 90.85% | Indels: | 10 |
| DB: | 16 | Gaps: | 2 |

US-09-674-716B-18 (1-1335) x US-10-474-832-5 (1-447)

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Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20

QY 61 TCTGTGCAGTACAGGATTCATTCTAGTGTGCTAGTCTCTGGTCCGCCAGGCT 120

Db 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrThrMetSerTrpValArgGlnAla 40

QY 121 CACGGAAGGGGCTCAGTGGTGTGAAATAGATTGAAATCTGAAATCTGAAATATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaThrIle-----SerGlyGlyGlyHisThr 57
QY 181 CATTATGCGGAGTCTCTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db 58 TyrTrpLeuAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 77
QY 241 CTCTATCTCCAAATGAACAGCCCTGAAACCGAGGACACAGCCGTGTATTACTGTACAGAT 300
Db 78 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysThrArg 97
QY 301 -----TTCATAGACTGGGCGCAGGGAACACTAGTACCGCTCTCC 339
Db 98 GlyPheGlyAspGlyTyrPheAspValTrpGlyGlnGlyThrLeuValThrValSer 117
QY 340 TCAGCCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCTCCAGAGCACCTCT 399
Db 118 SerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSer 137
QY 400 GGGGGACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGCAACCGGTGAGGTG 459
Db 138 GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrVal 157
QY 460 TCCTGGAACCTCAGGCGCCCTGACAGCGGTGCACACCTTCCCGGCTGTCTCAGAGTCC 519
Db 158 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 177
QY 520 TCAGGACTCTTCTCTCAGAGCGGTGTGACGTGCTCCCTCCAGAGCTTGGGACCCAG 579
Db 178 SerGlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGln 197
QY 580 ACCTACATCTGCAACGTGAATCACAGCCAGCAACACCAAGGTGCACAAAGAGTGGAG 639
Db 198 ThrTrpIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGlu 217
QY 640 CCAAAATCTTGACAAAACACTCACATGCCACCGTGTCCAGACCTGAATCTCGGGGG 699
Db 218 ProLysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGly 237
QY 700 GCACGCTCAGTCTTCTCTTCCCCCAAAACCCAGGACACCTCATGATCTCCGGGACC 759
Db 238 GlyProSerValPheLeuPheProLysProLysAspThrLeuMetLysSerArgThr 257
QY 760 CTTGAGGTACATGCTGCTGTGTGGACGTGAGCCAGAACAGCCCTGAGGTCAAGTTCAAC 819
Db 258 ProGluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsn 277
QY 820 TGGTACGTGAGCGGCTGGAGTGCATATGCCAGACAAAGCCCGGGAGGAGCAGTAC 879
Db 278 TrpTrpValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyr 297
QY 880 AACAGACAGTACCGTGTGTGTCAGCGTCTCACCGTCTCTGCACAGGACTGGGTGAATGCG 939
Db 298 GlnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly 317
QY 940 AAGGAGTACAGTGAAGGTCTCCAAAGAGCCCTCCAGAGCCCTCCAGAGAAACCATC 999
Db 318 LysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIle 337
QY 1000 TCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTACACCTGCCCTCCCGGAT 1059
Db 338 SerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAsp 357
QY 1060 GAGCTGACCAAGAACAGGTTCAGCTGTGCTGCTGCTCAAAGGCTTCTATCCAGCGCAC 1119
Db 358 GluLeuThrTrpLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAsp 377
QY 1120 ATCGCGCTGGAGTGGAGAGCAATGGCAGCGGAGAACAACTACAAAGACCAACGCTCC 1179
Db 378 IleAlaValGluTrpGluSerAsnGlyGlnProGluAsnThrLysThrThrProPro 397
QY 1180 GTGCTGGACTCCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGCAGAGCAGG 1239

398 ValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArg 417
1240 TGGCAGCAGGGGACGCTTCTCATGCTCCCTGATGATGAGGCTTCGCAACCACTAC 1299
418 TrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyr 437
1300 ACGCAGAGAGAGCTCTCCCTCTCTCCGGGT 1329
438 ThrGlnLysSerLeuSerLeuSerProGly 447

RESULT 7
US-10-226-435A-12
; Sequence 12, Application US/10226435A
; Publication No. US20040043418A1
; GENERAL INFORMATION:
; APPLICANT: ELI LILLY AND COMPANY and WASHINGTON UNIVERSITY
; TITLE OF INVENTION: Humanized Antibodies that Sequester Amyloid Beta Peptide
; FILE REFERENCE: 8792/293
; CURRENT APPLICATION NUMBER: US/10/226.435A
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/06191
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,601
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/254,465
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/254,498
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibodies
US-10-226-435A-12

Alignment Scores:
Pred. No.: 2,29e-133 Length: 442
Score: 2183.00 Matches: 414
Percent Similarity: 95.72% Conservative: 11
Best Local Similarity: 93.24% Mismatches: 17
Query Match: 90.77% Indels: 2
DB: 12 Gaps: 1
US-09-674-716B-18 (1-1335) x US-10-226-435A-12 (1-442)

QY 1 GAGGTGCGAGCTGTGGAGCTTGGTAAAGCCGGGGTCCCTTAGACTC 60
DB 1 GluValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCCTGTGCGAGCTAGCGGATTCACATTTTCAGTGGCTACTGGATGCTCCTGGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerArgTyrSerMetSerTrpValArgGlnAla 40
QY 121 CGAGGAGAGGGCTCGAGTGGTTCGAAATAGATTGAATCTGATTAATTGCAACA 180
DB 41 ProGlyLysGlyLeuGluLeuValAlaGlnLeu-----AsnSerValGlyAsnSerThr 58
QY 181 CATTATGCGAGCTGTGTGAAGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
DB 59 TyrTyrProAspThrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThr 78
QY 241 CTGTATCTGCAATGAACAGCTGAAACCCGAGGACACAGCGGTGTATTACTGTACAGAT 300
DB 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaSer 98
QY 301 TTCATAGACTGGGCGGAGGACACTAGTTCACCGCTCTCTCAGCTCCACCAAGGGCCCA 360
DB 99 GlyAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyPro 118

QY 361 TCGGTCTTCCCTCGGCACCCCTCTCAAGAGACCTCTGGGGGCACACGGCCCTGGGC 420
DB 119 SerValPheProLeuAlaProSerSerLysSerThrSerGlyThrAlaAlaLeuGly 138
QY 421 TGCTGTGTCAGAGCTACTTCCCGAAACCGGTGACCGGTCTGTGGAACCTCAGCGCCCTG 480
DB 139 CysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu 158
QY 481 ACCAGCGGGTGCACACCTTCCCGGGTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGC 540
DB 159 ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSer 178
QY 541 AGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAAT 600
DB 179 SerValValThrValProSerSerLeuGlyThrGlnThrTyrIleCysAsnValAsn 198
QY 601 CACAAGCCAGCAACACCCAGGTGGACAGAAAGTGGAGCCCAATCTTGTGCAAACT 660
DB 199 HisLysProSerAsnThrLysValAspLysValGluProLysSerCysAspLysThr 218
QY 661 CACACATGCCCCACCGTGGCCAGCACCTGAACCTCGCGGGGCGCCAGTCTCTCTCTTC 720
DB 219 HisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPhe 238
QY 721 CCCCCAAAACCCAGACACCCCTCATGATCTCCCGACCCCTGAGGTACATCGGTGGT 780
DB 239 ProProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCysValVal 258
QY 781 GTGAGCTGTAGCCAGCAAGACCCCTGAGGTCAAGTTCAGTGTGCTGACGTGACGCGGTGGAG 840
DB 259 ValAspValSerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGlu 278
QY 841 GTGCATAATGCCAAGCAAGCCCGGAGGAGCAGTACAACAGCAGTACCGGTGGTGC 900
DB 279 ValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValVal 298
QY 901 AGCGTCTCTACCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTCCAAGTTC 960
DB 299 SerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluLysCysLysVal 318
QY 961 TCCACAAAAGCCCTCCCGACCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCC 1020
DB 319 SerAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnPro 338
QY 1021 CGAGAACCCAGGTGTACACCTGCCCTGCCCATCCCGGATGAGCTGACCAAGACCCAGTCC 1080
DB 339 ArgGluProGlnValTyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnVal 358
QY 1081 AGCTGACCTCGCTGTCAAGGCTTCTATCCCGAGCATCCCGCTGGAGTGGGAGAGC 1140
DB 359 SerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTyrGluSer 378
QY 1141 AATGGGAGCCGAGAACAACTACAAGACACGCTCCCGTGTGCTGCTCCGACCGGCTCC 1200
DB 379 AsnGlyGlnProGluAsnAsnTyrLysThrThrProProValLeuAspSerAspGlySer 398
QY 1201 TTCTTCTCTACAGCAGCTCACCGTGGCAAGAGCAGGTGGCGAGCGGGAACGCTCTTC 1260
DB 399 PhePheLeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPhe 418
QY 1261 TCATGTCTCGGTGATGAGTCTGTGCACAAACCTACACGAGAGAGCCCTCTCCCTG 1320
DB 419 SerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu 438
QY 1321 TCTCCCGGTAAA 1332
DB 439 SerProGlyLys 442

RESULT 8
US-10-320-231A-79
; Sequence 79, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:

```

; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 79
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-79

Alignment Scores:
Pred. No.: 2,29e-133 Length: 445
Score: 2183.00 Matches: 415
Percent Similarity: 94.85% Conservative: 9
Best Local Similarity: 92.84% Mismatches: 15
Query Match: 90.77% Indels: 8
DB: 14 Gaps: 3

US-09-674-716B-18 (1-1335) x US-10-320-231A-79 (1-445)

QY 10 CTGCTGGCTCTGGGGAGGCTTGTAAAGCCGGGGGCTCCCTAGACTCTCTGTGCA 69
Db 1 LeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeuSerCysAla 20
QY 70 GCTAGCGGATTCACATTACAGTGGCTACTGATGCTGCTGGCTCCGCGAGGCTCCAGGGAAG 129
Db 21 AlaSerGlyPheThrPheSerSerTyraMetSerTyrValArgGlnAlaProGlyLys 40
QY 130 GGGCTCGAGTGGTCTGCAATTAAGATTGAATCTGTAATCTGTAATTAAGCAACATATCGG 189
Db 41 GlyLeuGluTrpValSerAlaIle-----SerGlySerGlyGlySerThrTyrrTyra 58
QY 190 GAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGACTGTATCTG 249
Db 59 AspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyrrLeu 78
QY 250 CAATGAACAGCTGAAACCCAGGACACAGCCGTGTATTACTGTACA-----GATTTC 303
Db 79 GlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrrTyrrCysAlaArgArgAspPhe 98
QY 304 ATAGAC-----TGGGGCCAGGAAACACAGTACCGCTCTCCAGCTCCACCC 351
Db 99 PheAlaHisPheAspValTrpGlyGlnGlyThrLeuValThrValSerAlaSerThr 118
QY 352 AAGGGCCCATCGGTCTTCCCTCGCACCCCTCTCCCAAGAGACACCTCTGGGGGCACAGCG 411
Db 119 LysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAla 138
QY 412 GCCTGGGTCTGGTCTGACAGACTACTCCCGAACCGGTGACGGTCTCGTGGACTCA 471
Db 139 AlaLeuGlyCysLeuValLysAspTyrrPheProGluProValThrValSerTrpAsnSer 158
QY 472 GCGCGCTCAGCAGGCGGTGCACACCTTCCCGGTGTCTACAGTCTCAGGACTCTAC 531
Db 159 GlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrr 178
QY 532 TCCTCAGCAGGCTGTGACCGTCTCCAGCAGCTTGGGACCCAGCAGCTACATCTGC 591
Db 179 SerLeuSerSerValValThrValProSerSerLeuGlyThrGlnThrTyrrileCys 198
QY 592 AAGCTGAATCACAAGCCCAAGCAACCAAGGTGGCAAGAAAGTGGAGCCCAAAATCTTGT 651
Db 199 AsnValAsnHisLysProSerAsnThrLysValAspLysValGluProLysSerCys 218

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QY 652 GACAAAACCTCACATGTCGCCACCGTCCCGAGCAGCTGAACTCGCGGGGCGCCGTCAGTTC 711
Db 219 AspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGlyProSerVal 238
QY 712 TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCGGACCCCTGAGTTCACA 771
Db 239 PheLeuPheProLysProLysAspThrLeuMetIleSerArgThrProGluValThr 258
QY 772 TGCGTGTGTGTCAGCTGAGCCACGAGACCTGAGTCAAGTTCACCTGAGTTCAGTGGAC 831
Db 259 CysValValValAspValSerHisGluAspProGluValLysPheAsnTrpTyrrValAsp 278
QY 832 GCGCTGGAGTGTCAATATCCAAAGCAAGCCGCGGAGGAGCAGTACACAGCAGTAC 891
Db 279 GlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTrpAsnSerThrTyrr 298
QY 892 CTGTGTGTCAGCTCTCCCTGTCACCGCTGTCACAGGACTGGCTGAATGGCAAGGATACAG 951
Db 299 ArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrrLys 318
QY 952 TGCAAGGTCTTCCAAACAAAGCCCTCCCGAGCCCTCCATCGAGAAAACCATCTCCAAAGCCAAA 1011
Db 319 CysLysValSerAsnLysAlaLeuProAlaProLeuGluLysThrIleSerLysAlaLys 338
QY 1012 GCGCAGCCCGGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACCAAG 1071
Db 339 GlyGlnProArgGluProGlnValTyrrThrLeuProProSerArgAspGluLeuThrLys 358
QY 1072 AACCAAGTCTGAGCTGACCTGCTGCTGCTCAAGGCTTCTATCCAGCAGACATCGCGTGGAG 1131
Db 359 AsnGlnValSerLeuThrCysLeuValLysGlyPheTyrrProSerAspIleAlaValGlu 378
QY 1132 TGGGAGAGCAATGGGAGCGGAGAGAACTCAAGACCAACGCGCTCCCTGCTGTGACTCC 1191
Db 379 TrpGluSerAsnGlyGlnProGluAsnAsnTyrrLysThrProProValLeuAspSer 398
QY 1192 GAGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1251
Db 399 AspGlySerPhePheLeuTyrrSerLysLeuThrValAspLysSerArgTrpGlnGlnGly 418
QY 1252 AACGCTCTTCTCATGCTCCGCTGATGATGAGGCTCTGCAACACCACTTACACGAGAGAGC 1311
Db 419 AsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrrThrGlnLysSer 438
QY 1312 CTCTCCCTGCTCCGGGTAAA 1332
Db 439 LeuSerLeuSerProGlyLys 445

RESULT 9
US-09-736-371B-21
; Sequence 21, Application US/09736371B
; Patent No. US20020131968A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
; CURRENT APPLICATION NUMBER: US/09/736,371B
; CURRENT FILING DATE: 2002-04-25
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: 9815909.8
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-371B-21

Alignment Scores:

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Pred. No.: 9,46e-133 Length: 449
Score: 2173.50 Matches: 412
Percent Similarity: 94.01% Conservative: 12
Best Local Similarity: 91.35% Mismatches: 18
Query Match: 90.37% Indels: 9
DB: 2 Gaps: 2

US-09-674-716B-18 (1-1335) x US-09-736-371B-21 (1-449)

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QY 1 GAGGTGACAGTGGTGGAGTCTGGGGGAGCTTGGTAAGCCCGGGGGTCCCTTAGACTC 60
DB 1 GluValGlnLeuLeuLeuSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCCTGTGACGTAGCGGATTCACTTTCAGTGGTACTGATGCTCTGGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerPheProMetAlaTrpValArgGlnAla 40
QY 121 CCAGGGAAGGGCTCGAGTGGTTCCTGAAATAGATTGAATCTGATAATTATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValSerThrile-----SerThrSerGlyGlyArgThr 58
QY 181 CATTATCGGGAGTCTGTAAGGGGAATTCACATCTCAAGAGATGATTCAAAATCTAGA 240
DB 59 TyrTyrArgAspSerValLysGlyArgPheThrileSerArgAspAsnSerLysAsnThr 78
QY 241 CTGTATCTGCAATCAACAGCCTGAAACCCGAGGACACAGCGGTGTATTACTGTACAGAT 300
DB 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTy-CysAlaLys 98
QY 301 TTCATAGAC-----TGGGGCCAGGGGAACAACACTAGTCACCGTCTCC 339
DB 99 PheArgGlnTyrSerGlyGlyPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 118
QY 340 TCAGCTCTCCACCAAGGGCCATCGGTCTTCCCTTGGCACCCCTCTCCAAAGAGCACCTCT 399
DB 119 SerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSer 138
QY 400 GGGGGACAGCGGCGCTGGCTGCTGTGTCAGGACTACTTCCCGAACCCGGTGCAGGTG 459
DB 139 GlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrVal 158
QY 460 TGTGGAATCTAGCGGCGCTGACAGCGCGTGCACACCTTCCCGGTCTCTCAAGTCC 519
DB 159 SerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 178
QY 520 TCAGGACTTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCAACCAG 579
DB 179 SerGlyLeuTy-SerLeuSerSerValValThrValProSerSerSerLeuGlyThrGln 198
QY 580 ACTATACCTGCAAGCTGATCACAGCCAGCACACCAAGGTGCACAAAGAAAGTGGAG 639
DB 199 ThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGlu 218
QY 640 CCCAAATCTTGACAAAACCTCACATACCCACCGTGCACAGACCTGAACTCCGGGG 699
DB 219 ProLysSerCysAspLysThrH.sThrCysProProCysProAlaProGluLeuGly 238
QY 700 GCACCGTGTGCTTCTTCTTCCCGGCAACCCAGGACACCTCATGATCTCCCGGACC 759
DB 239 GlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThr 258
QY 760 CTGAGGTTCACATGCTGTGTGGTGGACGTGAGCCACCAAGACCTCGAGTCAAGTTCAC 819
DB 259 ProGluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsn 278
QY 820 TGTACGTGAGCGGCTGAGGTGCTAATGCCAAGCAACCCCGGAGGAGAGGATAC 879
DB 279 TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyr 298
QY 880 AACAGACAGTACCGTGTGTCAGCGTCTCAGCTGCTCAGCAGGACTGGTGAATGCC 939
DB 299 AlaserThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGly 318
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QY 940 AAGGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAACCATC 999
DB 319 LysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrile 338
QY 1000 TCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGGAT 1059
DB 339 SerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProSerArgAsp 358
QY 1060 GAGCTCACCAAGAACAGGTTCAGCTGAGCTGCTCGTCAAAAGGTTCTATCCACGAC 1119
DB 359 GluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAsp 378
QY 1120 ATGCGGTGAGGAGAGAGCAATGGGAGCCCGGAGAACAACTACAGACCAAGCCCTCCC 1179
DB 379 IleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProPro 398
QY 1180 GTCTGTGACTCCACAGCGCTCTTCTCTCTACAGCAAGCTCACCCGTGGACAAAGACGAG 1239
DB 399 ValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArg 418
QY 1240 TGGCAGCAGGGGAACTCTTCTCATGCTCGTGTATGATGAGCTCTGCACAAACCACTAC 1299
DB 419 TrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyr 438
QY 1300 ACCGAGAGAGCGCTCTCCCTGTCTCCGGGTAAA 1332
DB 439 ThrGlnLysSerLeuSerLeuSerProGlyLys 449
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RESULT 10

US-10-463-442-21
; Sequence 21, Application US/10463442
; Publication No. US20040006216A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
; CURRENT APPLICATION NUMBER: US/10/463,442
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/736,371
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 9815909.8
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02380
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 21
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-463-442-21

Alignment Scores:

Pred. No.: 9,46e-133 Length: 449
Score: 2173.50 Matches: 412
Percent Similarity: 94.01% Conservative: 12
Best Local Similarity: 91.35% Mismatches: 18
Query Match: 90.37% Indels: 9
DB: 2 Gaps: 2

US-09-674-716B-18 (1-1335) x US-10-463-442-21 (1-449)

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QY 1 GAGGTGACAGTGGTGGAGTCTGGGGGAGCTTGGTAAGCCCGGGGGTCCCTTAGACTC 60
DB 1 GluValGlnLeuLeuLeuSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCCTGTGACGTAGCGGATTCACTTTCAGTGGTACTGATGCTCTGGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerPheProMetAlaTrpValArgGlnAla 40
QY 121 CCAGGGAAGGGCTCGAGTGGTTCCTGAAATAGATTGAATCTGATAATTATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValSerThrile-----SerThrSerGlyGlyArgThr 58
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454 ACAGTGTGCTGAACTCAGCGCCCTGACACGCGCGTGCACACCTTCCCGGCTGCTCTA 513
 159 ThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeu 178
 514 CAGTCTCAGACTCTACTCCTCAGCAGCGTGTGTGCGCTGCGCTCCAGCAGCTGGC 573
 179 GlnSerSerGlyLeuTySerLeuSerValValThrValProSerSerLeuGly 198
 574 ACCCAGACTCATCTGCAAGCTGAATCACAAGCCCAAGCAACCAAGGTGCACAAGAA 633
 199 ThrGlnThrTyIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLys 218
 634 GTGAGCCCAATCTGTGACAAACTCACAATGCCCGCTGCGCGCTGCGCTGCACTC 693
 219 ValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeu 238
 694 GCGGGGGCAGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 753
 239 LeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetLysSer 258
 754 CGGACCCCTGAGGTACATGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 813
 259 ArgThrProGluValThrCysValValValAspValSerHisGluAspProGluValLys 278
 814 TTCAACTGTGAGTGTGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 873
 279 PheAsnTrpTyValAspGlyValGluValHisAsnAlaLysThrLysProArgGluLeu 298
 874 CAGTCAACAGCAGCTACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 933
 299 GlnTyAsnSerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrpLeu 318
 934 ATGCAAGAGTACAGT 993
 319 AsnGlyLysGluTyLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLys 338
 994 ACCATCTCAAAGCAAGGGCAGCCCGAGAACACACAGGTGTGTGTGTGTGTGTGTGTGT 1053
 339 ThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyThrLeuProProSer 358
 1054 CCGGATGAGTACCAAGAACAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1113
 359 ArgAspGluLeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyPro 378
 1114 ACAGCATCGCTGGAGTGGAGAGCAATGGCAGCGGAGCAACAACTACAGACCAACG 1173
 379 SerAspIleAlaValGluTrpGlnSerAsnGlyGlnProGluAsnTyLysThrThr 398
 1174 CTTCCCGTCTGCTGACTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1233
 399 ProProValLeuAspSerAspGlySerPhePheLeuTySerLysLeuThrValAspLys 418
 1234 ACAGTGTGACAGCGGAGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1293
 419 SerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsn 438
 1294 CACTACAGCAGAGAGCT 1332
 439 HisTyThrGlnLysSerLeuSerLeuSerProGlyLys 451

RESULT 12

US-09-848-832-3
 ; Sequence 3, Application US/09848832
 ; Publication No. US20030165507A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hooper, Douglas
 ; APPLICANT: Dietzschold, Bernhard
 ; TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN
 ; MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
 ; FILE REFERENCE: H0001.NP0002
 ; CURRENT APPLICATION NUMBER: US/09/848,832
 ; CURRENT FILING DATE: 2001-05-04

; PRIOR APPLICATION NUMBER: 60/204,518
 ; PRIOR FILING DATE: 2000-05-16
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 474
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-848-832-3

Alignment Scores:
 Pred. No.: 1,1e-132 Length: 474
 Score: 2172.50 Matches: 411
 Percent Similarity: 93.22% Conservative: 15
 Best Local Similarity: 89.93% Mismatches: 16
 Query Match: 90.33% Indels: 15
 DB: 10 Gaps: 2

US-09-674-716B-18 (1-1335) x US-09-848-832-3 (1-474)

QY 1 GAGTCCAGCTGTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
 Db 20 GluValGlnLeuLeuGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
 QY 61 TCCTGTGCACTAGCGATTCACTTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT 120
 Db 40 SerCysAlaAlaSerGlyPheThrPheSerAsnTyAlaMetSerTrpValArgGlnAla 59
 QY 121 CGAGGAGGGCTCAGTGGGTTCGTAATTAGATTGAAATCTGATAATTATGCAACA 180
 Db 60 ProGlyLysGlyLeuGluTrpValSerAlaIle-----SerAlaSerGlyHisSerThr 77
 QY 181 CATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCATAATCTAGA 240
 Db 78 TyrLeuAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 97
 QY 241 CTGTATCTGCAATGAACAGCCCTGAAACCGAGGACACAGCCGTGTATTACTGTACA--- 297
 Db 98 LeuTyLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyTyCysAlaLys 117
 QY 298 -----GATTTCATAGACTGGGGCCAGGGA 321
 Db 118 AspArgGluValThrMetIleValLeuAsnGlyGlyPheAspTyTrpGlyGlnGly 137
 QY 322 ACCTAGTACCGTCTCTCAGCTCCACCAAGGGGCCATCGGTCTTCCCTCCCTGGGACCC 381
 Db 138 ThrArgValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaPro 157
 QY 382 TCCTCCAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
 Db 158 SerSerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyPhe 177
 QY 442 CCCGAACCGGTGACGGTGTCTGGAATCTCAGGGCCCTGACAGCGCGCTGCACACCTTC 501
 Db 178 ProGluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhe 197
 QY 502 CCGCTGTCTTACAGTCTCCTCAGGACTCTACTCCTCAGCAGCGTGTGTGACGCTGCCCTCC 561
 Db 198 ProAlaValLeuGlnSerSerGlyLeuTySerLeuSerValValThrValProSer 217
 QY 562 AGCAGCTTGGCACCCAGACTCATCTCAACCTGAATCACAAGCCCAAGCCCAACCAAG 621
 Db 218 SerSerLeuGlyThrGlnThrTyIleCysAsnValAsnHisLysProSerAsnThrLys 237
 QY 622 GTGACCAAGAAAGTGGAGCCCAATCTGTGACAAAACCTCACATGCCACCGTGGCCCA 681
 Db 238 ValAspLysArgValGluProLysSerCysAspLysThrHisThrCysProProCysPro 257
 QY 682 GCACCTGACTCGCGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 741
 Db 258 AlaProGluLeuLeuGlyGlyProSerValPheLeuPheProLysProLysAspThr 277
 QY 742 CTCATGATCTCCCGGACCCCTGAGGTGCATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 801

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:29:27 ; Search time 16.4527 Seconds
(without alignments)
4852.647 Million cell updates/sec

Title: US-09-674-716B-1
Perfect score: 753
Sequence: 1 aagctttacagtactacgc.....tggggccaaggacactagt 415

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/cpn2.1/USPTO.spool.p/US09674716/runat 30092004 070259 25882/app.query.fasta_1.3164
-DB=PIR 78 -QFMT=fasta -SUFFIX=rpr -MINMATCH=0.1 -LOOCL=0 -LOOPEXT=0
-UNITS=BITS -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09674716 @CGN 1.1.152 @runat 30092004 070259 25882 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query No. | Score | Match | Length | DB ID | Description |
|------------|-----------|-------|-------|--------|--------|--------------------|
| 1 | 519 | 68.9 | 115 | 2 | S38714 | Ig heavy chain v r |
| 2 | 518 | 68.8 | 139 | 2 | PC1213 | Ig heavy chain pre |
| 3 | 518 | 68.8 | 139 | 2 | G29380 | Ig heavy chain pre |
| 4 | 517.5 | 68.7 | 115 | 1 | AVMS06 | Ig heavy chain v-i |
| 5 | 515.5 | 68.5 | 113 | 1 | AVMSAB | Ig heavy chain v-i |
| 6 | 515.5 | 68.5 | 113 | 1 | AVMSG1 | Ig heavy chain v-i |
| 7 | 514.5 | 68.3 | 125 | 2 | S67945 | Ig heavy chain BrE |
| 8 | 510.5 | 67.8 | 115 | 2 | A25803 | Ig heavy chain v r |
| 9 | 509.5 | 67.7 | 113 | 1 | AVMSB7 | Ig heavy chain v-i |
| 10 | 507.5 | 67.4 | 113 | 1 | AVMS7 | Ig heavy chain v-i |
| 11 | 506.5 | 67.3 | 115 | 1 | AVMS82 | Ig heavy chain v-i |
| 12 | 505.5 | 67.1 | 113 | 1 | AVMS09 | Ig heavy chain v-i |
| 13 | 498 | 66.1 | 106 | 2 | S24521 | Ig heavy chain v r |
| 14 | 496.5 | 65.9 | 113 | 1 | HVMSAM | Ig heavy chain v r |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 15 | 495 | 65.7 | 137 | 2 | D34903 | Ig heavy chain pre |
| 16 | 492 | 65.3 | 137 | 2 | B34903 | Ig heavy chain pre |
| 17 | 479 | 63.6 | 137 | 2 | F34903 | Ig heavy chain pre |
| 18 | 469 | 62.3 | 137 | 2 | A34903 | Ig heavy chain pre |
| 19 | 468 | 62.2 | 111 | 1 | MMMS76 | Ig heavy chain v-i |
| 20 | 465.5 | 62.0 | 142 | 1 | EVRTK2 | Ig heavy chain pre |
| 21 | 463 | 61.5 | 137 | 2 | E34903 | Ig heavy chain pre |
| 22 | 453.5 | 60.2 | 121 | 2 | S09958 | Ig heavy chain v-D |
| 23 | 449.5 | 59.7 | 138 | 2 | A30561 | Ig heavy chain pre |
| 24 | 446 | 59.2 | 116 | 2 | H29380 | Ig heavy chain pre |
| 25 | 446 | 59.2 | 118 | 2 | A31485 | Ig heavy chain v r |
| 26 | 443 | 58.8 | 136 | 2 | S31587 | Ig heavy chain v r |
| 27 | 442.5 | 58.8 | 139 | 2 | S31678 | Ig heavy chain v r |
| 28 | 440.5 | 58.5 | 139 | 2 | I37781 | Ig variable region |
| 29 | 439.5 | 58.4 | 140 | 2 | S31588 | Ig heavy chain v r |
| 30 | 439 | 58.3 | 101 | 2 | S26460 | Ig heavy chain v r |
| 31 | 438 | 58.2 | 140 | 2 | S70442 | Ig heavy chain pre |
| 32 | 433.5 | 57.6 | 138 | 2 | S31666 | Ig heavy chain v r |
| 33 | 433.5 | 57.6 | 140 | 2 | S22857 | Ig heavy chain pre |
| 34 | 432 | 57.4 | 147 | 2 | I37780 | Ig variable region |
| 35 | 431 | 57.2 | 132 | 2 | PH1289 | Ig heavy chain pre |
| 36 | 430 | 57.1 | 119 | 2 | S31591 | Ig heavy chain v r |
| 37 | 430 | 57.1 | 137 | 2 | S42467 | Ig heavy chain v r |
| 38 | 429.5 | 57.0 | 134 | 2 | S31699 | Ig heavy chain v r |
| 39 | 427.5 | 56.8 | 138 | 2 | S09258 | Ig heavy chain v r |
| 40 | 427.5 | 56.8 | 140 | 2 | S31686 | Ig heavy chain v r |
| 41 | 427.5 | 56.8 | 160 | 2 | S05271 | Ig heavy chain pre |
| 42 | 427 | 56.7 | 119 | 2 | PH1293 | Ig heavy chain pre |
| 43 | 425.5 | 56.5 | 140 | 2 | A30532 | Ig heavy chain pre |
| 44 | 424 | 56.3 | 133 | 2 | PH1288 | Ig heavy chain pre |
| 45 | 423.5 | 56.2 | 135 | 2 | S31598 | Ig heavy chain v r |

ALIGNMENTS

RESULT 1
S38714
Ig heavy chain v region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C/Accession: S38714
R:Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38713
A:Accession: S38714
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <C1M>
A/Cross-references: EMBL:X76014; NID:G416092; PIDN:CAA53601.1; PID:G1334076
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-99/Domain: immunoglobulin homology <IMV>

Alignment Scores:
Pred. No.: 2,31e-43 Length: 115
Score: 519.00 Matches: 99
Percent Similarity: 92.79% Conservative: 4
Best Local Similarity: 89.19% Mismatches: 2
Query Match: 68.92% Indels: 6
DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) x S38714 (1-115)

| | | | |
|----|-----|---|-----|
| QY | 90 | GTGAAGCTTGAGGAGTCTGGAGGAGGCTTGTCACACCTGGAGGATCCATGAACCTCTCC | 149 |
| Db | 1 | VallyLeuValGluSerGlyGlyLeuValGlnProGlyGlySerMetIysLeuSer | 20 |
| QY | 150 | TGTTGAGCTCTGGAGTTACTTTCAGTGGCTCTGATCTCTGGGTCGCCAGTCTCCA | 209 |
| Db | 21 | CysValAlaSerGlyPheThrPheSerSerTyTrpMetSerTrpValArgIlnSerPro | 40 |
| QY | 210 | GAGAAGGGCTTGAGTGGGTTCTGAAATAGATTCAATCTGATAATATTCACACAT | 269 |

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Db 41 GluLysGlyLeuGluTrpIleAlaGluLeuArgLeuLysSerAspAsnTyrAlaThrHis 60
QY 270 TATGGGAGTCTGTGAAGGAGAGTTCACCATCTCAAGAGATGATTCCTCAAGAGTCTGTC 329
Db 61 TyrAlaGluSerValLysGlyPheThrIleSerArgAspSerLysSerArgLeu 80
QY 330 TACCTGCAATGACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA----- 383
Db 81 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrGlyIleTyrTyrCysThrAlaArg 100
QY 384 -----GATTTCATAGACTGGGGCCAAAGGACCA 410
Db 101 LeuGlyAspTyr-----TrpGlyGlnGlyThr 109
RESULT 2
PC1213
Ig heavy chain precursor V region (mAb H8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Jul-1999
C:Accession: PC1213
R:Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim,
Gene 121, 331-335, 1992
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m
A:Reference number: PC1213; MUID:93077049; PMID:1446832
A:Accession: PC1213
A:Molecule type: mRNA
A:Residues: 1-139 <HON>
A:Cross-references: GB:M98041; NID:G195092; PIDN:AAA38159, 1; PID:G195093
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Product: Ig heavy chain V region #status predicted <MAT>
F:134-119/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2,92e-43 Length: 139
Score: 518.00 Matches: 101
Percent Similarity: 82.84% Conservative: 15
Best Local Similarity: 75.37% Mismatches: 15
Query Match: 68.79% Indels: 8
DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) x PC1213 (1-139)
QY 36 ATGGATTTGGGCTG-----ATTTTATTATTGTTCTTTTAAAGGGCTCCAGAGTGA 89
Db 1 MetTyrLeuGlyLeuAsnTyrValPheIleValPheLeuLeuAsnGlyValGlnSerGlu 20
QY 90 GTGAAGCTTGAGGAGTCTGGAGGAGGCTTGTCGAACCTGGAGGATCCATGAAGACTCTCC 149
Db 21 ValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
QY 150 TGTGTAGCTCTGATTTACTTTTCTGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTC 209
Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60
QY 210 GAGAGGGGCTTGAGTGGGCTGCTGAAATAGATTTGAAATCTGATAATATGCAACACAT 269
Db 61 GluLysGlyLeuGluTrpValAlaGluLeuArgSerLysAlaHisAsnHisAlaThrTyr 80
QY 270 TATGGGAGTCTGTGAAGGAGGATTCACCATCTCAAGAGATGATTCCTCAAGAGTCTGTC 329
Db 81 TyrThrGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerAsnVal 100
QY 330 TACCTGCAATGACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA----- 383
Db 101 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrGlyIleTyrTyrCysThrArgasp 120
QY 384 -----GATTTCATAGACTGGGGCCAAAGGACCACTA 413
Db 121 TyrTyrGlyAlaGluPheAlaTyrTrpGlyGlnGlyThrLeu 134
RESULT 4
AVMS06
Ig heavy chain V-III region (J606) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: C92811; A02072
R:Johnson, N.; Slankard, J.; Paul, L.; Hood, L.
J. Immunol. 128, 302-307, 1982
A:Title: The complete V domain amino acid sequences of two myeloma inulin-binding protein
A:Reference number: A92811; MUID:82099361; PMID:6798111
A:Accession: C92811
A:Molecule type: protein
A:Residues: 1-115 <JOH>
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

```

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G29380
Ig heavy chain precursor V region (BC-1004) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Aug-1996
C:Accession: G29380
R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
A:Reference number: A92612; MUID:8807592; PMID:3115981
A:Accession: G29380
A:Molecule type: mRNA
A:Residues: 1-139 <CHE>
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:134-119/Domain: immunoglobulin homology <IMM>

```

```

Alignment Scores:
Pred. No.: 2,92e-43 Length: 139
Score: 518.00 Matches: 100
Percent Similarity: 82.84% Conservative: 11
Best Local Similarity: 74.63% Mismatches: 15
Query Match: 68.79% Indels: 8
DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) x G29380 (1-139)
QY 36 ATGGATTTGGGCTG-----ATTTTATTATTGTTCTTTTAAAGGGCTCCAGAGTGA 89
Db 1 MetTyrLeuGlyLeuAsnTyrValPheIleValPheLeuLeuAsnGlyValGlnSerGlu 20
QY 90 GTGAAGCTTGAGGAGTCTGGAGGAGGCTTGTCGAACCTGGAGGATCCATGAAGACTCTCC 149
Db 21 ValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
QY 150 TGTGTAGCTCTGATTTACTTTTCTGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTC 209
Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60
QY 210 GAGAGGGGCTTGAGTGGGCTGCTGAAATAGATTTGAAATCTGATAATATGCAACACAT 269
Db 61 GluLysGlyLeuGluTrpValAlaGluLeuArgSerLysAlaHisAsnHisAlaThrTyr 80
QY 270 TATGGGAGTCTGTGAAGGAGGATTCACCATCTCAAGAGATGATTCCTCAAGAGTCTGTC 329
Db 81 TyrThrGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerAsnVal 100
QY 330 TACCTGCAATGACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA----- 383
Db 101 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrGlyIleTyrTyrCysThrArgasp 120
QY 384 -----GATTTCATAGACTGGGGCCAAAGGACCACTA 413
Db 121 TyrTyrGlyAlaGluPheAlaTyrTrpGlyGlnGlyThrLeu 134
RESULT 4
AVMS06
Ig heavy chain V-III region (J606) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: C92811; A02072
R:Johnson, N.; Slankard, J.; Paul, L.; Hood, L.
J. Immunol. 128, 302-307, 1982
A:Title: The complete V domain amino acid sequences of two myeloma inulin-binding protein
A:Reference number: A92811; MUID:82099361; PMID:6798111
A:Accession: C92811
A:Molecule type: protein
A:Residues: 1-115 <JOH>
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

```

Alignment Scores:
 Pred. No.: 3,266-43 Length: 115
 Score: 517.50 Matches: 97
 Percent Similarity: 94.55% Conservative: 7
 Best Local Similarity: 88.18% Mismatches: 5
 Query Match: 68.73% Indels: 1
 DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x AVMS06 (1-115)

QY 87 GAAGTGAAGCTTGAGGAGCTTGGAGAGGCTTGGTGAACCTGGAGGATCCATGAATC 146
 |||||
 Db 1 GluValLysLeuGluGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
 |||||
 QY 147 TCCTGTGAGCTCTGGATTACTTTTCACTGCTACTCGATGCTCTGGTCCGCGAGTCT 206
 |||||
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyTrpMetAsnTrpValArgGlnSer 40
 |||||
 QY 207 CCAGAGAGGGCTTGAGTGGTGGCTGAATTAAGATTGAATCTGATATATGCAACA 265
 |||||
 Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnAsnTyAlaThr 60
 |||||
 QY 267 CATTATGCGAGTCTGTCGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 326
 |||||
 Db 61 HistyAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
 |||||
 QY 327 CTCTACCTGCAATGAACAGCTTAAGCTGAAGACAGTGGAGTCTTATTACTGT---ACA 383
 |||||
 Db 81 ValTyLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyTrpCysThrThr 100
 |||||
 QY 384 GATTTCATAGACTGGGGCCAAAGGACACTA 413
 |||||
 Db 101 GlyPheAlaTyTrpGlyGlnGlyThrLeu 110
 |||||

RESULT 5

AVMSAB
 Ig heavy chain V-III region (A4) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 31-Mar-1997
 C/Accession: A93818, A02072
 Rivrana, M.; Rudikoff, S.; Potter, M.
 Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
 A/Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
 A/Reference number: A93818; MUID:78158406; PMID:417344
 A/Accession: A93818
 A/Molecule type: protein
 A/Residues: 1-113 <VRA>
 C/Comment: This chain was isolated from a myeloma protein that binds inulin.
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:15-100/Domain: immunoglobulin homology <IMM>
 F:22-98/Disulfide bonds: #status predicted

Alignment Scores:
 Pred. No.: 5,146-43 Length: 113
 Score: 515.50 Matches: 97
 Percent Similarity: 93.64% Conservative: 6
 Best Local Similarity: 88.18% Mismatches: 6
 Query Match: 68.46% Indels: 1
 DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x AVMSAB (1-113)

QY 87 GAAGTGAAGCTTGAGGAGCTTGGAGAGGCTTGGTGAACCTGGAGGATCCATGAATC 146
 |||||
 Db 1 GluValLysLeuGluGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
 |||||
 QY 147 TCCTGTGAGCTCTGGATTACTTTTCACTGCTACTCGATGCTCTGGTCCGCGAGTCT 206
 |||||
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyTrpMetAsnTrpValArgGlnSer 40
 |||||
 QY 207 CCAGAGAGGGCTTGAGTGGTGGCTGAATTAAGATTGAATCTGATATATGCAACA 265
 |||||

Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyAlaThr 60
 |||||
 QY 267 CATTATGCGAGTCTGTCGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 326
 |||||
 Db 61 HistyAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
 |||||
 QY 327 CTCTACCTGCAATGAACAGCTTAAGCTGAAGACAGTGGAGTCTTATTACTGT---ACA 383
 |||||
 Db 81 ValTyLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyTrpCysThrThr 100
 |||||
 QY 384 GATTTCATAGACTGGGGCCAAAGGACACTA 413
 |||||
 Db 101 GlyPheAlaTyTrpGlyGlnGlyThrLeu 110
 |||||

RESULT 6

AVMS61
 Ig heavy chain V-III region (U61) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
 C/Accession: B93818, A02072
 Rivrana, M.; Rudikoff, S.; Potter, M.
 Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
 A/Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
 A/Reference number: A93818; MUID:78158406; PMID:417344
 A/Accession: B93818
 A/Molecule type: protein
 A/Residues: 1-113 <VRA>
 C/Comment: This chain was isolated from a myeloma protein that binds inulin.
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:15-100/Domain: immunoglobulin homology <IMM>
 F:22-98/Disulfide bonds: #status predicted

Alignment Scores:

Pred. No.: 5,146-43 Length: 113
 Score: 515.50 Matches: 97
 Percent Similarity: 93.64% Conservative: 6
 Best Local Similarity: 88.18% Mismatches: 6
 Query Match: 68.46% Indels: 1
 DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x AVMS61 (1-113)

QY 87 GAAGTGAAGCTTGAGGAGCTTGGAGAGGCTTGGTGAACCTGGAGGATCCATGAATC 146
 |||||
 Db 1 GluValLysLeuGluGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
 |||||
 QY 147 TCCTGTGAGCTCTGGATTACTTTTCACTGCTACTCGATGCTCTGGTCCGCGAGTCT 206
 |||||
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyTrpMetAsnTrpValArgGlnSer 40
 |||||
 QY 207 CCAGAGAGGGCTTGAGTGGTGGCTGAATTAAGATTGAATCTGATATATGCAACA 266
 |||||
 Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyAlaThr 60
 |||||
 QY 267 CATTATGCGAGTCTGTCGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGT 326
 |||||
 Db 61 HistyAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
 |||||
 QY 327 CTCTACCTGCAATGAACAGCTTAAGCTGAAGACAGTGGAGTCTTATTACTGT---ACA 383
 |||||
 Db 81 ValTyLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyTrpCysThrThr 100
 |||||

RESULT 7

S67945
 Ig heavy chain BrE-3 - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C/Accession: S67945


```

QY 384 GATTTCATAGACTGGGGCCAGGGACACTA 413
DB 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 10
AVMS57
Ig heavy chain V-III region (T957) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: A92810; A02072
R:Rudikoff, S.; Potter, M.
J. Immunol. 127, 191-194, 1981
A:Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a n
A:Reference number: A92810; MUID:81216632; PMID:6787122
A:Accession: A92810
A:Molecule type: protein
A:Residues: 1-113 <RUD>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 3,19e-42 Length: 113
Score: 507.50 Matches: 96
Percent Similarity: 91.82% Conservative: 5
Best Local Similarity: 87.27% Mismatches: 8
Query Match: 67.40% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x AVMS57 (1-113)

QY 87 GAAGTGAAGCTTGAGGAGCTTGAGGAGGCTTGTCGAACCTGGAGGATCCATGAACCTC 146
DB 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20

QY 147 TCCTGTGTAGCTCTGGATTACTTTCAGTGGCTACTGATGCTTGGGTCGCCAGTCT 206
DB 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40

QY 207 CCAGAGAAGGGCTTCAGTGGCTTGAATAGATTGAAATCTCTGATAATATGCAACA 266
DB 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60

QY 267 CATTTGCGGAGTCTCTGAAAGGAAAGTTCACCATCTCAAGAGATGATTCGAAAGTCT 326
DB 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspAspSerLysSer 80

QY 327 CTCTACTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTGTATTACTGT---ACA 383
DB 81 ValTyrLeuArgMetAsnAsnLeuArgProGluAspThrGlyIleTyrCysThrThr 100

RESULT 11
AVMS82
Ig heavy chain V-III region (W3082) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: D92811; A02072
R:Johnson, N.; Slankard, J.; Paul, L.; Hood, L.
J. Immunol. 128, 302-307, 1982
A:Title: The complete V domain amino acid sequences of two myeloma inulin-binding protei
A:Reference number: A92811; MUID:8209361; PMID:6798111
A:Accession: D92811
A:Molecule type: protein
A:Residues: 1-115 <JOH>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

```

```

F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 4.01e-42 Length: 115
Score: 506.50 Matches: 95
Percent Similarity: 92.73% Conservative: 7
Best Local Similarity: 86.36% Mismatches: 7
Query Match: 67.26% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x AVMS82 (1-115)

QY 87 GAAGTGAAGCTTGAGGAGCTTGAGGAGGCTTGTCGAACCTGGAGGATCCATGAACCTC 146
DB 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20

QY 147 TCCTGTGTAGCTCTGGATTACTTTCAGTGGCTACTGATGCTTGGGTCGCCAGTCT 206
DB 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40

QY 207 CCAGAGAAGGGCTTCAGTGGCTTGAATAGATTGAAATCTCTGATAATATGCAACA 266
DB 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60

QY 267 CATTTGCGGAGTCTCTGAAAGGAAAGTTCACCATCTCAAGAGATGATTCGAAAGTCT 326
DB 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspAspSerLysSer 80

QY 327 CTCTACTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTGTATTACTGT---ACA 383
DB 81 ValTyrLeuArgMetAsnAsnLeuArgProGluAspThrGlyIleTyrCysThrThr 100

RESULT 12
AVMS09
Ig heavy chain V-III region (B109) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: C93818; A02072
R:Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A:Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A:Reference number: A93818; MUID:78158406; PMID:417344
A:Accession: C93818
A:Molecule type: protein
A:Residues: 1-113 <VRA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 5.03e-42 Length: 113
Score: 505.50 Matches: 94
Percent Similarity: 93.64% Conservative: 9
Best Local Similarity: 85.45% Mismatches: 6
Query Match: 67.13% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x AVMS09 (1-113)

QY 87 GAAGTGAAGCTTGAGGAGCTTGAGGAGGCTTGTCGAACCTGGAGGATCCATGAACCTC 146
DB 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20

QY 147 TCCTGTGTAGCTCTGGATTACTTTCAGTGGCTACTGATGCTTGGGTCGCCAGTCT 206
DB 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40

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QY 207 CCAGAGAGGGGCTTGAAGTGGTCTGCTGAAATAGATTGAATCTGATAATTATGCAACA 266
 Db 41 ProGluLysGlyLeuGluTrpPheAlaGluLeuLeuValGlnProGlyArgSerMetLysLeu 60
 QY 267 CATTATCGGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 326
 Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSer 80
 QY 327 CTTCTACCTGCAAAATCAAGCAGCTTAAGAGCTGAAGAGCTGGAGTTATTACTGT---ACA 383
 Db 81 ValPheLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleHisTyrCysThr 100
 QY 384 GATTTCATAGACTGGGGCCAAAGGACACTA 413
 Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110
 RESULT 13
 IG heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S24521
 R:Kaartinen, M.
 submitted to the EMBL Data Library, October 1991
 A:Reference number: S24490
 A:Accession: S24521
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-106 <XAA>
 A:Cross-references: EMBL:X66664; NID:G51247; PIDN:CAA47226.1; PID:G51248
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:21-106/Domain: immunoglobulin homology <IMM>
 Alignment Scores:
 Pred. No.: 2,78e-41 Length: 106
 Score: 498.00 Matches: 92
 Percent Similarity: 96.19% Conservative: 9
 Best Local Similarity: 87.62% Mismatches: 4
 Query Match: 66.14% Indels: 0
 DB: 2 Gaps: 0
 US-09-674-716B-1 (1-415) x S24521 (1-106)
 QY 69 TTAAAGGGGCTCCAGAGTGAAGTGAAGCTTGAGAGTCTGAGAGGCTTGGTGAACCT 128
 Db 1 LeuLysGlyValGlnSerGluValLysLeuValGluSerGlyGlyLeuValGlnPro 20
 QY 129 GGAGATCCATGAACCTCCCTGCTAGCTCTGATTTACTTTCAGTGGCTACTGGATG 188
 Db 21 GlyGlySerMetLysLeuSerCysValAlaSerGlyPheThrPheAsnTyrTyrTrpMet 40
 QY 189 TCTTGGGTCGGCAGCTCCAGAGAGGGGCTTGAGTGGTTCCTGAAATAGATTGAAA 248
 Db 41 AsnTrpValArgGlnSerProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLys 60
 QY 249 TGTGATAATTATGCAACATATTGCGGAGTCTGAAAGGAAGTTCACCATCTCAAGA 308
 Db 61 SerAsnAsnTyrAlaThrHisTyrAlaGluSerValLysGlyArgPheThrIleSerArg 80
 QY 309 GATGATTCAAAAGTCTCTCTACTCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGA 368
 Db 81 AspAspSerLysSerSerValTyrLeuGlnMetAsnAsnPheArgSerGluAspThrGly 100
 QY 369 GTTATTACTGTACA 383
 Db 101 IleTyrTyrCysThr 105
 RESULT 14
 HVMSAM
 IG heavy chain V region (AMPC1) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 31-Mar-1997
 C:Accession: A02073
 R:Rudikoff, S.; Potter, M.
 J. Immunol. 127, 191-194, 1981
 A:Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a ne
 A:Reference number: A92810; MUID:81216632; PMID:6787122
 A:Accession: A02073
 A:Molecule type: protein
 A:Residues: 1-113 <RUD>
 C:Comment: This chain was isolated from a myeloma protein that binds inulin.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-100/Domain: immunoglobulin homology <IMM>
 F:22-98/Disulfide bonds: #status predicted
 Alignment Scores:
 Pred. No.: 3.92e-41 Length: 113
 Score: 496.50 Matches: 94
 Percent Similarity: 90.91% Conservative: 6
 Best Local Similarity: 85.45% Mismatches: 9
 Query Match: 65.94% Indels: 1
 DB: 1 Gaps: 1
 US-09-674-716B-1 (1-415) x HVMSAM (1-113)
 QY 87 GAAGTGAAGCTTGAGAGTCTGAGAGGCTTGTCACACCTGGAGGATCCATGAACTC 146
 Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyArgSerMetLysLeu 20
 QY 147 TCTGTGTAGCTCTGCTGATTTACTTTCAGTGGCTACTGATCTTGGTCCGCGAGTCT 206
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
 QY 207 CCAGAGAGGGGCTTGAGTGGTTCGTAATAGATTGAATCTGATTAATATGCAACA 266
 Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaIle 60
 QY 267 CATTATCGGGAGTCTGTAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCT 326
 Db 61 HisTyrAlaGlnSerValLysGlyArgPheThrIleSerArgAspSerLysSer 80
 QY 327 CTCTACTGCAAAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTTATTACTGT---ACA 383
 Db 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysSerThr 100
 QY 384 GATTTCATAGACTGGGGCCAAAGGACACTA 413
 Db 101 GlyPheProSerTrpGlyProGlyThrLeu 110
 RESULT 15
 D34903
 IG heavy chain precursor V region (9-40) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 23-Jul-1999
 C:Accession: D34903
 R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
 J. Biol. Chem. 265, 133-138, 1990
 A:Title: Active site structure and antigen binding properties of idiotypically cross-reac
 A:Reference number: A34903; MUID:90094387; PMID:2104617
 A:Accession: D34903
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-137 <BED>
 A:Cross-references: GB:M32378; GB:J05237; GB:J05238; NID:G639652; PIDN:AAA61587.1; PID:Gt
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-119/Domain: immunoglobulin homology <IMM>
 Alignment Scores:
 Pred. No.: 5.55e-41 Length: 137
 Score: 495.00 Matches: 95
 Percent Similarity: 82.58% Conservative: 14
 Best Local Similarity: 71.97% Mismatches: 17

```

Query Match:      65.74%      Indels:      6
DB:               2          Gaps:        2
US-09-674-716B-1 (1-415) x D34903 (1-137)

QY  36 ATGGATTTGGCTG-----ATTTTATTATGTTCTTTTAAAGGGGTCCACAGTGAA 89
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  1 MetTyrLeuGlyLeuSerCysValPheIleValPheLeuLeuLysGlyValGlnCysGlu 20
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  90 GTGAAGCTTGAGGAGCTCTGGAGGAGCTTGTCACCTGGAGGATCCATGAAACTCTCC 149
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  21 VallysLeuAspGluThrGlyGlyLeuValGlnProGlyArgProMetLysLeuSer 40
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  150 TGTGTAGCCTCTGGATTACTTTAGTGGCTACTGGATGTCCTTGGTCCGCCACTCTCCA 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  41 CysValAlaSerGlyPheThrPheSerAspTyrTrpMetAsnTrpValArgGlnSerPro 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  210 GAGTAGGGGCTTGAGTGGGTTCGCAATTAGATTGAATCTGATTAATTATGCAACACAT 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  61 GluLysGlyLeuGluTrpValAlaGlnIleArgAsnLysProTyrAsnTyrGluThrTyr 80
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  270 TATCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAGAGAGATGATCCAAAAGTCGTCTC 329
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  81 TyrSerAspSerValLysGlyArgPheThrIleSerArgAspSerLysSerSerVal 100
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  330 TACCTGCAANTGACAGCTTAAGAGCTGACAGACAGAGTGGAGTTTATTACTGTACAGATTTC 389
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  101 TyrLeuGlnMetAsnAsnLeuArgAlaGluAspMetGlyIleTyrTyrCysThrSerTyr 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  390 -----ATAGACTGGGGCCAGGGACACTA 413
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  121 GlyTyrHisGlyAlaTyrTrpGlyGlnGlyThrLeu 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: September 30, 2004, 08:56:59
Job time : 18.4527 secs

Blank sheet

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:20:22 ; Search time 9.00395 Seconds
(without alignments)
4799.922 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 753

Sequence: 1 aagctttacagttactcagc.....tggggccaaaggacactagt 415

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2.1/USPTO spool p/US09674716/runat 30092004 070257 25855/app query.fasta_1.3164
-DB=SwissProt 42-QFMT=fastan -SUFFIX=rs -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09674716 @CGN 1.1 82 @runat 30092004 070257 25855 -NCPU=6 -ICPU=3
-NO.WMAP -LARGQQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 517.5 | 69.7 | 115 | 1 HV32_MOUSE | P01801 mus musculus |
| 2 | 515.5 | 68.5 | 113 | 1 HV27_MOUSE | P01796 mus musculus |
| 3 | 515.5 | 68.5 | 113 | 1 HV28_MOUSE | P01797 mus musculus |
| 4 | 509.5 | 67.7 | 113 | 1 HV30_MOUSE | P01799 mus musculus |
| 5 | 507.5 | 67.4 | 113 | 1 HV31_MOUSE | P01800 mus musculus |
| 6 | 506.5 | 67.3 | 115 | 1 HV31_MOUSE | P01802 mus musculus |
| 7 | 505.5 | 67.1 | 113 | 1 HV29_MOUSE | P01798 mus musculus |
| 8 | 496.5 | 65.9 | 113 | 1 HV34_MOUSE | P01803 mus musculus |
| 9 | 468 | 62.2 | 111 | 1 HV35_MOUSE | P01804 mus musculus |
| 10 | 466.5 | 62.0 | 142 | 1 HV01_RAT | P01805 rattus norv |
| 11 | 412 | 54.7 | 117 | 1 HV36_MOUSE | P01764 homo sapien |
| 12 | 410.5 | 54.5 | 116 | 1 HV36_MOUSE | P01806 mus musculus |
| 13 | 405 | 53.8 | 136 | 1 HV16_MOUSE | P01783 mus musculus |
| 14 | 398.5 | 52.9 | 144 | 1 HV26_MOUSE | P01795 mus musculus |
| 15 | 396 | 52.6 | 117 | 1 HV54_MOUSE | P18523 mus musculus |
| 16 | 392.5 | 52.1 | 116 | 1 HV05_CARAU | P19181 carassius a |
| 17 | 387 | 51.4 | 117 | 1 HV59_MOUSE | P18530 mus musculus |
| 18 | 386.5 | 51.3 | 117 | 1 HV17_MOUSE | P01786 mus musculus |

ALIGNMENTS

RESULT 1
HV32_MOUSE STANDARD; PRT; 115 AA.
ID HV32_MOUSE
AC P01801;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=8209361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins".
RL J. Immunol. 128:302-307(1982).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; C92811; AVMS06.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT DOMAIN 1 114 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NONTER 115 115
SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;

Alignment Scores:

Pred. No.: 2,37e-51 Length: 115
Score: 517.50 Matches: 97
Percent Similarity: 94.55% Conservative: 7
Best Local Similarity: 88.18% Mismatches: 5
Query Match: 68.73% Indels: 1
DB: 1 Gaps: 1

P18526 mus musculus
P18529 mus musculus
P18524 mus musculus
P01790 mus musculus
P01791 mus musculus
P01766 homo sapien
P01789 mus sapien
P01768 homo sapien
P01787 mus musculus
P01798 mus musculus
P01794 mus musculus
P01792 mus musculus
P01807 mus musculus
P01810 mus musculus
P01770 homo sapien
P01775 homo sapien
P01793 mus musculus
P01771 homo sapien
P01808 mus musculus
P18527 mus musculus
P01763 homo sapien
P01774 homo sapien
P01765 homo sapien
P01811 mus musculus
P18528 mus musculus
P01781 homo sapien
P01785 canis famil

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US-09-674-716B-1 (1-415) x HV32_MOUSE (1-115)
QY 87 GAAGTGAAGCTTGAGAGCTCTGGAGAGCTGTGGCAACCTGGAGGATCCATGAATC 146
Db 1 GluValIysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetIysLeu 20
147 TCCTGTGTAGCCTCTGGATTACCTTTACCTTTCAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAGGGCTTGAGTGGTTCCTGAATTCAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAGGGCTTGAGTGGTTCCTGAATTCAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206
Db 41 ProGluIysGlyLeuGluTrpValAlaGluIleArgLeuLysSerHisAsnTyrAlaThr 60
QY 267 CATTATGCGGAGCTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 326
Db 61 HisTyrAlaGluSerValIysGlyArgPheThrIleSerArgAspSerIysSerSer 80
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT---ACA 383
Db 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrThr 100
QY 384 GATTTCATAGACTGGGGCCCAAGGGACACTA 413
Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 2
HV27_MOUSE
ID HV27_MOUSE STANDARD; PRT; 113 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region A4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RT proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93818; AVMSAB.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR ProSite; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 7658121C598285 CRC64;

Alignment Scores:
Pred. No.: 4,01e-51 Length: 113
Score: 515.50 Matches: 97
Percent Similarity: 93.64% Conservative: 6
Best Local Similarity: 88.18% Mismatches: 6
Query Match: 68.46% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x HV27_MOUSE (1-113)
QY 87 GAAGTGAAGCTTGAGAGCTCTGGAGAGCTGTGGCAACCTGGAGGATCCATGAATC 146
Db 1 GluValIysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetIysLeu 20
147 TCCTGTGTAGCCTCTGGATTACCTTTACCTTTCAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAGGGCTTGAGTGGTTCCTGAATTCAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAGGGCTTGAGTGGTTCCTGAATTCAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206
Db 41 ProGluIysGlyLeuGluTrpValAlaGluIleArgLeuLysSerHisAsnTyrAlaThr 60
QY 267 CATTATGCGGAGCTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 326
Db 61 HisTyrAlaGluSerValIysGlyArgPheThrIleSerArgAspSerIysSerSer 80
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGT---ACA 383
Db 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrThr 100
QY 384 GATTTCATAGACTGGGGCCCAAGGGACACTA 413
Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 3
HV28_MOUSE
ID HV28_MOUSE STANDARD; PRT; 113 AA.
AC P01797;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RT proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; B93818; AVMS61.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; Ig-like.
DR ProSite; PS00835; IG LIKE; 1.
DR SMART; SM00406; IGV; 1.
DR ProSite; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;

Alignment Scores:
Pred. No.: 4,01e-51 Length: 113
Score: 515.50 Matches: 97
Percent Similarity: 93.64% Conservative: 6
Best Local Similarity: 88.18% Mismatches: 6
Query Match: 68.46% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x HV28_MOUSE (1-113)
QY 87 GAAGTGAAGCTTGAGAGCTCTGGAGAGCTGTGGCAACCTGGAGGATCCATGAATC 146
Db 1 GluValIysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetIysLeu 20
147 TCCTGTGTAGCCTCTGGATTACCTTTACCTTTCAGTGGCTACTGGATCTCTGGTCCGCCAGTCT 206

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Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40
 QY 207 CCAGAGAGGGCTGAGTGGTTCGAAATAGATTGAATCTGATAATTATGCAACA 266
 Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60
 QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCCACCTCTCAAGAGATGATTCAAAAGTCGT 326
 Db 61 HistyAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
 QY 327 CTTCTACCTGCAATGAACAGCTTAAGAGCTCAAGAGATGATTCAAAAGTCGT 383
 Db 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrThr 100
 QY 384 GATTTCATAGACTGGGCGCAAGGACACTA 413
 Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 4
 HV30_MOUSE
 ID HV30_MOUSE STANDARD; PRT; 113 AA.
 AC P01799;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region ABE-47N.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77134726; PubMed=402936;
 RA Vrana M., Rudikoff S., Potter M.;
 RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
 protein.";
 RL Biochemistry 16:1170-1175(1977).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 BINDS INULIN.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A90400; AVMSB7.
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 >113 IG-LIKE.
 FT DISULFID 22 98 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Alignment Scores:
 Pred. No.: 1,966-50 Length: 113
 Score: 509.50 Matches: 96
 Percent Similarity: 92.73% Conservative: 6
 Best Local Similarity: 87.27% Mismatches: 7
 Query Match: 67.68% Indels: 1
 DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x HV30_MOUSE (1-113)

QY 87 GAAGTGAAGCTTGAGAGTCTGAGAGGCTTGGTGCACCTGGAGATCCATGAACCTC 146
 Db 1 GluValLysLeuGluLuserGlyGlyLeuValGlnProGlySerMetLysLeu 20
 QY 147 TCCTGTAGCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGTCCGCCAGTCT 206
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40
 QY 207 CCAGAGAGGGCTTGAGTGGTTCGAAATAGATTGAATCTGATAATTATGCAACA 266
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40
 QY 207 CCAGAGAGGGCTTGAGTGGTTCGAAATAGATTGAATCTGATAATTATGCAACA 266

Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60
 QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCCACCTCTCAAGAGATGATTCAAAAGTCGT 326
 Db 61 HistyAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
 QY 327 CTTCTACCTGCAATGAACAGCTTAAGAGCTCAAGAGATGATTCAAAAGTCGT 383
 Db 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrThr 100
 QY 384 GATTTCATAGACTGGGCGCAAGGACACTA 413
 Db 101 GlyPheAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 5
 HV31_MOUSE
 ID HV31_MOUSE STANDARD; PRT; 113 AA.
 AC P01800;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region T957.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81216632; PubMed=6787122;
 RA Rudikoff S., Potter M.;
 RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
 evidence for a new heavy chain joining segment.";
 RL J. Immunol. 127:191-194(1981).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 BINDS INULIN.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A92810; AVMS57.
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 >113 IG-LIKE.
 FT DISULFID 22 98 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12732 MW; 26618F626B59859E CRC64;

Alignment Scores:
 Pred. No.: 3,33e-50 Length: 113
 Score: 507.50 Matches: 96
 Percent Similarity: 91.82% Conservative: 5
 Best Local Similarity: 87.27% Mismatches: 8
 Query Match: 67.40% Indels: 1
 DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x HV31_MOUSE (1-113)

QY 87 GAAGTGAAGCTTGAGAGTCTGAGAGGCTTGGTGCACCTGGAGATCCATGAACCTC 146
 Db 1 GluValLysLeuGluLuserGlyGlyLeuValGlnProGlySerMetLysLeu 20
 QY 147 TCCTGTAGCTCTGGATTTACTTTCAGTGGCTACTGGATGTCTTGGTCCGCCAGTCT 206
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40
 QY 207 CCAGAGAGGGCTTGAGTGGTTCGAAATAGATTGAATCTGATAATTATGCAACA 266
 Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrGluThr 60
 QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCCACCTCTCAAGAGATGATTCAAAAGTCGT 326

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Db      61 HistyAlaGluSerVallysglyArgPheThrIleSerArgAspSerlySerSer 80
QY      327 CTCACCTCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATCTGT---ACA 383
Db      81 ValTyLeuGlnMetAsnIleLeuArgAlaGluAspThrGlyIleTyTy-CysThrThr 100
QY      384 GATTTCATAGACTGGGGCCAGGGACACTA 413
Db      101 GlyPheAlaTyTrpGlyGlnGlyThrLeu 110

RESULT 6
HV33_MOUSE
ID HV33_MOUSE STANDARD; PRT; 115 AA.
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Stankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; D92811; AVM882.
DR HSP; P01810; 2FBU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 114 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Alignment Scores:
Pred. No.: 4,366-50 Length: 115
Score: 506.50 Matches: 95
Percent Similarity: 92.73% Conservative: 7
Best Local Similarity: 86.38% Mismatches: 7
Query Match: 67.28% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x HV33_MOUSE (1-115)
QY 87 GAAGTGAAGCTTGAGAGCTTGAGAGAGCTTGTCGAACCTGGAGGATCCATGAATC 146
Db 1 GluVallyLeuGlnGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGATGCTCTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAAGGGCTTGAGTGGTTCCTCAATTAGATTAATCTGATAATATGCAACA 266
Db 41 ProGluLysGlyLeuGlnTrpValAlaGluIleArgLeuLysSerHisAsnTyAlaThr 60
QY 267 CATTATCGGAGCTCTGTGAAGGGAAGTTACCATCTCAAGAGATGATTCCTCAAAAGTCGT 326
Db 61 HistyAlaGluSerVallysglyArgPheThrIleSerArgAspSerlySerSer 80
QY 327 CTCACCTCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATCTGT---ACA 383

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Db      81 ValTyLeuArgMetAsnAsnLeuArgPrcGluAspThrGlyIleTyTy-CysThrThr 100
QY      384 GATTTCATAGACTGGGGCCAGGGACACTA 413
Db      101 GlyPheAlaTyTrpGlyGlnGlyThrLeu 110

RESULT 7
HV29_MOUSE
ID HV29_MOUSE STANDARD; PRT; 113 AA.
AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region E109.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RT proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; C93818; AVM509.
DR HSP; P01810; 2FBU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12647 MW; EE50F2F20EDB129B CRC64;

Alignment Scores:
Pred. No.: 5,666-50 Length: 113
Score: 505.50 Matches: 94
Percent Similarity: 93.64% Conservative: 9
Best Local Similarity: 85.45% Mismatches: 6
Query Match: 67.13% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x HV29_MOUSE (1-113)
QY 87 GAAGTGAAGCTTGAGAGCTTGAGAGAGCTTGTCGAACCTGGAGGATCCATGAATC 146
Db 1 GluVallyLeuGlnGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTAGCCTCTGGATTTACTTTCAGTGGCTACTGATGCTCTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAAGGGCTTGAGTGGTTCCTCAATTAGATTAATCTGATAATATGCAACA 266
Db 41 ProGluLysGlyLeuGlnTrpIleAlaGluIleArgLeuLysSerHisAsnTyAlaThr 60
QY 267 CATTATCGGAGCTCTGTGAAGGGAAGTTACCATCTCAAGAGATGATTCCTCAAAAGTCGT 326
Db 61 HistyAlaGluSerVallysglyArgPheThrIleSerArgAspSerlySerSer 80
QY 327 CTCACCTCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATCTGT---ACA 383
Db 81 ValPheLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleHisTyCysThrThr 100
QY 384 GATTTCATAGACTGGGGCCAGGGACACTA 413

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RESULT 9

Db 79 TyrGlyAspSerVallySgLYArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
QY 330 TACCTGCAAAATGACAGCTTAAGAGCTGAAGACAGCTGAGTTTATTACTGT 380
Db 99 TyrLeuGlnMetAsnSerLeuArgAlaGlnAspIlnzAlaValIlyrCys 115
RESULT 12
HV36_MOUSE
ID HV36_MOUSE STANDARD; PRT; 116 AA.
AC P01806;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region 441 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059449; PubMed=6795591;
RA Olio R., Auffray C., Sikorav J.-L., Rougeon F.;
RT "Mouse heavy chain variable regions: nucleotide sequence of a
RT germ-line VH gene segment";
RL Nucleic Acids Res. 9:4099-4109(1981).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
DR EMBL; V00774; CAA24152.1; -.
DR PIR; A02076; HVMS44.
DR HSSP; P01810; 2FEJ.
DR MGB; MGI:96432; Igh-VX24.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION 441.
FT DOMAIN 19 >116 IG-LIKE.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12911 MW; 684FF3EF9A95D9F3 CRC64;
Alignment Scores:
Pred. No.: 4,77e-39 Length: 116
Score: 410.50 Matches: 80
Percent Similarity: 81.03% Conservative: 14
Best Local Similarity: 68.97% Mismatches: 19
Query Match: 54.52% Indels: 3
DB: 1 Gaps: 2
US-09-674-716B-1 (1-415) x HV36_MOUSE (1-116)
QY 36 ATGGATTTGGCTGATTTTATTCTT---CTTTAAAGGGTCCAGAGTGAAGTG 92
Db 1 MetAspPheGlyLeuIlePhePheIleValAlaLeuLeuLeuGlyValGlnCysGluVal 20
QY 93 AAGCTTGAGGAGCTCGGAGGGCTTGGTGAACCTGGAGGATCCATGAACCTCTCTGT 152
Db 21 LysLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuLeuSerCys 40
QY 153 GTAGCTCTGGATTTACTTTTCAGTGGCTACCTGGATGCTTGGGTCGCGCAGTCTCCAGAG 212
Db 41 AlaAlaSerGlyPheAspPheSerArgTyrTrpMetSerTrpValArgGlnAlaProGly 60

QY 213 AAGGGCTTGAGTGGGTGCTGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCAT 272
Db 61 LysGlyLeuGluTrpIleGlyGluIle-----AsnProAspSerSerThrIleAsnTyr 78
QY 273 GCGAGTCTGTGAAGAGGAGTTCACCATCTCAAGAGATGATCCAAAGAGTCTCTCTAC 332
Db 79 ThrProSerLeuLysAspLysPheIleIleSerArgAspAsnAlaLysAsnThrLeuTyr 98
QY 333 CTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTGTATTACTGT 380
Db 99 LeuGlnMetSerLysValArgSerGluAspThrAlaLeuTyrTyrCys 114
RESULT 13
HV16_MOUSE
ID HV16_MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants";
RL Nature 265:299-304(1977).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00522; AAD15290.1; -.
DR PIR; E90809; GIMS21.
DR PDB; 1IGC; 03-JUN-95.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT NON_TER 1 1
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 2276A98DBDBF7016 CRC64;
Alignment Scores:
Pred. No.: 2,12e-38 Length: 136
Score: 405.00 Matches: 79

Percent Similarity: 74.81% Conservative: 19
 Best Local Similarity: 60.31% Mismatches: 19
 Query Match: 53.78% Indels: 14
 DB: 1 Gaps: 3

US-09-674-716B-1 (1-415) x HV16_MOUSE (1-136)

QY 48 CTGATTCTTTTATGTTCTTTAAAGGGTCCAGAGTGAAGTGAAGTCTGAGAGTCT 107
 Db 4 LeuValPheLeuValLeuLeuLeuValGlnCysAspValGlnLeuValGluSer 23
 QY 108 GGAGAGGGTTCGTCGCAACTCGAGAGTCCATGAAGTCTCTGTTGAGCCCTCTGGATT 167
 Db 24 GlyGlyGlyLeuValGlnProGlyGlySerArgLysLeuSerCysAlaAlaSerGlyPhe 43
 QY 169 ACTTTCAGTGGTACTGATGTTCTTGGTCCGCGAGTCCAGAGAGGGGCTTGAAGTG 227
 Db 44 ThrPheSerSerPheGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuGluTrp 63
 QY 228 GTTGCTGAATAGATTGAATCTCATATTATGCAACACATTAATGCGAGTCTGTGAAA 287
 Db 64 ValAlaTyrIle-----SerSerGlySerSerThrLeuHisTyrAlaAspThrValLys 81
 QY 288 GGAAGTTCACCATCTCAAGAGATGATCCAAAGTCTCTACCTCCAAATGAACAGC 347
 Db 82 GlyArgPheThrIleSerArgAspAsnProLysAsnThrLeuPheLeuGlnMetThrSer 101
 QY 348 TTAAGAGCTGAAGAGTGGAGTGTATTACTGTACA----- 383
 Db 102 LeuArgSerGluAspThrAlaMetTyrTyrCysAlaArgTrpGlyAsnTyrProTyrTyr 121
 QY 384 -----GATTTTCATAGACTGGGGCCCAAGGACA 410
 Db 122 AlaMetAspTyr-----TrpGlyGlnGlyThr 130

RESULT 14

HV26_MOUSE
 ID HV26_MOUSE STANDARD; PRT; 144 AA.
 AC P01795;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region M167 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93358330; PubMed=6101208;
 RA Kim S., Davis M., Sinn E., Patten P., Hood L.;
 RT "Antibody diversity: somatic hypermutation of rearranged VH genes.";
 RL Cell 27:573-581(1981).
 RN [2]
 RP SEQUENCE OF 20-142.
 RX MEDLINE=7622762; PubMed=819932;
 RA Rudikoff S., Potter M.;
 RT "Size differences among immunoglobulin heavy chains from
 RT phosphorylcholine-binding proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 73:2103-2112(1976).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
 CC THAT BINDS PHOSPHORYLCHOLINE.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC This SWISS-Prot entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J00516; AAC18867.2; ALT_TERM.
 CC DR

DR PIR; A90818; AVMS67.
 DR HSP, P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 CHAIN 20 144 IG HEAVY CHAIN V REGION M167.
 FT DOMAIN 20 133 IG-LIKE.
 FT CONFLICT 125 125 N -> D (IN REF. 2).
 FT NON TER 144 144
 SQ SEQUENCE 144 AA; 16219 MW; BECB4A2C956CF769 CRC64;

Alignment Scores:

Pred. No.: 1,2e-37 Length: 144
 Score: 398.50 Matches: 75
 Percent Similarity: 70.99% Conservative: 18
 Best Local Similarity: 57.25% Mismatches: 27
 Query Match: 52.92% Indels: 11
 DB: 1 Gaps: 1

US-09-674-716B-1 (1-415) x HV26_MOUSE (1-144)

QY 51 ATTTTCTTTTATGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGTCTGAGAGTCTGA 110
 Db 8 ValPheLeuLeuThrLeuLeuHisGlyIleGlnCysGluValLysValValGluSerGly 27
 QY 111 GGAGGCTTGGTCCAACTCGAGAGTCCATGAAGTCTCTGTTGAGCCCTCTGGATTACT 170
 Db 28 GlyGlyLeuValGlnProGlyGlySerLeuArgLeuSerCysAlaThrSerGlyPheThr 47
 QY 171 TTCAGTGGTCTACTGATGTTCTTGGTCCGCGAGTCCAGAGAGGGGCTTGAAGTGGTT 230
 Db 48 PheSerAspPheTyrMetGluTrpValArgGlnThrProGlyLysArgLeuGluTrpIle 67
 QY 231 GCTGAATAGATTGAATCTGATTAATGATCAACACATTAATGCGAGTCTGTGAAGGG 290
 Db 68 AlaAlaSerArgSerLysAlaHisAspTyrArgThrGluTyrSerAlaSerValLysGly 87
 QY 291 AGTTCACCATCTCAAGAGATGATCCAAAGTCTCTACCTGCAATGAACAGCTTA 350
 Db 88 ArgPheIleValSerArgAspThrSerGlnSerValLeuTyrLeuGlnMetAsnAlaLeu 107
 QY 351 AGAGCTGAGACAGTGGAGTCTTACTTACTGACAGATTTTCATAGAC----- 395
 Db 108 ArgAlaGluAspThrAlaThrTyrTyrCysThrArgAspAlaAspTyrGlyAsnSerTyr 127
 QY 396 -----TGGGGCCCAAGGACA 410
 Db 128 PheGlyTyrPheAspValTrpGlyAlaGlyThr 138

RESULT 15

HV54_MOUSE
 ID HV54_MOUSE STANDARD; PRT; 117 AA.
 AC P18525;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5-84 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BALB/cJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 RT the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).

Search completed: September 30, 2004, 08:42:43
Job time : 11.0039 secs

Blank sheet

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:27:18.; Search time 52.5503 Seconds
(without alignments)
4983.418 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 753
Sequence: 1 aagttttacattactacgc.....tggggccaaagggacactagt 415

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xl
-Q=/cgn2_1/USPTO_spool_p/US09674716/runat_30092004_070258_25867/app_query.fasta_1.3.164
-DB=SPTRMBL_25 -QPMT=fastan -SUFFIX=rpct -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=rpct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09674716@cgn_1_1_499@runat_30092004_070258_25867 -NCFU=6 -ICPU=3
-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rhodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 534.5 | 71.0 | 487 | 11 | Q80Z17 |

| | | | | | |
|----|-------|------|-----|----|--------|
| 2 | 468 | 62.2 | 479 | 11 | Q7TMK4 |
| 3 | 431 | 57.2 | 469 | 11 | Q8R3V9 |
| 4 | 422.5 | 56.1 | 597 | 4 | Q96BB9 |
| 5 | 420 | 55.8 | 613 | 4 | Q8WUK1 |
| 6 | 407.5 | 54.1 | 479 | 11 | Q91WP5 |
| 7 | 405 | 53.8 | 487 | 11 | Q99KA4 |
| 8 | 404 | 53.7 | 473 | 11 | Q91Z05 |
| 9 | 400 | 53.1 | 494 | 4 | Q96X68 |
| 10 | 395 | 52.5 | 573 | 4 | Q8WU38 |
| 11 | 394.5 | 52.4 | 113 | 4 | Q9UL90 |
| 12 | 393.5 | 52.3 | 480 | 11 | Q91XE1 |
| 13 | 391 | 51.9 | 484 | 11 | Q8VEA0 |
| 14 | 390.5 | 51.9 | 470 | 4 | Q7ZSW1 |
| 15 | 390.5 | 51.9 | 486 | 11 | Q91Z07 |
| 16 | 387.5 | 51.5 | 499 | 4 | Q8NSK4 |
| 17 | 386 | 51.3 | 95 | 4 | Q9ULB6 |
| 18 | 384.5 | 51.1 | 131 | 4 | Q9UL88 |
| 19 | 377.5 | 50.1 | 121 | 4 | Q9UL71 |
| 20 | 377 | 50.1 | 118 | 4 | Q9UL91 |
| 21 | 375.5 | 49.9 | 493 | 4 | Q8NCL6 |
| 22 | 375.5 | 49.9 | 521 | 4 | Q8N4Y9 |
| 23 | 370 | 49.1 | 112 | 4 | Q9HCC1 |
| 24 | 364.5 | 48.4 | 119 | 11 | Q920E7 |
| 25 | 362.5 | 48.1 | 116 | 4 | Q9UL93 |
| 26 | 352 | 46.7 | 147 | 4 | Q9Y509 |
| 27 | 351 | 46.6 | 122 | 4 | Q9UL84 |
| 28 | 350 | 46.5 | 298 | 11 | Q9QIF0 |
| 29 | 348 | 46.2 | 118 | 4 | Q9UL72 |
| 30 | 344.5 | 45.8 | 482 | 4 | Q7Z351 |
| 31 | 332 | 44.1 | 437 | 11 | Q9R1A4 |
| 32 | 311 | 41.3 | 482 | 11 | Q8K172 |
| 33 | 309 | 41.0 | 463 | 11 | Q93LC4 |
| 34 | 304.5 | 40.4 | 634 | 11 | Q7TMT6 |
| 35 | 304 | 40.4 | 278 | 11 | Q921K1 |
| 36 | 304 | 40.4 | 613 | 11 | Q8VCX7 |
| 37 | 303.5 | 40.3 | 168 | 11 | Q8VDC9 |
| 38 | 303.5 | 40.3 | 473 | 11 | Q9D8L4 |
| 39 | 302 | 40.1 | 143 | 11 | Q924P9 |
| 40 | 299 | 39.7 | 488 | 11 | Q8K0F2 |
| 41 | 295 | 39.2 | 143 | 11 | Q91V67 |
| 42 | 294.5 | 39.1 | 112 | 4 | Q9UGP3 |
| 43 | 291.5 | 38.7 | 470 | 11 | Q7TMK1 |
| 44 | 291 | 38.6 | 137 | 11 | Q924R6 |
| 45 | 289.5 | 38.4 | 117 | 11 | Q9QXF0 |

ALIGNMENTS

RESULT 1

ID Q80Z17 PRELIMINARY; PRT; 487 AA.

AC Q80Z17; SEQUENCE FROM N.A.

DT 01-JUN-2003 (TREMREL. 24, Created)

DT 01-JUN-2003 (TREMREL. 24, Last sequence update)

DT 01-OCT-2003 (TREMREL. 25, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP STRAIN=FVB/N; TISSUE=Colon;

RC Strausberg R.;

RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC049143; AAH49143.1; -

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig_3.

DR SMART; SMC0409; IG; 3.

DR SMART; SM00407; IGV; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IGV; 4.
 DR PROSITE; PS00290; IGV; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 487 AA; 53019 MW; 312C893900A4D80 CRC64;

Alignment Scores:
 Pred. No.: 2,228-51 Length: 487
 Score: 534.50 Matches: 103
 Percent Similarity: 83.82% Conservative: 11
 Best Local Similarity: 75.74% Mismatches: 11
 Query Match: 70.98% Indels: 11
 DB: 11 Gaps: 2

US-09-674-716B-1 (1-415) x Q80Z17 (1-487)

QY 36 ATGGATTTGGGCTG-----ATTTTATTATGTTCTTTAAAGGGTCCAGAGTCAA 89
 Db 1 MetTyrLeuGlyLeuAsnCysValPheLeuLeuLysGlyValGlnSerGlu 20
 QY 90 GTCAAGCTTACAGAGTCTCGAGAGGCTGTCGCAACTGGAGGATCCATGAACCTCTCC 149
 Db 21 ValLysLeuGluGluAlaGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
 QY 150 TGTGTAGCTCTGGATTTACTTTCAGTGGCTACTGCTGCTTGGTCCGCCAGTCTCCA 209
 Db 41 CysAlaAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSerPro 60
 QY 210 GAGAGGGCTTACAGAGTCTCGAGAGGCTGTCGCAACTGGAGGATCCATGAACCTCAACAT 269
 Db 61 GluLysGlyLeuGluTrpValAlaGluLeuArgSerAsnAsnTyrAlaThrHis 80
 QY 270 TATGGAGCTCTGTGAAGGGAGTTTACCATCTCAAGAGATGATTCGAAAGTCTGCTC 329
 Db 81 TyrAlaGluSerValLysGlyArgPheThrThrLeuSerArgAspSerLysSerSerVal 100
 QY 330 TACCTCAATGAACAGCTTAAGAGTGAAGAGTGAAGAGTGAAGTATTAATGACATACAT 386
 Db 101 TyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrArgArg 120
 QY 387 -----TTCATAGACTGGGCCCAAGGACA 410
 Db 121 GlyTyrGlyAspProAsnTrpTyrPheAspValTrpGlyAlaGlyThr 136

RESULT 2
 Q7TMK4 PRELIMINARY; PRT; 479 AA.
 ID Q7TMK4
 AC Q7TMK4
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Shenmen C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska D., Smalls D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 KW EMBL; BC055905; AAH5905.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 479 AA; 52209 MW; 532DED9D46D0AED CRC64;

Alignment Scores:
 Pred. No.: 7,2e-44 Length: 479
 Score: 468.00 Matches: 90
 Percent Similarity: 81.54% Conservative: 16
 Best Local Similarity: 69.23% Mismatches: 16
 Query Match: 62.15% Indels: 8
 DB: 11 Gaps: 3

US-09-674-716B-1 (1-415) x Q7TMK4 (1-479)

QY 36 ATGGATTTGGGCTG-----ATTTTATTATGTTCTTTAAAGGGTCCAGAGTCAA 89
 Db 1 MetTyrLeuGlyLeuSerCysValPheLeuLeuLysGlyValGlnCysGlu 20
 QY 90 GTCAAGCTTACAGAGTCTCGAGAGGCTGTCGCAACTGGAGGATCCATGAACCTCTCC 149
 Db 21 ValLysLeuAspGluThrGlyGlyLeuValGlnProGlyArgProMetLysLeuSer 40
 QY 150 TGTGTAGCTCTGGATTTACTTTCAGTGGCTACTGCTGCTTGGTCCGCCAGTCTCCA 209
 Db 41 CysValAlaSerGlyPheThrPheGlyAspTyrTrpMetAsnTrpValArgGlnSerPro 60
 QY 210 GAGAGGGCTTACAGAGTCTCGAGAGGCTGTCGCAACTGGAGGATCCATGAACCTCAACAT 269
 Db 61 GluLysGlyLeuGluTrpValSerGlnIleArgAsnLysProTyrAsnTyrGluThrTyr 80
 QY 270 TATGGCGAGTCTGTGAAGGGAGTTTACCATCTCAAGAGATGATTCGAAAGTCTGCTC 329
 Db 81 TyrSerAspSerValLysGlyArgPheThrThrLeuSerArgAspSerLysSerGlyVal 100
 QY 330 TACCTCAATGAACAGCTTAAGAGTGAAGAGTGAAGAGTGAAGTATTAATGACATACAT 383
 Db 101 TyrLeuGlnMetAsnAsnLeuArgProGluAspMetGlyIleTyrTyrCysThrValGlu 120
 QY 384 -----GATTTCATAGACTGGGCCCAAGG 407
 Db 121 GlyMetAspTyr-----TrpGlyArgGly 128

RESULT 3
 Q8R3V9 PRELIMINARY; PRT; 469 AA.
 ID Q8R3V9
 AC Q8R3V9
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN IGH-4
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 EMBL; BC024405; AAH24405.1; -.
 DR

DR PIR: B45837; B45837.
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Hypothetical protein.
 KW SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;
 SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;
 Alignment Scores:
 Pred. No.: 1.09e-39 Length: 469
 Score: 431.00 Matches: 83
 Percent Similarity: 72.93% Conservative: 14
 Best Local Similarity: 62.41% Mismatches: 24
 Query Match: 57.24% Indels: 12
 DB: 11 Gaps: 1
 US-09-674-716B-1 (1-415) x Q96BB9 (1-469)
 QY 51 ATTTTATTTTATGTTCTTTTAAAGGGCTCCAGAGTGAAGCTTGAGGAGTCTGGA 110
 Db 8 ILePheLeuValThrLeuLeuAsnGlyIleGlnCysGluValAlaSerGly 27
 QY 111 GGAGCTTGGTGCACACCTGGAGGATCCATGAACCTCTCTGTGAGCTCTGGAATTACT 170
 Db 28 GlyGlyLeuValGlnProGlySerLeuArgLeuSerCysAlaAlaSerGlyPheThr 47
 QY 171 TTCAGTGGCTACTGATCTCTGGTCCGCCAGTCTCCAGAGAGGGCTTGAGTGGTT 230
 Db 48 PheThrAspTyrTyrMetSerTrpValArgGlnProGlyLysAlaLeuGluTrpLeu 67
 QY 231 GCTGAATATAGATTGAAATCGATTAATTATGACACACATTTATGCGAGTCTGTGAAAGGG 290
 Db 68 GlyPheIleArgAsnLysAlaAsnGlyTyrThrThrGluTyrSerAlaSerValLysGly 87
 QY 291 AAGTTCACATCTCAAGAGATGATCCAAAGTCTCTCTACCTGCAATGAACAGCTTA 350
 Db 88 ArgPheThrIleSerArgAspAsnSerglnSerIleLeuTyrLeuGlnMetAsnAlaLeu 107
 QY 351 ACAGCTGAAGACAGTGGAGTTTATTACTGT----- 380
 Db 108 ArgAlaGluAspSerAlaThrTyrTyrCysAlaArgAspArgSerTyrTyrTyr 127
 QY 381 -----ACAGATTTCATAGACTGGGGCCCAAGGCACACTA 413
 Db 128 SerGlyThrSerPheAlaTyrTrpGlyGlnGlyThrLeu 140
 RESULT 4
 Q96BB9 PRELIMINARY; PRT; 597 AA.
 AC Q96BB9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015760; AAH15760.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 DR Hypothetical protein.
 KW SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
 Alignment Scores:
 Pred. No.: 1.03e-38 Length: 597
 Score: 422.50 Matches: 85
 Percent Similarity: 72.73% Conservative: 19
 Best Local Similarity: 59.44% Mismatches: 18
 Query Match: 56.11% Indels: 21
 DB: 4 Gaps: 4
 US-09-674-716B-1 (1-415) x Q96BB9 (1-597)
 QY 36 ATGGAATTTGGGCTG-----ATTITTTTATGTTCTTTTAAAGGGTCCAGAGTGA 89
 Db 1 MetGluPheGlyLeuSerTrpLeuValAlaIleLeuLysGlyValGlnCysGlu 20
 QY 90 GTGAAGCTTGAGGAGTCTGGAGGAGCTTGGTGCACCTGGAGGATCCATGAACCTCTCC 149
 Db 21 ValGlnLeuGluSerGlyGlyLeuValGlnProGlySerLeuArgLeuSer 40
 QY 150 TGTGTAGCTCTGGATTTTACTTTTCAGTGGCTACTGGATCTTTGGTCCGCCAGTCTCCA 209
 Db 41 CysAlaAlaSerGlyPheSerSerTyrAlaMetAsnTrpValArgGlnAlaPro 60
 QY 210 GAGAAGGGCTTGAGTGGTTCCTGAAATAGATTGAAATCTGATTAATTATGCAACACAT 269
 Db 61 GlyLysGlyLeuGluTrpValSerAlaIle-----SerGlySerGlyGlySerThrTyr 78
 QY 270 TATGCGGAGTCTGTGAAAGGGAAGTTTCCACATCTCAAGAGATGATTCCAAAGTCTGCTC 329
 Db 79 TyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerArgAspThrLeu 98
 QY 330 TACTGCAATGAACAGCTTAAGAGCTGAAGAGCAGTGGAGTATTACTGTACA----- 383
 Db 99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAlaLysAsp 118
 QY 384 -----GATTTCATAGACTGGGGCAA 404
 Db 119 ProArgGlyTyrSerAlaSerGlyAsnTyrThrArgGluAspTyr-----TrpGlyGln 136
 QY 405 GGGACACTA 413
 Db 137 GlyThrLeu 139
 RESULT 5
 Q9WUK1 PRELIMINARY; PRT; 613 AA.
 AC Q9WUK1;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tonsil;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020240; AAH20240.1; -.
 DR PIR; P10120; P10120.
 DR PIR; S15590; S15590.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 5.

36 ATGGATTTTGGG-----CTGATTTTATTTTATTTTATTTTAAAGGGGTCAGAGTCAA 89
 1 MetAsnPheGlyLeuSerLeuValLeuValLeuValLeuValGlnCysGlu 20
 90 GTGAAGCTTGGAGCTCTGGAGGAGCTTGGTGGCACTGAGAGTCAATCAAACTCTCC 149
 21 ValGlnLeuValGluSerGlyGlyLeuValValValValValValValValValVal 40
 150 TGTGTAGCTCTGGATTTTCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 209
 41 CysAlaAlaSerGlyPheThrPheSerSerTyraAlaMetSerTrpValArgGlnThrPro 60
 210 GAGAGGGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 266
 61 GluValArgLeuGluTrpValAlaThrIle-----SerAspGlyGlySerTyThr 77
 267 CATTAATGGAGCTCTGTAAGGAGGAGTTCACCTCTCAAGAGAGTGAATTCATAATATGCA 326
 78 TyrTrpProAspAsnValValValValValValValValValValValValValVal 97
 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGTGAAGTGAAGTGAAGTGAAGT 380
 98 LeuTyraLeuGlnMetSerHisLeuValValValValValValValValValValVal 117
 381 -----ACAGATTTTCATAGACTGGGGCCAGGAGCA 410
 118 AspMetGlyGlySerProTyraGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyThr 137

RESULT 8
 Q91Z05 PRELIMINARY; PRT; 473 AA.
 ID Q91Z05 (TREMBLrel. 19, Created)
 AC Q91Z05 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN AU04919.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010327; AAH10327.1; -.
 DR MGD; MGI:2144967; AU04919.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000345; Cytochrome_B.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00190; CYTOCHROME C; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00230; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AP12 CRC64;

Alignment Scores:
 Pred. No.: 1,22e-36 Length: 473
 Score: 404.00 Matches: 79
 Percent Similarity: 76.74% Conservative: 20
 Best Local Similarity: 61.24% Mismatches: 18
 Query Match: 53.65% Indels: 12
 DB: 11 Gaps: 3

US-09-674-716B-1 (1-415) x Q91Z05 (1-473)

7 LeuValPheLeuValLeuLeuLeuValGlnCysGluValGlnValGlnValGluSer 26
 108 GGAGGAGCTTGGTGGCACTGAGGATCCATGAACCTCTCTGTGTAGCCTCTGGATTT 167
 27 GlyGlyGlyLeuValValValValValValValValValValValValValValVal 46
 168 ACTTTCAGTGGCTGAGTGTCTTGGTCCGCCACTCTCCAGAGAGGGCTTGGATGG 227
 47 ThrPheSerAspTyraGlyMetHisTrpValArgGlnAlaProGluValGlyLeuGluTrp 66
 228 GTTGTGTAATAGATTGAATCTGATAATATGCAACACATTATCGGAGTCTGTGAAA 287
 67 ValAlaThrIle-----AsnSerGlySerThrThrIleTyraAlaAspThrValLys 84
 288 GGAAGTTCACCATCTCAAGAGAGTGAATCAAAAGTCTCTTACCTGCAATGAACAGC 347
 85 GlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuPheLeuGlnMetThrSer 104
 348 TTAAGAGCTGAACAGACAGTGGAGTTTATTCTGTACA----- 383
 105 LeuArgSerGluAspThrAlaMetTyraCysAlaArgGluLeuTrpLeuArgArgIle 124
 384 GATTTCATAGACTGGGGCCAGGAGCA 410
 125 AspTyra-----TrpGlyGlnGlyThr 131

RESULT 9
 Q96K68 PRELIMINARY; PRT; 494 AA.
 ID Q96K68 (TREMBLrel. 19, Created)
 AC Q96K68 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ14473.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-Mammary gland;
 RA ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wakatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakami K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
 RA Nimomiyama K., Iwayanagi T.;
 RL "NEDO human cDNA sequencing project."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK027379; BAB55072.1; -.
 DR PIR; S21205; S21205.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00230; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AEE4C0E CRC64;

Alignment Scores:
 Pred. No.: 3,48e-36 Length: 494
 Score: 400.00 Matches: 79
 Percent Similarity: 72.46% Conservative: 21
 Best Local Similarity: 57.25% Mismatches: 24
 Query Match: 53.12% Indels: 14
 DB: 4 Gaps: 3

US-09-674-716B-1 (1-415) x Q96K68 (1-494)

36 ATGGATTTTGGGCTG-----ATTTTATTTTATTTTATTTTAAAGGGGTCAGAGTCAA 89

Db 41 ProGlyLysGlyLeuGluTrpValAlaPheLeuArgTyrAspGlySerAsn-----Lys 58
 QY 267 CATTATGGGAGCTGTGTAAGAGGGAAGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCGT 326
 Db 59 TyrTyrAlaAspSerValGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 78
 QY 327 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGCTGAGTTTATTACTGTACA--- 383
 Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 98
 QY 384 GATTTCATAGACTGGGCCCAAGGACACTA 413
 Db 99 AspLeuAsnTyrTrpGlyGlnGlyThrLeu 108
 RESULT 12
 Q91XE1
 ID Q91XE1 PRELIMINARY; PRT; 480 AA.
 AC Q91XE1
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue=Colon;
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC010798; AAH10798.1; -.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 4.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS0835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 2.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;
 Alignment Scores:
 Pred. No.: 1-88e-35 Length: 480
 Score: 393.50 Matches: 78
 Percent Similarity: 75.57% Conservative: 21
 Best Local Similarity: 59.54% Mismatches: 23
 Query Match: 52.26% Indels: 9
 DB: 11 Gaps: 3
 US-09-674-716B-1 (1-415) x Q91XE1 (1-480)
 QY 39 GATTTCGGG-----CTGATTTTATTGTTCTTTTAAAGGGGTCAGAGTGAAGTGTG 92
 Db 1 AsnPheGlyLeuSerLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeuVal 20
 QY 93 AACCTTGAGAGCTGAGAGGCTGTGGTCAACCTGGAGGATCCATGAACCTCTCTCTGT 152
 Db 21 LysLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeuSerCys 40
 QY 153 GTAGCTCTGATTTACTTTCAGTGGCTACTGATGCTTGGTCCGCGAGTCTCCAGAG 212
 Db 41 AlaAlaSerGlyPheIlePheSerAsnSerTyrMetSerTrpValArgGlnThrProGlu 60
 QY 213 AAGGGCTTCAGTGGGTGTGCTGAATCTGAAATCTGATTAATATGCAACACACATTA 272
 Db 61 LysArgLeuGluTrpValAlaThrIle-----SerAsnSerGlyTyrAlaThrHisTyr 78
 QY 273 GCGAGTCTGTGAAGGGAAGTTCCACCATCTCAAGAGATGATTCCTCAAAAGTCTCTCTAC 332
 Db 79 ProAspSerMetLysGlyArgPheThrIleSerArgAspAsnAlaGlnAsnThrValLeu 98

QY 333 CTGCAAAATGAACAGCTTAAGAGCTGAAGAGTGGAGTTTATTACTGTACAGAT----- 386
 Db 99 LeuGlnMetThrSerLeuAsnSerGluAspThrAlaValTyrTyrCysThrArgGlyAsp 118
 QY 387 -----TTCATAGACTGGGCCCAAGGAC 410
 Db 119 TyrTrpTyrPheAspValTrpGlyAlaGlyThr 129
 RESULT 13
 Q8VEA0
 ID Q8VEA0 PRELIMINARY; PRT; 484 AA.
 AC Q8VEA0
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC019425; AAH19425.1; -.
 DR MGD: MGI:96486; IGH-VJ558.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 4.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS0835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 484 AA; 52859 MW; P2522DF5ED6288A6 CRC64;
 Alignment Scores:
 Pred. No.: 3.6e-35 Length: 484
 Score: 391.00 Matches: 75
 Percent Similarity: 73.02% Conservative: 17
 Best Local Similarity: 59.52% Mismatches: 28
 Query Match: 51.93% Indels: 6
 DB: 11 Gaps: 1
 US-09-674-716B-1 (1-415) x Q8VEA0 (1-484)
 QY 51 ATTTTATTTTATGTTCTTTTAAAGGGGTCAGAGTGAAGTGAAGTTCAGAGTCTCGA 110
 Db 8 IlePheLeuValThrLeuLeuAsnGlyPheGlnCysGluValLysLeuValGluSerGly 27
 QY 111 GGAGCTTGTCSCAACCTGGAGGATCCATGAACTCTCTGTGTAGCTCTGGATTACT 170
 Db 28 GlyGlyLeuValGlnProGlyThrSerLeuThrLeuSerCysAlaThrSerGlyPheThr 47
 QY 171 TTCAGTGGCTACTGATGTCCTGGTCCGCGAGTCTCCAGAGAGGGCTTGAGTGGTT 230
 Db 48 PheThrGluTyrTyrMetSerTrpValArgGlnProGlyArgAlaLeuGluTrpLeu 67
 QY 231 GCTGAAATTAGATTGAAATCTGATAATTATCAACACACATTAATGCGAGTCTGTGAAAGG 290
 Db 68 GlyPheIleArgAsnArgAlaAsnGlyTyrThrProGluTyrSerAlaSerValGlnGly 87
 QY 291 AAGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCTCTCTACCTGCAAAATGAACAGCTTA 350
 Db 88 ArgPheThrIleSerArgAspAsnSerGlnAsnLeuLeuTyrLeuGlnMetAsnThrLeu 107
 QY 351 AGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT-----TTCATA 392
 Db 108 ArgAlaGluAspSerAlaThrTyrTyrCysAlaArgAlaTyrSerAsnTyrTyrPheAsp 127
 QY 393 GACTGGGCCCAAGGAC 410

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Db 128 AsnTrpGlyGlnGlyThr 133
RESULT 14
Q725W1 PRELIMINARY; PRT; 470 AA.
AC Q725W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Xie H.F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyvinski M.I., Skalska U., Smallos J.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAHS3984.1; -.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483B1A CRC64;

Alignment Scores:
Pred. No.: 4,08e-35 Length: 470
Score: 390.50 Matches: 80
Percent Similarity: 70.29% Conservative: 17
Best Local Similarity: 57.97% Mismatches: 26
Query Match: 51.86% Indels: 15
DB: 4 Gaps: 3

US-09-674-716B-1 (1-415) X Q725W1 (1-470)

QY 36 ATGAGTTTGGGTG-----ATTTTATTTATGTTCTTTTAAAGGGTCCAGAGTCAA 89
Db 1 MetGluGlyLeuSerTrpValPheLeuValValIleLeuGluGlyValGlnCysGlu 20

QY 90 GTCAAGCTTGAGAGTCTGAGAGGCTTGTCGCACTGGAGGAGTCCATGAATCTCC 149
Db 21 ValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeuSer 40

QY 150 TGTGTAGCTCTGGATTACTTTTCTAGTGGCTACTGATGTTCTGGTCCGCCAGTCTCCA 209
Db 41 CysValAlaSerGlyPheThrLeuAsnAspMetHisTrpValArgGlnGlyIle 60

QY 210 GAGAGGGCTTCAGTGGGCTTCTGAAATAGATTGAATCTGAATATTCACACAT 269
Db 61 GlyLysGlyLeuGluTrpValSerIleGlyThrAlaGlyAspArgTrp-----77

US-09-674-716B-1 (1-415) X Q91Z07 (1-486)

QY 36 ATGAGTTTGGGTG-----CTGATTTTATTTATGTTCTTTTAAAGGGTCCAGAGTCAA 89
Db 1 MetAsnPheGlyLeuArgLeuLeuPheLeuValLeuAlaLeuLysGlyValGlnCysGlu 20

QY 90 GTCAAGCTTGAGAGTCTGAGAGGCTTGTCGCACTGGAGGAGTCCATGAATCTCC 149
Db 21 ValHisLeuValGluSerGlyGlyLeuValGlyProGlyGlySerLeuLysLeuSer 40

QY 150 TGTGTAGCTCTGGATTACTTTTCTAGTGGCTACTGATGTTCTGGTCCGCCAGTCTCCA 209
Db 41 CysValValSerGlyPheSerPheThrSerTrpAspMetSerTrpValArgGlnThrPro 60

QY 210 GAGAGGGCTTCAGTGGGCTTGCTGAAATAGATTGAATCTGAATATTCACACAT 269
Db 61 GluArgGluGluTrpValAlaIle-----ThrSerGlyGlyAsnThrTrp 77

QY 270 TATGCGGAGTCTGTGAAAGGAAAGTTCCACATCTCAAGAGATGATTCCTGCTCTC 329
Db 78 TyrProAspAsnValLysGlyArgPheThrValSerArgAspAsnAlaLysTrpThrLeu 97

QY 330 TACTGCAATGAACAGCTTAAGAGCTCAAGACAGTGGAGTTTATTACTGTACA-----383
Db 98 TyrLeuGlnMetAsnSerLeuArgValGlyAspAlaValIleTrpCysAlaArgGly 117

QY 384 -----GATTTATAGACTGGGGCCAAAGGACACTA 413
Db 118 AlaGlyArgTrpAlaProLeuGlyAlaPheAspIleTrpGlyGlnGlyThrMet 135

RESULT 15
Q91Z07 PRELIMINARY; PRT; 486 AA.
AC Q91Z07;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAH10324.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Alignment Scores:
Pred. No.: 4.1e-35 Length: 486
Score: 390.50 Matches: 78
Percent Similarity: 72.66% Conservative: 23
Best Local Similarity: 56.12% Mismatches: 21
Query Match: 51.86% Indels: 17
DB: 11 Gaps: 3.

US-09-674-716B-1 (1-415) X Q91Z07 (1-486)

QY 36 ATGAGTTTGGGTG-----CTGATTTTATTTATGTTCTTTTAAAGGGTCCAGAGTCAA 89
Db 1 MetAsnPheGlyLeuArgLeuLeuPheLeuValLeuAlaLeuLysGlyValGlnCysGlu 20

QY 90 GTCAAGCTTGAGAGTCTGAGAGGCTTGTCGCACTGGAGGAGTCCATGAATCTCC 149
Db 21 ValHisLeuValGluSerGlyGlyLeuValGlyProGlyGlySerLeuLysLeuSer 40

QY 150 TGTGTAGCTCTGGATTACTTTTCTAGTGGCTACTGATGTTCTGGTCCGCCAGTCTCCA 209
Db 41 CysValValSerGlyPheSerPheThrSerTrpAspMetSerTrpValArgGlnThrPro 60

QY 210 GAGAGGGCTTCAGTGGGCTTGCTGAAATAGATTGAATCTGAATATTCACACAT 269
Db 61 GluArgGluGluTrpValAlaIle-----ThrSerGlyGlyAsnThrTrp 77

QY 270 TATGCGGAGTCTGTGAAAGGAAAGTTCCACATCTCAAGAGATGATTCCTGCTCTC 329
Db 78 TyrProAspAsnValLysGlyArgPheThrValSerArgAspAsnAlaLysTrpThrLeu 97

QY 330 TACTGCAATGAACAGCTTAAGAGCTCAAGACAGTGGAGTTTATTACTGT-----380
Db 98 TyrLeuGlnMetSerLeuLysSerGluAspThrAlaMetTrpTrpCysValArgPro 117

```

QY 381 -----ACAGATTTCATAGACTGGGGCCCAAGGACA 410
 Db 118 GluIleProIleTyrTyrSerGlySerTyrPheAspSerTyrGlyGlnGlyThr 136

Search completed: September 30, 2004, 08:53:35
 Job time : 57.5503 secs

Blank sheet

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:19:42 ; Search time 49.4398 Seconds
(without alignments)
4743.430 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 753

Sequence: 1 aagcttacagttactcagc.....tggggccaaggacactagt 415

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DB=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0

-Q/cn2_1/USPTO_spuol_p/US09674716/runat_30092004_070257_25848/app_query.fasta_1.3164
-DB=A_Geneseq_29Jan04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09674716 @CGN 1.1 475 @runat_30092004_070257_25848 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRAIDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|---------------------|
| 1 | 715 | 95.0 | 137 | 3 AAY32260 | Aay32260 Mouse ant |
| 2 | 573.5 | 76.2 | 151 | 4 AAU76696 | Aau76696 Mouse hea |
| 3 | 573.5 | 76.2 | 151 | 4 AAB35292 | Aab35292 Murine PS |
| 4 | 561.5 | 74.6 | 142 | 2 AAW06212 | Aaw06212 MAB Br-3 |
| 5 | 561.5 | 74.6 | 142 | 2 AAW85059 | Aaw85059 Mouse Br- |
| 6 | 561.5 | 74.6 | 142 | 6 ABUS5893 | Abu5893 Mouse ant |
| 7 | 561.5 | 74.6 | 143 | 2 AAR09423 | Aar09423 Br-3 Heavy |
| 8 | 553.5 | 73.5 | 160 | 2 AAR70829 | Aar70829 MAB 4197X |
| 9 | 531.5 | 70.6 | 134 | 2 AAR12358 | Aar12358 Heavy cha |
| 10 | 531.5 | 70.6 | 134 | 2 AAR12236 | Aar12236 Mouse MAB |

| | | | | | |
|----|-------|------|-----|------------|---------------------|
| 11 | 531 | 70.5 | 444 | 3 AAY32263 | Aay32263 Humanised |
| 12 | 524.5 | 69.7 | 134 | 2 AAR52771 | Aar52771 Murine Br |
| 13 | 524.5 | 69.7 | 134 | 2 AAR52789 | Aar52789 Murine Br |
| 14 | 521.5 | 69.3 | 570 | 2 AAY39451 | Aay39451 Antibody |
| 15 | 518.5 | 68.9 | 123 | 6 ABO10742 | Abol10742 Variable |
| 16 | 518.5 | 68.9 | 123 | 6 ABR44686 | Abr44686 Murine Mu |
| 17 | 518 | 68.8 | 139 | 2 AAR30484 | Aar30484 VH region |
| 18 | 511.5 | 67.9 | 119 | 2 AAW46958 | Aaw46958 Amino aci |
| 19 | 511.5 | 67.9 | 554 | 2 AAR70827 | Aar70827 Anti-cata |
| 20 | 507 | 67.3 | 120 | 2 AAW01589 | Aaw01589 Lead bind |
| 21 | 503.5 | 66.9 | 116 | 2 AAY03869 | Aay03869 SM3 heavy |
| 22 | 503 | 66.8 | 114 | 2 AAR25410 | Aar25410 Heavy cha |
| 23 | 500.5 | 66.5 | 134 | 2 AAR52807 | Aar52807 Humanised |
| 24 | 500 | 66.4 | 286 | 4 AAB50426 | Aab50426 Antibody |
| 25 | 498.5 | 66.2 | 119 | 2 AAW01588 | Aaw01588 Lead bind |
| 26 | 497.5 | 66.1 | 136 | 2 AAR12326 | Aar12326 Heavy cha |
| 27 | 497.5 | 66.1 | 503 | 5 AAU72874 | Aau72874 3B10P5-2 |
| 28 | 495 | 65.7 | 100 | 4 AAE06973 | Aae06973 Mouse ger |
| 29 | 493 | 65.5 | 256 | 5 AAU72866 | Aau72866 PS-3 sing |
| 30 | 491 | 65.2 | 114 | 3 AAY90816 | Aay90816 113F1 hyb |
| 31 | 490 | 65.1 | 122 | 3 AAY90812 | Aay90812 2G3 hybri |
| 32 | 489.5 | 65.0 | 123 | 6 ABO10743 | Abol10743 Consensus |
| 33 | 489.5 | 65.0 | 123 | 6 ABR44687 | Abr44687 Murine J4 |
| 34 | 488 | 64.8 | 299 | 4 AAB50425 | Aab50425 Mouse ant |
| 35 | 483.5 | 64.2 | 129 | 2 AAR85908 | Aar85908 Monoclonal |
| 36 | 483 | 64.1 | 255 | 5 AAU72870 | Aau72870 PS-23 sin |
| 37 | 481 | 63.9 | 133 | 6 ABO10730 | Abol10730 Variable |
| 38 | 481 | 63.9 | 133 | 6 ABR44674 | Abr44674 Murine J4 |
| 39 | 480.5 | 63.8 | 253 | 2 AAR72599 | Aar72599 Anti-dans |
| 40 | 480 | 63.7 | 116 | 6 ABO10726 | Abol10726 Variable |
| 41 | 480 | 63.7 | 116 | 6 ABR44670 | Abr44670 Murine J4 |
| 42 | 476 | 63.2 | 116 | 6 ABO10728 | Abol10728 Variable |
| 43 | 476 | 63.2 | 116 | 6 ABR44672 | Abr44672 Murine J4 |
| 44 | 475 | 63.1 | 507 | 5 ABG71552 | Abg71552 Murine sc |
| 45 | 473 | 62.8 | 116 | 6 ABO10734 | Abol10734 Consensus |

ALIGNMENTS

RESULT 1

AAY32260

ID AAY32260 standard; protein; 137 AA.

XX AC AAY32260;

XX AC 15-FEB-2000 (first entry)

XX DE Mouse anti-CD23 MAB C11 heavy chain variable region.

XX KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

XX FT Region 59..63

XX FT Region /note= "CDR H1"

XX FT Region 78..96

XX FT Region /note= "CDR H2"

XX FT Region 129..131

XX FT Region /note= "CDR H3"

XX PN WO9958679-A1.

XX PD 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.
 XX 09-MAY-1998; 98GB-00009839.
 PA (GLAX) GLAXO GROUP LTD.
 XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 DR WPI; 2000-053101/04.
 DR N-PSDB; AAZ34745.
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis.
 XX Claim 8; Fig 1; 81pp; English.
 XX This sequence represents the heavy chain variable region (VH) of murine
 CC anti-CD23 (FCER1I) monoclonal antibody C11. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies (see
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid
 CC sequences of the C11 light and heavy chain complementarity determining
 CC regions (see AAY32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies are
 CC used to block soluble CD23 formation in human therapy, for the treatment
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX SQ Sequence 137 AA;

Alignment Scores:
 Pred. No.: 3 67e-70 Length: 137
 Score: 715.00 Matches: 137
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 94.95% Indels: 0
 DB: 3 Gaps: 0

US-09-674-716B-1 (1-415) x AAY32260 (1-137)

QY 3 GCTTACAGTACTACGACACAGGACCTCACCATGGATTGGCGTATTTTATT 62
 DB 1 AlaLeuGlnLeuSerThrGlnAspLeuThrMetAspPheGlyLeuIlePheHelle 20
 QY 63 GTTCTTTAAAGGGGTCACAGAGTGAAGTGAAGTTCGAGAGTCTGGAGAGGCTTGTG 122
 DB 21 ValLeuLeuLysGlyValGlnSerGluValLysLeuGluLysGlyGlyLeuVal 40
 QY 123 CAACCTGGAGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTTTAGTGGCTAC 182
 DB 41 GlnProGlyGlySerMetLysLeuSerCysValAlaSerGlyPheThrPheSerGlyTyr 60
 QY 183 TGGATGCTTGGTTCGCGCAGTCTCCAGAGAGGGGCTTGGTGGCTTGCCTCAATTTAGA 242
 DB 61 TrpMetSerTrpValArgGlnSerProGluLysGlyLeuGluTrpValAlaGluLeuArg 80
 QY 243 TTGAATCTGATTAATATGACACATTAATGCGAGTCTGTGAAGGGAGTTCACCATC 302
 DB 81 LeuLysSerAspSerTyrAlaThrHisTyrAlaGluSerValLysGlyLysPheThrIle 100
 QY 303 TCAGAGATGATTCGAAAGTCTCTCTACCTGCAATCAAGCTTAGAGCTGAAGAC 362
 DB 101 SerArgAspSerLysSerArgLeuTyrLeuGlnMetAsnSerLeuArgAlaGluasp 120
 QY 363 AGTGGAGTTTATTCTGTACAGATTTTCATAGACTGGGCGCAAGGACACTA 413

Db 121 SerGlyValTyrTyrCysThrAspPheIleAspTrpGlyGlnGlyThrLeu 137
 RESULT 2
 AAU76696
 ID AAU76696 standard; protein; 151 AA.
 XX
 AC AAU76696;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Mouse heavy chain variable domain region of PSCA antibody 2H9 protein.
 XX
 KW Mouse; prostate stem cell antigen; PSCA; antibody; immunogen;
 KW prostate cancer; bladder cancer; pancreatic cancer; immunoconjugate;
 KW PSCA-associated cancer; heavy chain variable domain region; PSCA antigen;
 KW PSCA antibody 2H9.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 45..54
 FT Region /note= "Complementarity determining region 1 (CDR1)"
 FT Region 69..87
 FT Region /note= "Complementarity determining region 2 (CDR2)"
 FT Region 120..125
 FT Region /note= "Complementarity determining region 3 (CDR3)"
 XX
 US2001055751-A1.
 PD 27-DEC-2001.
 XX
 PF 03-MAY-2000; 2000US-00564329.
 XX
 PR 10-MAR-1997; 97US-0228816P.
 PR 12-JAN-1998; 98US-0071141P.
 PR 13-FEB-1998; 98US-0074675P.
 PR 10-MAR-1998; 98US-00038261.
 PR 02-DEC-1998; 98US-0020939.
 PR 21-DEC-1998; 98US-0113230P.
 PR 17-FEB-1999; 99US-00251835.
 PR 17-FEB-1999; 99US-0120536P.
 PR 16-MAR-1999; 99US-0124858P.
 PR 25-MAY-1999; 99US-00318503.
 PR 20-JUL-1999; 99US-00359326.
 XX
 PA (REIT/) REITER R E.
 PA (WITT/) WITTE O N.
 PA (SAFF/) SAFFRAN D C.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Reiter RE, Witte ON, Safran DC, Jakobovits A;
 XX
 DR WPI; 2001-159478/16.
 DR N-PSDB; ABK09984.
 XX
 PT Antibodies binding to prostate stem cell antigen inhibit the growth of
 PT cancer cells and are used to detect and treat prostate, pancreatic or
 PT bladder cancers.
 XX
 PS Example 21; Fig 60; 127pp; English.
 XX
 CC The present invention relates to new antibodies that specifically bind a
 CC novel prostate stem cell antigen (PSCA), which is widely over-expressed
 CC across all stages of prostate cancer. The antibodies of the invention are
 CC useful to kill tumour cells expressing PSCA and as PSCA expression is
 CC observed in prostate tumour cells and in other human cancers,
 CC particularly bladder and pancreatic carcinomas, the antibodies are useful
 CC therapeutically to treat these diseases. In particular, monoclonal
 CC antibodies can be administered to subjects suffering from PSCA-associated
 CC cancers, e.g. prostate, bladder or pancreatic cancer or metastatic
 CC prostate, bladder or pancreatic cancer, to inhibit the cancer and prolong
 CC the subject's life. The antibodies can be combined with a therapeutic
 CC agent in immunoconjugates useful to treat subjects suffering from

CC malignant diseases, characterised by cells having PSA antigen on the
 CC cell surface e.g. cancers, by killing the cells. The antibodies and
 CC immunoconjugates may also be included with a carrier in pharmaceutical
 CC compositions useful to kill human cells expressing PSA antigen on the
 CC cell surface. The antibodies are also useful diagnostically to detect
 CC cancers, especially prostate cancer, to isolate prostate cancer cells
 CC e.g. to enable culture growth to evaluate candidate therapeutic
 CC compounds, assist in identification of rare genes associated with
 CC prostate cancer, and to isolate and purify PSA and PSA homologues. The
 CC present amino acid sequence represents the mouse heavy chain variable
 CC domain region of the PSA monoclonal antibody 2H9 of the invention
 XX
 SQ Sequence 151 AA;

Alignment Scores:
 Pred. No.: 1,64e-54 Length: 151
 Score: 573.50 Matches: 109
 Percent Similarity: 92.31% Conservative: 11
 Best Local Similarity: 83.85% Mismatches: 5
 Query Match: 76.16% Indels: 5
 DB: 4 Gaps: 2

US-09-674-716B-1 (1-415) x AAU76696 (1-151)

QY 39 GATTTTGGCTG-----ATTTTATTGTTCTTTTAAAGGGTCCAGAGTCAAGTG 92
 DB 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
 QY 93 AAGCTTGAGGAGCTCGGAGGAGCTGTGTGCAACCTGGAGGATCCATGAAATCTCTCTGT 152
 DB 22 ArgLeuGluGluSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
 QY 153 GTAGCTCTGGATTACATTGAGTGGCTACTGGATGCTTGGTCCGCCAGTCTCCAGAG 212
 DB 42 ValAlaSerGlyPheThrPheSerAsnTrpMetThrTrpValArgGlnSerProGlu 61
 QY 213 AAGGGCTTGAGTGGTCTGCTCAATAGATTGAATCTGATAATTATGCAACACATTAT 272
 DB 62 LysGlyLeuGluTrpValAlaGluLeuArgLeuArgSerGluAsnTrpAlaThrHisTyr 81
 QY 273 GCGAGTCTGTGAAGGGAAGTTCACATCTCAAGAGATGATCCAAAGTCTCTCTAC 332
 DB 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
 QY 333 CTGCAAAATCAACAGCTTAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
 DB 102 LeuGlnMetAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
 QY 393 -----GACTGGGGCCCAAGGACACTA 413
 DB 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 3
 AAB35292
 ID AAB35292 standard; protein; 151 AA.

XX
 AC AAB35292;
 XX
 DT 08-MAY-2001 (first entry)
 XX
 DE Murine PSA antibody 2H9 H chain V region.
 XX
 KW Prostate stem cell antigen; PSA; human; mouse; prostate cancer;
 KW diagnosis; treatment; chromosome 8q24.2.
 OS
 XX Mus sp.
 XX
 FN WO200105427-A1.
 XX
 PD 25-JAN-2001.
 XX
 PF 20-JUL-2000; 2000WO-US019967.

PR 20-JUL-1999; 99US-00359326.
 XX 03-MAY-2000; 2000US-00564329.
 XX (ZEGC) UNIV CALIFORNIA.
 PA (UROC-) UROGENESYS.
 XX
 PI Reiter R, Witte O, Saffran DC, Jakobovits A;
 XX WPI; 2001-159478/16.
 DR N-PSDB; AAF27975.
 XX
 PT Antibodies binding to prostate stem cell antigen inhibit the growth of
 PT cancer cells and are used to detect and treat prostate, pancreatic or
 PT bladder cancers.
 XX
 PS Example 21; Fig 60; 229pp; English.
 XX
 CC The present invention describes a method of treating cancer associated
 CC with prostate stem cell antigen (PSCA) by administering an antibody which
 CC selectively binds to PSCA and inhibits the growth of the cancer cells.
 CC The PSCA gene is found on human chromosome 8q24.2. The invention provides
 CC the human and murine PSCA protein and coding sequences, which can be used
 CC not only in the treatment of, but also in detection and prognosis of
 CC prostate cancer
 XX
 SQ Sequence 151 AA;

Alignment Scores:
 Pred. No.: 1,64e-54 Length: 151
 Score: 573.50 Matches: 109
 Percent Similarity: 92.31% Conservative: 11
 Best Local Similarity: 83.85% Mismatches: 5
 Query Match: 76.16% Indels: 5
 DB: 4 Gaps: 2

US-09-674-716B-1 (1-415) x AAB35292 (1-151)

QY 39 GATTTTGGCTG-----ATTTTATTGTTCTTTTAAAGGGTCCAGAGTCAAGTG 92
 DB 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
 QY 93 AAGCTTGAGGAGCTCGGAGGAGCTGTGTGCAACCTGGAGGATCCATGAAATCTCTCTGT 152
 DB 22 ArgLeuGluGluSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
 QY 153 GTAGCTCTGGATTACATTGAGTGGCTACTGGATGCTTGGTCCGCCAGTCTCCAGAG 212
 DB 42 ValAlaSerGlyPheThrPheSerAsnTrpMetThrTrpValArgGlnSerProGlu 61
 QY 213 AAGGGCTTGAGTGGTCTGCTCAATAGATTGAATCTGATAATTATGCAACACATTAT 272
 DB 62 LysGlyLeuGluTrpValAlaGluLeuArgLeuArgSerGluAsnTrpAlaThrHisTyr 81
 QY 273 GCGAGTCTGTGAAGGGAAGTTCACATCTCAAGAGATGATCCAAAGTCTCTCTAC 332
 DB 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
 QY 333 CTGCAAAATCAACAGCTTAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
 DB 102 LeuGlnMetAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
 QY 393 -----GACTGGGGCCCAAGGACACTA 413
 DB 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 4
 AAB06212
 ID AAB06212 standard; protein; 142 AA.

XX
 AC AAB06212;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-FEB-1997 (first entry)

Db 61 GluLysGlyLeuGluTrpValAlaGluLeuLeuLysSerAsnAsnTyrAlaThrHis 329

QY 270 TATCGGAGTCTGTCAAAGGGAAGTTCCACCATCTCAAGAGATGATTCCAAAGTCGTCTC 329

Db 81 TyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSerVal 100

QY 330 TACCTGCAATCAACAGCTTAAGAGCTCAAGACAGTCGAGCTTTATTACTGTACA----- 383

Db 101 TyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrPheGly 120

QY 384 ---GATTCTAGACTGGGGCCAAAGGCACACTA 413

Db 121 AsnGlnPheAlaTyrTrpGlyGlnGlyThrLeu 131

RESULT 5

AAW85059

ID AAW85059 standard; protein; 142 AA.

XX AC AAW85059;

XX XX

DT 20-MAR-2003 (revised)

DT 16-APR-1999 (first entry)

XX XX

XX Mouse Br-3 heavy chain variable region.

XX XX

KW Heavy chain variable region; murine antibody Br-3; antibody ING-1;

KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;

KW treatment; human cancer.

XX XX

OS Mus sp.

XX XX

PN US5843685-A.

XX XX

PD 01-DEC-1998.

XX XX

PF 06-JUN-1995; 95US-00466034.

XX XX

PR 06-SEP-1988; 88US-00240624.

PR 08-SEP-1988; 88US-00241744.

PR 13-SEP-1988; 88US-00243739.

PR 04-OCT-1988; 88US-00253002.

PR 19-JUN-1989; 89US-00367841.

PR 21-JUL-1989; 89US-00382768.

PR 06-SEP-1989; 89WO-US003852.

PR 06-MAY-1991; 91US-00659401.

PR 27-DEC-1994; 94US-00364001.

XX XX

PA (XOMA) XOMA CORP.

XX XX

PI Horwitz AH, Lei S, Chang CP, Better MD, Robinson RR;

XX XX

DR WPI; 1999-045474/04.

DR N-PSDB; AAV71155.

XX XX

PT Chimeric antibody specific for human tumour antigen - useful as

PT immunoassay, imaging or antitumour agent.

XX XX

PS Example 3; Fig 15; 92pp; English.

XX XX

CC The present sequence represents the heavy chain variable region of murine

CC antibody Br-3. The sequence was used to create chimeric mouse-human

CC immunoglobulins which recognise the human tumour antigen bound by

CC antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The

CC chimeric antibodies also have an antigen-binding site that competitively

CC inhibits the binding of antibody ING-1, and mediate complement-dependent

CC cytotoxicity of target cells or antibody-dependent cellular cytotoxicity to

CC target cells. The chimeric antibodies can be used for therapeutic

CC purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to

CC correct PR field.)

XX XX

SQ Sequence 142 AA;

QY 384 ---GATTTCATAGACTGGGGCCCAAGGCACACTA 413
 Db 121 AsnGlnPheAlaTyrTrpGlyGlnGlyThrLeu 131

RESULT 7

AAR09423
 ID AAR09423 standard; protein; 143 AA.

XX AC AAR09423;

XX 25-MAR-2003 (revised)

DT 04-MAR-1993 (first entry)

XX Br-3 Heavy Chain V Region (mouse).

XX Monoclonal antibody; chimera; light; heavy; chain; constant; variable;
 KW antigen; diagnosis; cancer; tumour.

XX Mus musculus.

OS WO9002569-A.

XX 22-MAR-1990.

XX 08-SEP-1988; 88US-00241744.

XX 06-SEP-1988; 88US-00241744.

PR 13-SEP-1988; 88US-00243739.

PR 04-OCT-1988; 88US-00253002.

PR 19-JUN-1989; 89US-00367641.

PR 21-JUL-1989; 89US-00382768.

XX (ITGE-) INT GENETIC ENG. INC.

PA (INGE-) INGENE INT GENETIC.

XX Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;

XX WPI; 1990-115825/15.

DR N-PSDB; AAQ06605.

XX Chimeric mouse-human antibodies - prep. using genes coding for constant

PT human region murine variable region, esp. to 3 tumour antigen.

XX Claim 13; Page 123 + Fig 15; 173pp; English.

XX The sequence is used in the prodn. of a chimeric antibody mol. comprising

CC two light chains and two heavy chains, each having a constant region

CC (human) and a variable region (murine) having specificity to an antigen

CC bound by murine monoclonal antibody (Mab) Br-3. The chimeric antibodies

CC can be used for any purpose for which the original murine Mabs can be

CC used, with the advantage that they are more compatible with the human

CC body. They are esp. used for the diagnosis and treatment of cancer.

CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 143 AA;

SQ

Alignment Scores:

Pred. No.: 3 43e-53 Length: 143

Score: 561.50 Matches: 108

Percent Similarity: 89.31% Conservative: 9

Best Local Similarity: 82.44% Mismatches: 9

Query Match: 74.57% Indels: 5

DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) x AAR09423 (1-143)

QY 36 ATGATTTGGGCTG-----ATTGTTTATGTTCTTTAAAGGGTCCAGAGTGA 89

Db 1 MetTyrLeuGlyLeuAsnCysValPheLeuValPheLeuLeuGlyValGlnSerGlu 20

QY 90 GTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGCACACTGGAGGATCCATGAACCTCTCC 149

Db 21 ValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
 QY 150 TGTGTAGCCTCTGGATTACTTTCACTGGTCTACTGGATGCTCTTGGTCCGCCAGTCTCCA 209
 Db 41 CysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSerPro 60
 QY 210 GAGAAGCGGCTTGAGTCGGTCTGCTGAATAGATTGAAATCTGATTAATATGCAACAT 269
 Db 61 GluLysGlyLeuGluTrpValAlaGluIleArgLeuLysSerAsnAsnTyrAlaThrHis 80
 QY 270 TATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCTCAAGAGTCTCTC 329
 Db 81 TyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSerVal 100
 QY 330 TACCTGCAATGAACAGCTTAAGAGCTGAAGAGCAGTGGAGTTTATTACTGTACA----- 383
 Db 101 TyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrTrpCysThrPheGly 120
 QY 384 ---GATTTCATAGACTGGGGCCCAAGGCACACTA 413
 Db 121 AsnGlnPheAlaTyrTrpGlyGlnGlyThrLeu 131

RESULT 8

AAR70829

ID AAR70829 standard; protein; 160 AA.

XX AAR70829;

AC AAR70829;

XX 25-MAR-2003 (revised)

DT 31-AUG-1995 (first entry)

XX MAB 4197X heavy chain variable region.

XX Immunotoxin; heavy chain; light chain; variable region; antibody;

KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;

KW pHB19; 4197X; monoclonal antibody; MAB.

XX Synthetic.

XX Key Location/Qualifiers

XX 69...73

XX /label= CDR1

XX /note= "complementarity determining region 1"

XX 87...106

XX /label= CDR2

XX /note= "complementarity determining region 2"

XX 139...144

XX /label= CD3

XX /note= "complementarity determining region 3"

XX WO9503828-A1.

XX 09-FEB-1995.

XX 15-JUL-1994; 94WO-US007919.

XX 02-AUG-1993; 93US-00101329.

XX (HOUS-) HOUSTON BIOTECHNOLOGY INC.

XX Wood MS, Gould RM, Kelleher PJ, Wallace TL;

XX WPI; 1995-082036/11.

XX N-ESDB; AAQ85388.

XX New single chain immuno:toxin - binds specifically to epithelial cells,

XX for inhibiting development of sec. cataracts after extra:capsular

XX cataract extraction.

XX Disclosure; Fig 2; 68pp; English.

XX An immunotoxin (given in AAR70827) comprises the heavy (VH) and light

XX chain (VL) variable regions of anti-lens epithelium IgG3 Mab 4197X linked

CC

CC to ricin-A. cDNAs encoding the VL and VH regions of 4197X (AAQ85387-88, CC respectively) were obtained from hybridoma mRNA, amplified by PCR, and CC engineered for inclusion in the immunotoxin construct (AAQ85386). CC (Updated on 25-MAR-2003 to correct PN field.) XX

SQ Sequence 160 AA;

Alignment Scores:

Pred. No.: 2,69e-52 Length: 160
Score: 553.50 Matches: 106
Percent Similarity: 88.64% Conservative: 11
Best Local Similarity: 80.30% Mismatches: 10
Query Match: 73.51% Indels: 5
DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) x AAR70829 (1-160)

QY 33 ACCATGGATTGGGCTG-----ATTGTTTATTGTTCTTTAAAGGGTCCAGAGT 86
DB 19 ThrMetTyrLeuGlyLeuAsnCysValPheValLeuGlyValGlnSer 38
QY 87 GAAGTGAAGCTTTGAGGAGTCTGGAGGAGCTTGGTCAACCTGGAGGATCCATGAATC 146
DB 39 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 58
QY 147 TCCTGTGAGCTCTGGATTACTTTCACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCT 206
DB 59 SerCysValAlaSerGlyPheThrPheSerAsnPheTrpMetAsnTrpValArgGlnSer 78
QY 207 CCAGAGAGGGGCTTGAGTGGGCTGCTGAAATAGATTGAATCTGATAATTATGCAACA 266
DB 79 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnAsnTyrProThr 98
QY 267 CATTATGGGAGTCTGTGAAGGAGTTCACCTCTCAAGAGATGATTCGAAAGTCTGT 326
DB 99 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 118
QY 327 CTTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGTGGAGTTTATTACTGTACA--- 383
DB 119 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrCysThrThr 138
QY 384 -----GATTTCATAGACTGGGGCCCAAGGGACACTA 413
DB 139 AspSerProPheAlaTyrTrpGlyGlnGlyThrLeu 150

RESULT 9

AAR12358
ID AAR12358 standard; protein; 134 AA.

XX AAR12358;
AC AC
DT 25-MAR-2003 (revised)
DT 15-AUG-1991 (first entry)
XX Heavy chain variable region of murine 1C11 immunoglobulin.
DE DE
KW Chimeric antibodies; immunoconjugates; HIV; AIDS.

OS Mus musculus.

XX WO9107493-A.

XX 30-MAY-1991.

XX 13-NOV-1989; 89US-00433730.

XX 13-NOV-1989; 89US-00433730.

XX (XOMA) XOMA CORP.

PA (GEC) GREEN CROSS CORP.

XX Better MD, Horwitz AH, Ghoshdasti P, Robinson R;

DR WPI; 1991-178105/24.
DR N-PSDB; AAQ12060.
XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV
PT -1 antigen from sample.
XX

PS Disclosure; Fig 12; 107pp; English.

XX This is the heavy-chain variable (V) region of a mouse mono- clonal
CC antibody (MAB), 1C11, and is specific for an HIV-1 viral antigen. It is
CC used in the construction of a chimeric MAB comprising heavy and light
CC chains having murine V regions and human C regions. The chimeric MABs are
CC more effective than murine MAB 1C11 since they have an increased
CC compatibility in humans. The heavy and light chain V-regions are joined
CC by manipulating their respective joining (J) regions, to generate
CC restriction enzyme recognition sites. The chimeric MABs can be used as
CC immunoconjugates, in association with e.g. toxins for HIV treatment. They
CC can also be used in diagnosis of HIV. See also AAQ12056-59 and AAQ12061-
CC 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003
CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)
XX

SQ Sequence 134 AA;

Alignment Scores: Length: 134
Pred. No.: 7e-50 Matches: 103
Score: 531.50 Conservative: 10
Percent Similarity: 87.60% Mismatches: 13
Best Local Similarity: 79.84% Indels: 3
Query Match: 70.58% Gaps: 2
DB: 2

US-09-674-716B-1 (1-415) x AAR12358 (1-134)

QY 36 ATGATTTTGGGCTG-----ATTGTTTATTGTTCTTTAAAGGGTCCAGAGTGA 89
DB 1 MetTyrLeuGlyLeuAsnTyrValPheValPheLeuLeuAsnGlyValGlnSerGlu 20
QY 90 GTGAAGCTTCAGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAATCTCC 149
DB 21 ValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
QY 150 TGTGATGCTCTGATTTACTTTTCAGTGGCTACTGATGTCTTGGTCCGCCAGTCTCCA 209
DB 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60
QY 210 GAGGAGGGCTTGAGTGGTGTGCTGAATTAGATTGAATCTGATTAATTATGCAACAT 269
DB 61 GluLysLeuGluTrpValAlaGluIleArgSerLysAlaAsnAsnHisAlaThrTyr 80
QY 270 TATCGGAGTCTGTGAAGGGAAGTTCCACCATCTCAAGAGATGATTCGAAAGTCTCTC 329
DB 81 TyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerVal 100
QY 330 TACCTGCAATGAACAGCTTAAGAGCTGAAGAGTGGAGTGGTATTACTCTACAGAT--- 386
DB 101 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrGlyIleTyrCysThrAspTrp 120
QY 387 TTCATAGACTGGGGCCCAAGGGACACTA 413
DB 121 PheAlaTyrTrpGlyGlnGlyThrLeu 129

RESULT 10

AAR12236
ID AAR12236 standard; protein; 134 AA.

XX AAR12236;

XX 25-MAR-2003 (revised)

DT 19-AUG-1991 (first entry)

XX Mouse MAB 1C11 H chain V region.

XX HIV-1; chimera.

XX MUS SP.
 OS
 PN WO9107494-A.
 XX
 PD 30-MAY-1991.
 XX
 XX 13-NOV-1989; 89US-00433703.
 XX
 PR 13-NOV-1989; 89US-00433703.
 XX
 PA (XOMA) XOMA CORP.
 PA (GREC) GREEN CROSS CORP.
 PA (ZOMA-) ZOMA CORP.
 XX
 PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
 XX
 XX WPI; 1991-178106/24.
 DR N-PSDB; AAQ12106.
 XX
 XX New chimeric mouse human antibodies - used in treatment, diagnosis and
 PT prophylaxis of HIV infections.
 PS Disclosure; Fig 12; 108pp; English.
 XX
 CC The mouse VH gene product may be used to produce chimeric mouse- human
 CC Abs against HIV-1 comprising human Ig constant regions and murine
 CC variable regions. These novel sequence are useful in treatment, diagnosis
 CC and prophylaxis of HIV infections, and may be produced by a bacterial,
 CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 134 AA;
 Alignment Scores:
 Pred. No.: 7e-50 Length: 134
 Score: 531.50 Matches: 103
 Percent Similarity: 87.60% Conservative: 10
 Best Local Similarity: 79.84% Mismatches: 13
 Query Match: 70.58% Indels: 3
 DB: 2 Gaps: 2
 US-09-674-716B-1 (1-415) x AAR12236 (1-134)
 QY 36 ATCGATTTCGGGTG-----ATTTCCTTATGTCCTTTAAAGGGTCCAGAGTGAA 89
 Db 1 MetTyLeuGlyLeuAsnTyValPheLeuLeuAsnGlyValGlnSerGlu 20
 QY 90 GTGAAGCTTGAGAGCTGGAGGAGCTGGTGCACCTGGAGGATCCATGAATCTCTCC 149
 Db 21 ValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
 QY 150 TGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGGATCTCTGGTCCGCGAGTCTCA 209
 Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60
 QY 210 GAGAAGGGGCTTCAGTGGGTTCGTGAATTCAGATTCGAATTCGAATTCACACACAT 269
 Db 61 GluLysGlyLeuGluTrpValAlaGluLeuArgSerLysAlaAsnHisAlaThrTy 80
 QY 270 TATCGAGTCTGTGAAGGAGTTCACATCTCAAGAGATGATTCACAAAGTCTGCTC 329
 Db 81 TyAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerVal 100
 QY 330 TACTCTCAATGACAGCTTAGAGCTGAAGAGCTGGAGTTTATCTACTGTACAGAT--- 386
 Db 101 TyLeuGlnMetAsnSerLeuArgAlaGluAspThrGlyIleTyrcysThrAspTrp 120
 QY 387 TTCATAGCTGGGGCCCAAGGACACTA 413
 Db 121 PheAlaTyTrpGlyGlnGlyThrLeu 129
 RESULT 11

AAV32263
 ID AAY32263 standard; protein; 444 AA.
 XX
 AC AAY32263;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Humanised anti-CD23 MAb C11 heavy chain.
 XX
 KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..30
 FT /note= "framework region 1"
 FT Region 31..35
 FT /note= "CDR 1"
 FT Region 36..49
 FT /note= "framework region 2"
 FT Region 50..58
 FT /note= "CDR 2"
 FT Region 59..100
 FT /note= "framework region 3"
 FT Region 101..103
 FT /note= "CDR 3"
 FT Region 104..111
 FT /note= "framework region 4"
 FT Region 112..444
 FT /note= "constant region"
 XX
 PN WO9958679-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-GB001434.
 XX
 PR 09-MAY-1998; 98GB-00009839.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX
 DR WPI; 2000-053101/04.
 DR N-PSDB; AAZ34748.
 XX
 PT Cell receptor specific antibodies useful for treating e.g. arthritis,
 XX diabetes, multiple sclerosis and psoriasis.
 PS Claim 9; Fig 4; 81pp; English.

This amino acid sequence represents the heavy chain of humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human framework (H5IGKVIT) and the heavy chain complementarity determining regions (see AAY32257-59) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,

CC glomerulonephritis, inflammatory bowel disease, ulcerative colitis,
CC Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
CC malignancies (claimed). They are also useful for studying interactions
CC between CD23 and various ligands and determining the binding agents
XX
XX
SQ Sequence 444 AA;

Alignment Scores:
Pred. No.: 1.03e-49 Length: 444
Score: 531.00 Matches: 97
Percent Similarity: 95.41% Conservativeness: 7
Best Local Similarity: 88.95% Mismatches: 5
Query Match: 70.52% Indels: 0
DB: 3 Gaps: 0

US-09-674-716B-1 (1-415) x AAY32263 (1-444)

QY 87 GAAGTGAAGCTTGAGGAGTCTGAGGAGGCTTGTCGAACCTGGAGGATCCATGAACCTC 146
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlyGlySerLeuArgueu 20
QY 147 TCTGTGTAGCTCTGGATTTACTTTCAAGTGCTACTCGATGTCTTGGTCCGCCAGTCT 206
Db 21 SerCysAlaAlaSerGlyPheThrPheSerGlyTyrTrpMetSerTrpValArgGlnAla 40
QY 207 CCAGAGAGGGCTTGAGTGGCTTCTGTAATAGATTCGAATCTGATAATATGCAACA 266
Db 41 ProGlyGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAspAsnTyrAlaThr 60
QY 267 CATTATGCCGAGTCTGTGAAGGAGGAGTTCACCATCTCAAGAGAGATGATTCACAAAGTGGT 326
Db 61 HistTyrAlaGluSerValLysGlyLysPheThrLysSerArgAspSerLysSerArg 80
QY 327 CTCCTACCTCAATAGACAGCTAGAGCTAGAGCTGAAGACAGCTGGAGTTTATCTGTACAGAT 386
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrAsp 100
QY 387 TTCATAGACTGGGGCCCAAGGGACACTA 413
Db 101 PheLeuAspTrpGlyGlnGlyThrLeu 109

RESULT 12

AAR52771

ID AAR52771 standard; protein; 134 AA.

XX AAR52771;

XX 25-MAR-2003 (revised)

DT 24-JAN-1995 (first entry)

XX Murine BrE-3 immunoglobulin heavy chain variable domain.

XX Immunoglobulin variable domain; primer; polymerase chain reaction;

XX chimeric antibody; human milk fat globule; BrE-3 VH-chain.

XX Mus musculus.

XX Key Location/Qualifiers

FT Protein 20..134

FT Region /label= BrE-3_VH-chain

FT Region 50..54

FT Region /label= CDR1

FT Region 69..87

FT Region /label= CDR2

FT Region 120..123

FT Region /label= CDR3

XX WO9411508-A2.

XX 26-MAY-1994.

XX 15-NOV-1993; 93WO-US011316.
XX 13-NOV-1992; 92US-00977706.
PR 13-NOV-1992; 92US-00977707.
PR 28-SEP-1993; 93US-00128015.
XX (CANC-) CANCER RES FUND CONTRA COSTA.
XX WPI; 1994-183509/22.
DR N-PSDB; AAQ62750.
XX Chimeric human-murine polypeptide(s) specific for human mammary fat
PT globule antigen - for imaging, diagnosing and treating neoplasia, with
PT less undesirable immunogenic response.
XX Example 10; Page 32; 54pp; English.
XX Primers JO2, JO3, JO4, JO14 and VH1BACK (AAQ62740-Q62744) were all used
CC to prepare cDNAs that encode the BrE-3 mouse Ig variable domains. The
CC amplified V-regions lacked constant regions so as to produce less
CC immunogenic polypeptides. A hybrid polypeptide was prepared using human
CC constant regions with the murine V regions. The chimeric polypeptide
CC retained the binding affinity of BrE-3 for human milk fat globule.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 134 AA;

Alignment Scores:
Pred. No.: 4.16e-49 Length: 134
Score: 524.50 Matches: 102
Percent Similarity: 88.37% Conservativeness: 12
Best Local Similarity: 79.07% Mismatches: 12
Query Match: 69.65% Indels: 3
DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) x AAR52771 (1-134)

QY 36 ATGATTTTGGGCTG-----ATTTTTTATTTGTTCTTTTAAAGGGTCCAGAGTAA 89
Db 1 MetTyrLeuGlyLeuAsnTyrValPheLeuLeuLeuGlyValGlnSerGlu 20
QY 90 GTGAGCTTGGAGAGTCTGGAGGAGGCTTGGTCAACCTGGAGATCCATGAACCTCTCC 149
Db 21 ValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
QY 150 TGTGTAGCTCTGTGATTTACTTTTTCAGTGGCTACTGTGATGTCTTGGGTCCGCCAGTCTCCA 209
Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60
QY 210 GAGAAGGGGCTTGAGTGGTGTCTGAAATAGATTGAATCTGATATATTATGCAACAT 269
Db 61 GluLysGlyLeuGluTrpValAlaGluLeuArgAsnLysAlaAsnHisAlaThrTyr 80
QY 270 TATCGGAGTCTGTGAAAGGAGAGTTCACCATCTCAAGAGATGATTCAAAAGTCGTCTC 329
Db 81 TyrAspGluSerValLysGlyArgPheThrLysSerArgAspSerLysSerArgVal 100
QY 330 TACCTGCAATGAACAGCTTAAGAGCTGAACAGAGTGGAGTTTATTACTGTAC---GAT 386
Db 101 TyrLeuGlnMetIleSerLeuArgAlaGluAspThrGlyLeuTyrTyrCysThrGlyGlu 120
QY 387 TTCATAGACTGGGGCCCAAGGGACACTA 413
Db 121 PheAlaAsnTrpGlyGlnGlyThrLeu 129

RESULT 13

AAR52789

ID AAR52789 standard; protein; 134 AA.

XX AAR52789;

XX 25-MAR-2003 (revised)

DT 25-MAR-2003 (revised)

DT 24-JAN-1995 (first entry)
 XX Murine BrE-3 immunoglobulin heavy chain variable domain.
 DE
 XX
 XX Immunoglobulin variable domain; primer; polymerase chain reaction;
 KW chimeric antibody; human milk fat globule; BrE-3 VH-chain.
 XX
 XX Mus musculus.

Key Location/Qualifiers
 FT Protein 20..134
 FT /label= BrE-3_VH-chain
 FT Region 50..154
 FT /label= CDR1
 FT Region 69..187
 FT /label= CDR2
 FT Region 120..123
 FT /label= CDR3

XX WO9411509-A2.

XX 26-MAY-1994.

XX 16-NOV-1993; 93WO-US011445.

XX 16-NOV-1992; 92US-00977696.

XX 30-SEP-1993; 93US-00129930.

XX 08-OCT-1993; 93US-00134346.

XX (CANC-) CANCER RES FUND CONTRA COSTA.

XX Do Couto FJR, Ceriani RL, Peterson JA, Padlan EA;

XX WPI; 1994-183510/22.

XX New analogue peptide(s) comprising antibody variable regions - used to
 develop prods. for use in the detection, diagnosis, therapy and
 prevention of neoplasms.

XX Example 11; Page 48; 109pp; English.

XX Primers J02, J03, J04, J014 and VHLBACK (AAQ62765-Q62769) were all used
 to prepare cDNAs that encode the BrE-3 mouse Ig variable domains. The
 amplified V-regions lacked constant regions so as to produce less
 immunogenic polypeptides. A hybrid polypeptide was prepared using human
 constant regions with the murine V regions. The chimeric polypeptide
 retained the binding affinity of BrE-3 for human milk fat globule.
 CC (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 134 AA;

Alignment Scores:
 Pred. No.: 4,156-49 Length: 134
 Score: 524.50 Matches: 102
 Percent Similarity: 88.37% Conservative: 12
 Best Local Similarity: 79.07% Mismatches: 12
 Query Match: 69.65% Indels: 3
 DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) x AAR52789 (1-134)

QY 36 ATGATTTGGGTG-----ATTTTATTTATGTTTAAAGGGTCCAGACTGAA 89
 Db 1 MetTyrLeuGlyLeuAsnTyrValPheIleValPheLeuLeuLeuGlyValGlnSerGlu 20
 QY 90 GTCAAGCTTGAGAGCTGGAGAGGCTTGGTGCAACTGGGAGGATCCATGAAGACTCTCC 149
 Db 21 ValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
 QY 150 TGTGTAGCTCTGGATTTACTTTTCAGTGGCTACTGGATCTTGGGTCCGCCAGTCTCCA 209
 Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTyrMetAspTrpValArgGlnSerPro 60

QY 210 GAGAAAGGGCTTGAGTGGTGTGCTGAAATAGATTGAATCTGATTAATATGCAACACAT 269
 Db 61 GluLysGlyLeuGluTrpValAlaGluIleArgAsnLysAlaAsnHisAlaThrTyr 80
 QY 270 TATCGGAGCTGTGAAAGGGAAGTTCCACCATCTCAAGAGATGATTCCAAAGTCGTCTC 329
 Db 81 TyrAspGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerArgVal 100
 QY 330 TACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA--GAT 386
 Db 101 TyrLeuGlnMetIleSerLeuArgAlaGluAspThrGlyLeuTyrCysThrGlyGlu 120
 QY 387 TTCATAGACTGGGCGCCAGGACACTA 413
 Db 121 PheAlaAsnTrpGlyGlnGlyThrLeu 129

RESULT 14

AA39451

ID AAY39451 standard; protein; 570 AA.

XX AAY39451;

DT 19-NOV-1999 (first entry)

DE Antibody ABX-CBL heavy chain sequence.

XX Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
 KW organ transplant rejection disease; lymphoma; pancreatic disease;
 KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Homo sapiens.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

XX 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LI, Hales J;
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX N-PSDB; AAZ20419.

XX New monoclonal antibody, used for treating e.g. graft versus host
 disease, cancers, autoimmune diseases and inflammatory diseases.

XX Disclosure; Page 58; 245pp; English.

XX This sequence represents the heavy chain of the antibody ABX-CXL. The
 invention relates to a monoclonal antibody (mAb) with an isotype that
 fixes complement and a variable region that binds to the epitope on CD147
 bound by the IGM mAb ABX-CBL, providing that the antibody is not CBL1.
 CC The mAb can selectively kill activated T-cells, activated B-cells or
 CC resting or activated monocytes. The products and methods can be used for
 CC treating diseases involving activated T-cells or B-cells or monocytes,
 CC e.g. graft versus host disease (GVHD), organ transplant rejection
 CC diseases (e.g. renal transplant, ocular transplant), cancers (e.g.
 CC cancers of the blood (e.g. leukaemia's and lymphomas) and pancreatic),
 CC autoimmune diseases (e.g. lupus), and inflammatory diseases (e.g.
 CC arthritis)

XX Sequence 570 AA;

Alignment Scores:

Pred. No.: 1,22e-48 Length: 570
 Score: 521.50 Matches: 97

Percent Similarity: 95.43% Conservative: 8
Best Local Similarity: 88.18% Mismatches: 4
Query Match: 69.26% Indels: 1
DB: 2 Gaps: 1

US-09-674-716B-1 (1-415) x AAY39451 (1-570)

QY 87 GAAGTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGAACCTGGAGAGTCCATGAATC 146
Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTGTAGCTCTGGATTACTTTTCACTGCTACTGATGCTTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAAGGGCTTCACTGGCTTCTGAAATAGATTCAAATCTGATATTCACAA 266
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnTyrAlaThr 60
QY 267 CATTATGGGAGCTCTGAAAGGAGTTCACATCTCAAGAGATGATCCAAAGTCT 326
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerA-GASPSPSerLysSer 80
QY 327 CTTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTCTGTACAGAT 386
Db 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyr-Tyr-CysThrAsp 100
QY 387 TTC---ATAGACTGGGGCCAGGACACTA 413
Db 101 TyrAspAlaTyrTrpGlyGlnGlyThrLeu 110

RESULT 15

ID ABO10742

XX ID ABO10742 standard; protein; 123 AA.

AC ABO10742;

XX 20-AUG-2003 (first entry)

XX Variable region of murine antibody MuVHIIC.

XX Modified antibody; deimmunised antibody; anti-PSMA antibody;

XX prostate specific membrane antigen; immunogenic; CDR; murine;

XX complementarity determining region; J591; J415; J533; E99; mouse;

XX prostatic disorder; cancerous disorder; genitourinary inflammation;

XX prostaticitis; benign enlargement; prostatic cancer; testicular cancer;

XX solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;

XX antiinflammatory; cycostatic; framework region; variable heavy chain;

XX variable light chain; VH; VL; variable region.

XX Mus musculus.

OS WO200298897-A2.

PN 12-DEC-2002.

XX 30-MAY-2002; 2002WO-US017068.

XX 01-JUN-2001; 2001US-0295214P.

PR 20-SEP-2001; 2001US-0323585P.

PR 08-MAR-2002; 2002US-0362810P.

XX (CORR) CORNELL RES FOUND INC.

XX Bander N, Carr FU, Hamilton A;

PI WPI; 2003-156839/15.

DR New modified anti-prostate specific membrane antigen (PSMA)

XX immunoglobulins, useful for treating or preventing a prostatic or

PT cancerous disorder, e.g. genitourinary inflammation, prostaticitis, or

PT prostatic or testicular cancer.

XX

PS Disclosure; Fig 7C; 254pp; English.

XX The present invention relates to modified (e.g. deimmunised) antibodies

CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA

CC antibodies are less immunogenic compared to the unmodified anti-PSMA

CC antibodies. The modified antibodies comprise complementarity determining

CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415,

CC J533 or E99), and framework sequences that are less immunogenic in humans

CC (e.g. less antigenic than the murine frameworks in which a murine CDR

CC naturally occurs). The modified antibodies bind with PSMA, preferably

CC human PSMA, with high affinity and specificity. The anti-PSMA antibodies

CC are useful for treating or preventing a prostatic or cancerous disorder,

CC e.g. genitourinary inflammation, prostaticitis, benign enlargement,

CC prostatic cancer or testicular cancer, or solid tumours, soft tissue

CC tumours or metastatic lesions, and its associated pain. The present

CC sequence represents a variable region from a murine antibody

XX Sequence 123 AA;

Alignment Scores:

Pred. No.: 1.88e-48 Length: 123

Score: 518.50 Matches: 98

Percent Similarity: 88.14% Conservative: 6

Best Local Similarity: 83.05% Mismatches: 5

Query Match: 68.86% Indels: 9

DB: 6 Gaps: 1

US-09-674-716B-1 (1-415) x ABO10742 (1-123)

QY 87 GAAGTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGAACCTGGAGATCCATGAATC 146

Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20

QY 147 TCCTGTGTAGCTCTGGATTACTTTTCACTGCTACTGATGCTTGGTCCGCCAGTCT 206

Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40

QY 207 CCAGAGAAGGGCTTCACTGGCTTCTGAAATAGATTCAAATCTGATATTCACAA 266

Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAsnTyrAlaThr 60

QY 267 CATTATGGGAGCTCTGAAAGGAGTTCACATCTCAAGAGATGATCCAAAGTCT 326

Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerA-GASPSPSerLysSer 80

QY 327 CTTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTCTGTACAGAT 386

Db 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyr-Tyr-CysThrThr 100

QY 387 -----TTCATAGACTGGGGCCAGGACACTA 413

Db 101 GlyGlyTyrGlyGlyArgG-SerTrpPheAlaTyr-TrpGlyGlnGlyThrLeu 118

Search completed: September 30, 2004, 08:40:50

Job time : 54.4398 secs

Blank Sheet

| Score | Match | Length | DB | ID | Description |
|-------|-------|--------|----|----|-------------|
|-------|-------|--------|----|----|-------------|

; PRIOR APPLICATION NUMBER: 60/124,658
 ; PRIOR FILING DATE: 1999-03-16
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 09/203,939
 ; PRIOR FILING DATE: 1998-12-02
 ; PRIOR APPLICATION NUMBER: 09/251,835
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 09/308,503
 ; PRIOR FILING DATE: 1999-05-25
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: SCID Mice
 ; US-09-564-329A-15

Alignment Scores:
 Pred. No.: 5,19e-51 Length: 151
 Score: 573.50 Matches: 109
 Percent Similarity: 92.31% Conservative: 11
 Best Local Similarity: 83.85% Mismatches: 5
 Query Match: 76.16% Indels: 5
 DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) X US-09-564-329A-15 (1-151)

```

QY 39 GATTTGGGCTG-----ATTGTTTATGTTCTTTTAAAGGGTCAGAGTGAAGTG 92
Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGAGTCTCGAGAGGCTTGGTGCACCTGAGGATCCATGAAACTCTCCGT 152
Db 22 ArgLeuGluGlySerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCCTCTGGATTTACTTTCAGTGGCTACTGATGCTGGTCCGCGAGTCTCCAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTCAGTGGCTTCTGAAATGAGTGAATCTGAATCTGAATATGCAACATTA 272
Db 62 LysGlyLeuGluTrpValAlaGluIleArgLeuArgSerGlyLeuValAlaThrHisTyr 81
QY 273 GCGAGTCTGTGAAGGGAAGTTCCACATCTCAAGAGATGATTCACAAAGTCTCTAC 332
Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
QY 333 CTGCAATGAACAGCTTAAGACTGAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

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RESULT 2

US-09-855-153-15
 ; Sequence 15, Application US/09855153
 ; Patent No. US20020102666A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; TITLE OF INVENTION: PSICA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US14
 ; CURRENT APPLICATION NUMBER: US/09/855,153
 ; CURRENT FILING DATE: 2001-05-14
 ; PRIOR APPLICATION NUMBER: 09/564,329
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 09/359,326
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 08/814,279

; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 60/113,230
 ; PRIOR FILING DATE: 1998-12-21
 ; PRIOR APPLICATION NUMBER: 60/120,536
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 60/124,658
 ; PRIOR FILING DATE: 1999-03-16
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 09/203,939
 ; PRIOR FILING DATE: 1998-12-02
 ; PRIOR APPLICATION NUMBER: 09/251,835
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 09/308,503
 ; PRIOR FILING DATE: 1999-05-25
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: SCID Mice
 ; US-09-855-153-15

Alignment Scores:

Pred. No.: 5,19e-51 Length: 151
 Score: 573.50 Matches: 109
 Percent Similarity: 92.31% Conservative: 11
 Best Local Similarity: 83.85% Mismatches: 5
 Query Match: 76.16% Indels: 5
 DB: 2 Gaps: 2

US-09-674-716B-1 (1-415) X US-09-855-153-15 (1-151)

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QY 39 GATTTGGGCTG-----ATTGTTTATGTTCTTTTAAAGGGTCAGAGTGAAGTG 92
Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGAGTCTCGAGAGGCTTGGTGCACCTGAGGATCCATGAAACTCTCCGT 152
Db 22 ArgLeuGluGlySerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCCTCTGGATTTACTTTCAGTGGCTACTGATGCTGGTCCGCGAGTCTCCAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTCAGTGGCTTCTGAAATGAGTGAATCTGAATCTGAATATGCAACATTA 272
Db 62 LysGlyLeuGluTrpValAlaGluIleArgLeuArgSerGlyIleTyrCysThrAspGlyLeu 81
QY 273 GCGAGTCTGTGAAGGGAAGTTCCACATCTCAAGAGATGATTCACAAAGTCTCTAC 332
Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
QY 333 CTGCAATGAACAGCTTAAGACTGAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

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RESULT 3

US-09-854-811-15
 ; Sequence 15, Application US/09854811
 ; Patent No. US20020119157A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; APPLICANT: Saffran, Douglas C.

; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/854,811
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-854-811-15

Alignment Scores:
Pred. No.: 5,19e-51 Length: 151
Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 9 Gaps: 2

US-09-674-716B-1 (1-415) x US-09-854-811-15 (1-151)

QY 39 GATTTGGGCTG-----ATTGTTTATGTTCTTTTAAAGGGGTCCAGAGTGAAGTG 92
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QY 93 AAGCTTGAGAGCTCGAGAGGCTTGGTGCACCTGGAGATCCATGAACTCTCCNGT 152
Db 22 ArgLeuGluGlySerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCTCTGGATTACTTTTCAGTGGTCTACTGGATGCTTGGGTCCCGCAGTCTCCAGAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTGAGTGGTCTGCTCAATGAACTGAACTGATAATGATGCAACACATTAT 272
Db 62 LysGlyLeuGluTrpValAlaGluLeuArgLeuArgSerGluAsnTyAlaThrHisTy 81
QY 273 GCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCTCTCTAC 332
Db 82 AlaGluSerValLysGlyPheThrIleSerArgSerArgSerArgLeuTy 101
QY 333 CTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTCTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnLeuArgProGluAspSerGlyIleTyTyrcysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGCACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 4

US-09-934-773-15
; Sequence 15, Application US/09934773
; Patent No. US20020136689A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/934,773
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141

; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-934-773-15

Alignment Scores:

Pred. No.: 5,19e-51 Length: 151
Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 9 Gaps: 2

US-09-674-716B-1 (1-415) x US-09-934-773-15 (1-151)

QY 39 GATTTGGGCTG-----ATTGTTTATGTTCTTTTAAAGGGGTCCAGAGTGAAGTG 92
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QY 93 AAGCTTGAGAGCTCGAGAGGCTTGGTGCACCTGGAGATCCATGAACTCTCTCTGT 152
Db 22 ArgLeuGluGlySerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCTCTGGATTACTTTTCAGTGGTCTACTGGATGCTTGGGTCCCGCAGTCTCCAGAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTGAGTGGTGTGCTGAAATGAAATGAAATCTGATAATGCAACACATTAT 272
Db 62 LysGlyLeuGluTrpValAlaGluLeuArgLeuArgSerGluAsnTyAlaThrHisTy 81
QY 273 GCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCTCTCTAC 332
Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgSerArgSerArgLeuTy 101
QY 333 CTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTCTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnLeuArgProGluAspSerGlyIleTyTyrcysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGCACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 5

US-09-963-620-15
; Sequence 15, Application US/09963620
; Patent No. US20020141941A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14

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; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; TYPE: PRT
; LENGTH: 151
; ORGANISM: SCID Mice
US-09-963-620-15

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Alignment Scores:
Pred. No.: 151
Score: 573.50
Percent Similarity: 92.31%
Best Local Similarity: 83.85%
Query Match: 76.16%
Indels: 5
Gaps: 2
DB:

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US-09-674-716B-1 (1-415) X US-09-963-620-15 (1-151)

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QY 39 GATTGGGCTG-----ATTGTTTATTGTTCTTTTAAAGGGGTCAGAGTGAAGTG 92
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QY 93 AAGCTTGAGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAACTCTCCTGT 152
DB 22 ArgLeuGluSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCCTCTGGATTACTTTCAGTGCTACTGGATGCTTGGTCCGCGAGTCCAGAG 212
DB 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTCAGTGGTTCGCTGAATAGATTGAATCTGATAATTCACACATTAT 272
DB 62 LysGlyLeuGluTrpValAlaGluIleArgLeuArgSerGlyLeuAsnTyrAlaThrHisTyr 81
QY 273 GCGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCTCTTAC 332
DB 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
QY 333 CTCGAAATGACAGCTTAGAGCTGAAGACAGTGGAGTTTATCTACTGTCACATTTCATA 392
DB 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----CACTGGGGCCCAAGGCACACTA 413
DB 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

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US-09-855-632-15
; Sequence 15, Application US/09855632
; Publication No. US20030113816A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Safiran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435,54US14
; CURRENT APPLICATION NUMBER: US/09/855,632
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; TYPE: PRT
; LENGTH: 151
; ORGANISM: SCID Mice
US-09-855-632-15

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Alignment Scores:

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Pred. No.: 151
Score: 573.50
Percent Similarity: 92.31%
Best Local Similarity: 83.85%
Query Match: 76.16%
Indels: 5
Gaps: 2
DB:

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US-09-674-716B-1 (1-415) X US-09-855-632-15 (1-151)

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QY 39 GATTGGGCTG-----ATTGTTTATTGTTCTTTTAAAGGGGTCAGAGTGAAGTG 92
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QY 93 AAGCTTGAGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAACTCTCCTGT 152
DB 22 ArgLeuGluSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCCTCTGGATTACTTTCAGTGCTACTGGATGCTTGGTCCGCGAGTCCAGAG 212
DB 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTCAGTGGTTCGCTGAATAGATTGAATCTGATAATTCACACATTAT 272
DB 62 LysGlyLeuGluTrpValAlaGluIleArgLeuArgSerGlyLeuAsnTyrAlaThrHisTyr 81
QY 273 GCGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCTCTTAC 332
DB 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101

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QY 333 CTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----GACTGGGCGCAAGGACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131
RESULT 7
US-10-225-784-15
; Sequence 15, Application US/10225784
; Publication No. US20030113820A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSKA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/225,784
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-225-784-15
Alignment Scores:
Pred. No.: 5,19e-51 Length: 151
Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 14 Gaps: 2
US-09-674-716B-1 (1-415) x US-10-225-784-15 (1-151)
QY 39 GATTTGGCTG-----ATTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGTG 92
Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGGAGTCTGAGGAGGCTTGTCGAACCTGGAGGATCCATGAACTCTCCCTGT 152
Db 22 ArgLeuGluGlnSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCTCTGGAATTTACTTTCAGTGGCTACTCGATGTCTTGGTCCGCCAGTCTCCAGAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTGAGTGGTCTGCTGAATAGATTGAATCTGATAATATATCAACACATAT 272

Db 62 LysGlyLeuGluTrpValAlaGluIleArgLeuArgSerGluAsnTyrAlaThrHisTyr 81
QY 273 GCGAGTCTGTGAAGGAGTTCACCATCTCAAGAGATGATCCAAAGTCCGTCTCTAC 332
Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspAspSerArgSerArgLeuTyr 101
QY 333 CTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----GACTGGGCGCAAGGACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131
RESULT 8
US-10-224-720-15
; Sequence 15, Application US/10224720
; Publication No. US20030147806A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSKA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/224,720
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US/09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-224-720-15
Alignment Scores:
Pred. No.: 5,19e-51 Length: 151
Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 14 Gaps: 2
US-09-674-716B-1 (1-415) x US-10-224-720-15 (1-151)
QY 39 GATTTGGCTG-----ATTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGTG 92
Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGGAGTCTGAGGAGGCTTGTCGAACCTGGAGGATCCATGAACTCTCCCTGT 152
Db 22 ArgLeuGluGlnSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41

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QY 153 GTAGCCTCTGATTTACTTTCTAGTGCTACTGATGCTTGGTCCGCGAGTCTCCAGAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTGTAGTGGTGTCTGAAATAGATTGAAATCTGATAATATGCAACACATTAT 272
Db 62 LysGlyLeuGlnTrpValAlaGluIleArgLeuArgSerGluAsnTyrAlaThrHisTyr 81
QY 273 GCGAGTCTGTGAAGGAGTTCACCATCTCAAGAGATGATCCAAAGTCTCTCTAC 332
Db 82 AlaGluSerValysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
QY 333 CTCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131
RESULT 9
US-10-225-779-15
; Sequence 15, Application US/10225779
; Publication No. US20030153016A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/225,779
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-225-779-15
Alignment Scores:
Pred. No.: 5,19e-51 Length: 151
Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 14 Gaps: 2
US-09-674-716B-1 (1-415) x US-10-225-779-15 (1-151)
QY 39 GATTTGGGCTG-----ATTTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGTG 92

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Db 2 AspPheGlyLeuSerTrpValPheIleIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTTCAGAGTCTGAGGAGGCTTGGTCAACCTGGAGGATCCCATGAACTCTCCTGT 152
Db 22 ArgLeuGlnGluSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCCTCTGATTTACTTTCTAGTGGCTACTGGATGCTCTGGCTCCGCGAGTCTCCAGAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTGTAGTGGTGTCTGAAATAGATTGAAATCTGATAATATGCAACACATTAT 272
Db 62 LysGlyLeuGlnTrpValAlaGluIleArgLeuArgSerGluAsnTyrAlaThrHisTyr 81
QY 273 GCGAGTCTGTGAAGGAGTTCACCATCTCAAGAGATGATCCAAAGTCTCTCTAC 332
Db 82 AlaGluSerValysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
QY 333 CTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCATA 392
Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131
RESULT 10
US-10-374-381-15
; Sequence 15, Application US/10374381
; Publication No. US20030228318A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/374,381
; CURRENT FILING DATE: 2003-02-25
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US/09/564,329A
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-374-381-15
Alignment Scores:
Pred. No.: 5,19e-51 Length: 151
Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5

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DB: 15 Gaps: 2
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QY 39 GATTTCGGCTG-----ATTTCCTTTTAAAGGGTCCAGAGTGAAGTG 92
Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGAGTCTGGAGGAGCTTGGTCAACCTGGAGGATCCATGAATCTCCTGT 152
Db 22 ArgLeuGluGlySerGlyGlyGlyTrpValGlnProGlySerMetLysLeuSerCys 41
QY 153 GTAGCCTCGGATTACTTCAGTGGCTACTGGATGCTTGGGTCCGCCAGTCTCCAGAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTGAGTGGTCTGCTGAATAGATGAATCTGAATCTGAATCTGAATCTGAATCT 272
Db 62 LysGlyLeuGluTrpValAlaGluLeuArgLeuArgLeuArgLeuArgLeuArgLeu 81
QY 273 GCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCTCTCTAC 332
Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
QY 333 CTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTACTGTACAGATTTTATA 392
Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 11
US-10-446-542-15
; Sequence 15, Application US/10446542
; Publication No. US20040018571A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSMA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/446,542
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/855,153
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: "Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-446-542-15

Alignment Scores: 5,19e-51 Length: 151
Score: 575.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 15 Gaps: 2
US-09-674-716B-1 (1-415) x US-10-446-542-15 (1-151)
QY 39 GATTTCGGCTG-----ATTTCCTTTTAAAGGGTCCAGAGTGAAGTG 92
Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGAGTCTGGAGGAGCTTGGTCAACCTGGAGGATCCATGAATCTCCTGT 152
Db 22 ArgLeuGluGlySerGlyGlyGlyTrpValGlnProGlySerMetLysLeuSerCys 41
QY 153 GTAGCCTCGGATTACTTCAGTGGCTACTGGATGCTTGGGTCCGCCAGTCTCCAGAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTyrTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTGAGTGGTCTGCTGAATAGATGAATCTGAATCTGAATCTGAATCTGAATCT 272
Db 62 LysGlyLeuGluTrpValAlaGluLeuArgLeuArgLeuArgLeuArgLeuArgLeu 81
QY 273 GCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCTCTCTAC 332
Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
QY 333 CTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTACTGTACAGATTTTATA 392
Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

RESULT 12
US-09-947-839-13
; Sequence 13, Application US/09947839
; Publication No. US20030138428A1
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; Ceriani Dr., Roberto L.
; Peterson Dr., Jerry A.
; Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; Carcinoma Specificity, and Kit and
; Diagnostic Vaccination and
; Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/947,839
; FILING DATE: 06-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/976,288
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. US20030138428A1ember 16, 1992

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; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-947-839-13

Alignment Scores:
Pred. No.: 6 53e-46 Length: 134
Score: 524.50 Matches: 102
Percent Similarity: 88.37% Conservative: 12
Best Local Similarity: 79.07% Mismatches: 12
Query Match: 69.65% Indels: 3
DB: 10 Gaps: 2

US-09-674-716B-1 (1-415) X US-09-947-839-13 (1-134)
QY 36 ATGGATTGGGTG-----ATTGTTTATTGTTCTTTTAAAGGGTCCAGAGTGAA 89
Db 1 MetTyrLeuGlyLeuAsnTyrValPheIleValPheLeuLeuLysGlyValGlnSerGlu 20
QY 90 GTCAAGCTTCAGAGCTCGAGGAGCTGGTGCACACTGGAGGATCCATGAATCTCC 149
Db 21 ValLysLeuGlnGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
QY 150 TGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGATGCTCTGGTCCGCCAGTCTCCA 209
Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTyrMetAspTyrValArgGlnSerPro 60
QY 210 GAGAGGGCTTCAGCGGTTCGTGAATAGATTGAATTCGAAATCGAATATTCACACAT 269
Db 61 GluLysGlyLeuGlnTyrPheValAlaGluIleArgAsnLysAlaAsnHisAlaThrTyr 80
QY 270 TATCCGGAGCTCTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTC 329
Db 81 TyrAspGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerArgVal 100
QY 330 TACTGCAATGAACAGCTTACAGCTGAAGACAGTGGAGCTTATTACTGTACA---GAT 386
Db 101 TyrLeuGlnMetIleSerLeuArgAlaGluAspThrGlyLeuTyrCysThrGlyGlu 120
QY 387 TTCATAGACTGGGGCCCAAGGACACTA 413
Db 121 PheAlaAsnTyrGlyGlnGlyThrLeu 129

RESULT 13
US-10-160-506-69
; Sequence 69, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
; APPLICANT: Bandex, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
; FILE REFERENCE: 10448-162001
; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-449-379-69
; APPLICANT: Bandex, Neil H.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 10448-163002
; CURRENT APPLICATION NUMBER: US/10/449,379
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 10/160,505
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/323,595
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,810
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/295,214
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-449-379-69

Alignment Scores:
Pred. No.: 2 72e-45 Length: 123
Score: 518.50 Matches: 98
Percent Similarity: 88.14% Conservative: 6
Best Local Similarity: 83.05% Mismatches: 5
Query Match: 68.86% Indels: 9
DB: 14 Gaps: 1

US-09-674-716B-1 (1-415) X US-10-160-506-69 (1-123)
QY 87 GAAGTGAAGCTTCAGGAGTCTGGAGGAGGCTTGGTGCACACTGGAGGATCCATGAATC 146
Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGGAATGCTTGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTyrMetAsnTyrValArgGlnSer 40
QY 207 CCAGAGAAGGGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 266
Db 41 ProLysGlyLeuGluTyrPheValAlaGluIleArgLeuLysSerAspAsnTyrAlaThr 60
QY 267 CATATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTGT 326
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
QY 327 CTCTACCTGCAATGACAGCTTAAAGAGCTGAAGACAGTGGAGCTTATTACTGTACAGAT 386
Db 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrCysThrThr 100
QY 387 -----TTCATAGACTGGGGCCCAAGGACACTA 413
Db 101 GlyGlyTyrGlyArgSerTyrPheAlaTyrTyrGlyGlnGlyThrLeu 118

RESULT 14
US-10-449-379-69
; Sequence 69, Application US/10449379
; Publication No. US20040120958A1
; GENERAL INFORMATION:
; APPLICANT: Bandex, Neil H.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 10448-163002
; CURRENT APPLICATION NUMBER: US/10/449,379
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 10/160,505
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/323,595
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,810
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/295,214
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-449-379-69

Alignment Scores:
Pred. No.: 2 72e-45 Length: 123
Score: 518.50 Matches: 98
Percent Similarity: 88.14% Conservative: 6
Best Local Similarity: 83.05% Mismatches: 5
Query Match: 68.86% Indels: 9
DB: 14 Gaps: 1

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DB: 16 Gaps: 1
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DB 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTAGCTCTGGAATTTACTTTAGTCTGCTACTGATGCTTGGTCCGCGAGTCT 206
DB 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrTrpValArgGlnSer 40
QY 207 CCAGAGAGGGCTTGAGTGGTCTGCAATAGATTGAAATCTGATAATTATGCAACA 266
DB 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAspAsnTyrAlaThr 60
QY 267 CATTATGGGGAGCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCAAAAGTCGT 326
DB 61 HistyAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80
QY 327 CTCCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
DB 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrCysThrThr 100
QY 387 -----TTCATAGACTGGGGCCAAAGGACACTA 413
DB 101 GlyGlyTyrGlyGlyArgSerTrpPheAlaTyrTrpGlyGlnGlyThrLeu 118

RESULT 15

US-10-688-015-69
; Sequence 69, Application US/10688015
; Publication No. US20040136998A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: INSULIN-RELATED DISORDERS USING BINDING AGENTS SPECIFIC FOR
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
; FILE REFERENCE: 10448-196001
; CURRENT APPLICATION NUMBER: US/10/688,015
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/422,396
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-688-015-69

Alignment Scores:

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|------------------------|----------|---------------|-----|
| Pred. No.: | 2,72e-45 | Length: | 123 |
| Score: | 518.50 | Matches: | 98 |
| Percent Similarity: | 88.14% | Conservative: | 6 |
| Best Local Similarity: | 83.05% | Mismatches: | 5 |
| Query Match: | 68.86% | Indels: | 9 |
| DB: | 16 | Gaps: | 1 |

US-09-674-716B-1 (1-415) x US-10-688-015-69 (1-123)

QY 87 GAAGTGAAGCTTGAGAGCTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAACTC 146
DB 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTAGCTCTGGAATTTACTTTAGTCTGCTACTGATGCTTGGTCCGCGAGTCT 206
DB 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrTrpValArgGlnSer 40
QY 207 CCAGAGAGGGCTTGAGTGGTCTGCAATAGATTGAAATCTGATAATTATGCAACA 266
DB 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerAspAsnTyrAlaThr 60
QY 267 CATTATGGGGAGCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCAAAAGTCGT 326

Search completed: September 30, 2004, 09:48:28

Job time : 57.4329 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:41:28 ; Search time 10.1499 Seconds
(without alignments)
4221.672 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 753

Sequence: 1 aagctttacagtactacgc.....tggggccaaggacactagt 415

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORW=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09674716 @CGN 1 1 107 @runat_30092004_070259_25901 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:

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- 2: /cgn2_6/prodata/2/aaa/5B COMB.pcp:*
- 3: /cgn2_6/prodata/2/aaa/5A COMB.pcp:*
- 4: /cgn2_6/prodata/2/aaa/5B COMB.pcp:*
- 5: /cgn2_6/prodata/2/aaa/PCTUS COMB.pcp:*
- 6: /cgn2_6/prodata/2/aaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 573.5 | 76.2 | 151 | 4 | US-09-564-329A-15 |
| 2 | 524.5 | 69.7 | 134 | 1 | US-07-977-696C-13 |
| 3 | 524.5 | 69.7 | 134 | 1 | US-08-129-930B-13 |
| 4 | 524.5 | 69.7 | 134 | 4 | US-08-976-288A-13 |
| 5 | 507.67 | 67.3 | 120 | 3 | US-08-767-128-28 |
| 6 | 500 | 66.4 | 285 | 3 | US-09-318-661-4 |
| 7 | 500 | 66.4 | 285 | 4 | US-09-883-758-4 |
| 8 | 498.5 | 66.2 | 119 | 3 | US-08-767-128-26 |
| 9 | 491 | 65.2 | 114 | 3 | US-08-483-749A-10 |
| 10 | 480 | 65.1 | 122 | 3 | US-08-483-749A-2 |
| 11 | 488 | 64.8 | 298 | 2 | US-09-318-661-2 |
| 12 | 488 | 64.8 | 298 | 4 | US-09-883-758-2 |

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| 13 | 463 | 61.5 | 119 | 1 | US-08-192-102-5 | Sequence 5, Appl |
| 14 | 463 | 61.5 | 119 | 1 | US-08-324-799-5 | Sequence 5, Appl |
| 15 | 463 | 61.5 | 119 | 2 | US-08-192-861A-5 | Sequence 5, Appl |
| 16 | 463 | 61.5 | 119 | 3 | US-09-133-119-5 | Sequence 5, Appl |
| 17 | 463 | 61.5 | 119 | 3 | US-08-192-093A-5 | Sequence 5, Appl |
| 18 | 458.5 | 60.9 | 227 | 1 | US-08-681-432-2 | Sequence 6, Appl |
| 19 | 452 | 60.0 | 139 | 3 | US-09-136-315-6 | Sequence 6, Appl |
| 20 | 452 | 60.0 | 139 | 4 | US-09-767-888-6 | Sequence 6, Appl |
| 21 | 451 | 59.9 | 242 | 2 | US-08-224-591-14 | Sequence 14, Appl |
| 22 | 451 | 59.9 | 242 | 2 | US-08-392-338A-23 | Sequence 23, Appl |
| 23 | 451 | 59.9 | 242 | 2 | US-08-926-789-14 | Sequence 14, Appl |
| 24 | 451 | 59.9 | 242 | 3 | US-09-166-750-23 | Sequence 23, Appl |
| 25 | 451 | 59.9 | 242 | 3 | US-09-166-093-23 | Sequence 23, Appl |
| 26 | 451 | 59.9 | 242 | 3 | US-09-172-019-23 | Sequence 23, Appl |
| 27 | 451 | 59.9 | 242 | 3 | US-09-166-094-23 | Sequence 23, Appl |
| 28 | 451 | 59.9 | 242 | 4 | US-09-443-213-23 | Sequence 23, Appl |
| 29 | 451 | 59.9 | 244 | 5 | PCT-US93-11138-14 | Sequence 14, Appl |
| 30 | 450 | 59.8 | 115 | 1 | US-08-468-661-1 | Sequence 1, Appl |
| 31 | 450 | 59.8 | 115 | 1 | US-08-466-272A-1 | Sequence 1, Appl |
| 32 | 450 | 59.8 | 115 | 1 | US-08-478-857-1 | Sequence 1, Appl |
| 33 | 450 | 59.8 | 115 | 2 | US-08-471-771-1 | Sequence 1, Appl |
| 34 | 450 | 59.8 | 115 | 3 | US-09-130-783-1 | Sequence 13, Appl |
| 35 | 450 | 59.8 | 244 | 2 | US-08-392-338A-13 | Sequence 13, Appl |
| 36 | 450 | 59.8 | 244 | 3 | US-09-166-750-13 | Sequence 13, Appl |
| 37 | 450 | 59.8 | 244 | 3 | US-09-166-093-13 | Sequence 13, Appl |
| 38 | 450 | 59.8 | 244 | 3 | US-09-172-019-13 | Sequence 13, Appl |
| 39 | 450 | 59.8 | 244 | 3 | US-09-166-094-13 | Sequence 13, Appl |
| 40 | 450 | 59.8 | 244 | 4 | US-09-443-213-13 | Sequence 13, Appl |
| 41 | 447 | 59.4 | 250 | 2 | US-08-392-338A-15 | Sequence 15, Appl |
| 42 | 447 | 59.4 | 250 | 3 | US-09-166-750-15 | Sequence 15, Appl |
| 43 | 447 | 59.4 | 250 | 3 | US-09-166-093-15 | Sequence 15, Appl |
| 44 | 447 | 59.4 | 250 | 3 | US-09-172-019-15 | Sequence 15, Appl |
| 45 | 447 | 59.4 | 250 | 3 | US-09-166-094-15 | Sequence 15, Appl |

ALIGNMENTS

RESULT 1

US-09-564-329A-15

; Sequence 15, Application US/09564329A

; Patent No. 6541212

; GENERAL INFORMATION:

; APPLICANT: Reiter, Robert E.

; APPLICANT: Witte, Owen N.

; FILE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

; FILE REFERENCE: 30435.54US14

; CURRENT APPLICATION NUMBER: US/09/564,329A

; CURRENT FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: 09/359,326

; PRIOR FILING DATE: 1999-07-20

; PRIOR APPLICATION NUMBER: 08/814,279

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: 60/071,141

; PRIOR FILING DATE: 1998-01-12

; PRIOR APPLICATION NUMBER: 60/074,675

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: 60/113,230

; PRIOR FILING DATE: 1998-12-21

; PRIOR APPLICATION NUMBER: 60/120,536

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: 60/124,658

; PRIOR FILING DATE: 1999-03-16

; PRIOR APPLICATION NUMBER: 09/038,261

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 09/203,939

; PRIOR FILING DATE: 1998-12-02

; PRIOR APPLICATION NUMBER: 09/251,835

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: 09/308,503

; PRIOR FILING DATE: 1999-05-25

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 15
LENGTH: 151
TYPE: PRT
ORGANISM: SCID Mice
US-09-564-329A-15

Alignment Scores:
Pred. No.: 2,68e-62 Length: 151
Score: 573.50 Matches: 109
Percent Similarity: 92.31% Conservative: 11
Best Local Similarity: 83.85% Mismatches: 5
Query Match: 76.16% Indels: 5
DB: 4 Gaps: 2

US-09-674-716B-1 (1-415) X US-09-564-329A-15 (1-151)

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QY 39 GATTTGGCTG-----ATTATTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGTG 92
Db 2 AspPheGlyLeuSerTrpValPheIleValLeuLeuLysGlyValArgSerGluVal 21
QY 93 AAGCTTGAGAGTCTGGAGGAGCTTGTGCAACCTGGAGGATCCATGAACCTCTCTGT 152
Db 22 ArgLeuGluSerGlyGlyTrpValGlnProGlyGlySerMetLysLeuSerCys 41
QY 153 GTAGCTCTGGATTACTTTCAGTGGCTACTGATGCTTGGTCCGCGAGTCTCCAGAG 212
Db 42 ValAlaSerGlyPheThrPheSerAsnTrpMetThrTrpValArgGlnSerProGlu 61
QY 213 AAGGGCTTGAGTGGCTTGTGAAATAGATTGAAATCTGAAATATGCAACACATTAT 272
Db 62 LysGlyLeuGluTrpValAlaGluIleArgLeuArgSerGluAsnTrpAlaThrHisTyr 81
QY 273 GCGAGTCTGTGAAGAGGAGTTCACATCTCAAGAGATGATCCAAAGTCTCTAC 332
Db 82 AlaGluSerValLysGlyLysPheThrIleSerArgAspSerArgSerArgLeuTyr 101
QY 333 CTCCAATGAACAGCTTAAGAGCTGAAGACAGTGAAGTGTATTAATCTACATACATTCATA 392
Db 102 LeuGlnMetAsnAsnLeuArgProGluAspSerGlyIleTyrCysThrAspGlyLeu 121
QY 393 -----GACTGGGGCCCAAGGACACTA 413
Db 122 GlyArgProAsnTrpGlyGlnGlyThrLeu 131

```

RESULT 2

US-07-977-696C-13
Sequence 13, Application US/07977696C
Patent No. 5792852

GENERAL INFORMATION:

APPLICANT: do Couto, Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
TITLE OF INVENTION: and Therapeutic Methods.
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38227
TELEPHONE: (510) 748-6668
TELEFAX: (510) 748-6668
TELEX: n.a.

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-977-696C-13

Alignment Scores:
Pred. No.: 2,86e-56 Length: 134
Score: 524.50 Matches: 102
Percent Similarity: 88.37% Conservative: 12
Best Local Similarity: 79.07% Mismatches: 12
Query Match: 69.65% Indels: 3
DB: 1 Gaps: 2

US-09-674-716B-1 (1-415) X US-07-977-696C-13 (1-134)

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QY 36 ATGATTTTGGCTG-----ATTATTTTATTGTTCTTTTAAAGGGTCCAGAGTGAA 89
Db 1 MetTyrLeuGlyLeuAsnTrpValPheIleValPheLeuLeuLysGlyValGlnSerGlu 20
QY 90 GTGAAGCTTCAGAGAGTCTGGAGGAGCTTGGTCAACCTGGAGGATCCATGAACCTCTCC 149
Db 21 ValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
QY 150 TGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGATGCTTTGGTCCGCGAGTCTCCA 209
Db 41 CysAlaAlaSerGlyPheThrPheSerArgAspAlaTrpMetAspTrpValArgGlnSerPro 60
QY 210 GAGNAGGGCTTTCAGTGGTTCGTAATAGATTCGAATTCATATTCATATTCACACAT 269
Db 61 GluLysGlyLeuGluTrpValAlaGluIleArgAsnLysAlaAsnAsnHisAlaThrTyr 80
QY 270 TATCGCGAGTCTGTGAAGGAAAGTTCCACCATCTCAAGAGATGATTCCTCAAGTCTCTC 329
Db 81 TyrAspGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerArgVal 100
QY 330 TACTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTGGAGTTTACTGTACA---GAT 386
Db 101 TyrLeuGlnMetIleSerLeuArgAlaGluAspThrGlyLeuTyrCysThrGlyGlu 120
QY 387 TTCATAGACTGGGCGCCCAAGGACACTA 413
Db 121 PheAlaAsnTrpGlyGlnGlyThrLeu 129

```

RESULT 3

US-08-129-930B-13
Sequence 13, Application US/08129930B
Patent No. 5804187

GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California

APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESS: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFCC-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-129-930B-13

Alignment Scores:
Pred. No.: 2,86e-56 Length: 134
Score: 524.50 Matches: 102
Percent Similarity: 88.37% Conservative: 12
Best Local Similarity: 79.07% Mismatches: 12
Query Match: 69.65% Indels: 3
DB: 1 Gaps: 2

US-09-674-716B-1 (1-415) x US-08-129-930B-13 (1-134)

QY 36 ATGGATTGGCTG-----ATTTTATTGTTCTTTTAAAGGGTCCAGAGTCAA 89
Db 1 MetTyrLeuGlyLeuAsnTyrValPheLeuValPheLeuLeuGlyValGlnSerGlu 20
QY 90 GTGAAGCTTGGAGAGCTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAATCTCC 149
Db 21 ValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
QY 150 TGTGTAGCTCTGGATTCTTCTTCTAGTGGCTACTGGATGCTTGGCTCGGCGAGTCTCA 209
Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60
QY 210 GAGAAGGGCTTGGAGTGGTCTGCTGAATTTAGATTGAATCTGAATTTATGCAACACAT 269
Db 61 GluLysGlyLeuGluTrpValAlaGluLeuArgAsnLysAlaAsnHisAlaThrTyr 80
QY 270 TATCGGAGTCTGTGAAGGGAGAGTTCACCATCTCAAGAGATGATTCACAAAGTCGTCTC 329
Db 81 TyrAspGluSerValLysGlyArgPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60
QY 330 TACCTGCAATGAACAGCTTAAGAGCTGAAGAGTGAAGAGTGAAGTGAAGTGAAGTGAAG 413
Db 101 TyrLeuGlnMetLysLeuArgAlaGluAspThrGlyLeuTyrCysThrGlyGlu 120
QY 387 TTCATAGCTGGGCGCAAGGACACTA 413
Db 121 PheAlaAsnTrpGlyGlnGlyThrLeu 129

RESULT 4

US-08-976-288A-13
Sequence 13, Application US/08976288A
Patent No. 6315997
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.

APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESS: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-288A-13

Alignment Scores:
Pred. No.: 2,86e-56 Length: 134
Score: 524.50 Matches: 102
Percent Similarity: 88.37% Conservative: 12
Best Local Similarity: 79.07% Mismatches: 12
Query Match: 69.65% Indels: 3
DB: 4 Gaps: 2

US-09-674-716B-1 (1-415) x US-08-976-288A-13 (1-134)

QY 36 ATGGATTGGCTG-----ATTTTATTGTTCTTTTAAAGGGTCCAGAGTCAA 89
Db 1 MetTyrLeuGlyLeuAsnTyrValPheLeuLeuGlyValGlnSerGlu 20
QY 90 GTGAAGCTTGGAGAGCTCTGGAGAGGCTTGGTGCACCTGGAGATCCATGAATCTCC 149
Db 21 ValLysLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeuSer 40
QY 150 TGTGTAGCTCTGGATTCTTCTTCTAGTGGCTACTGGATGCTTGGCTCGGCGAGTCTCA 209
Db 41 CysAlaAlaSerGlyPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60
QY 210 GAGAAGGGCTTGGAGTGGTCTGCTGAATTTAGATTGAATTTATGCAACACAT 269
Db 61 GluLysGlyLeuGluTrpValAlaGluLeuArgAsnLysAlaAsnHisAlaThrTyr 80
QY 270 TATCGGAGTCTGTGAAGGGAGAGTTCACCATCTCAAGAGATGATTCACAAAGTCGTCTC 329
Db 81 TyrAspGluSerValLysGlyArgPheThrPheSerAspAlaTrpMetAspTrpValArgGlnSerPro 60

QY 330 TACCTGCAATGACAGCTTAAGAGCTGAAGAGCTGGAGTTTATTACTGTACA---GAT 386
 Db 101 TyrLeuGlnMetIleSerLeuArgAlaGluAspThrGlyLeuTyrCysThrGlyGlu 120
 QY 387 TTCATAGACTGGGGCCCAAGGACACTA 413
 Db 121 PheAlaAsnTrpGlyGlnGlyThrLeu 129

RESULT 5
 US-08-767-128-28
 ; Sequence 28, Application US/08767128
 ; Patent No. 6111079
 ; GENERAL INFORMATION:
 ; APPLICANT: WYLIE, DWANE E.
 ; APPLICANT: LOPEZ, OSVALDO
 ; APPLICANT: MURRAY, PETER JOSEPH
 ; APPLICANT: GOEBEL, PETER
 ; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
 ; NUCLEOTIDES CODING THEREFORE
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
 ; STREET: 3100 No. 6111079west Center, 90 South Seventh St
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/767,128
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/09258
 ; FILING DATE: 05-JUN-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/541,373
 ; FILING DATE: 10-OCT-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/462,798
 ; FILING DATE: 05-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Carter, Charles G.
 ; REGISTRATION NUMBER: 35,093
 ; REFERENCE/DOCKET NUMBER: 8648.49USF1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 612/371-5278
 ; TELEFAX: 612/332-9081
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 120 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; US-08-767-128-28

Alignment Scores: 3.96e-54 Length: 120
 Pred. No.:

Score: 507.00 Matches: 95
 Percent Similarity: 89.57% Conservative: 8
 Best Local Similarity: 82.61% Mismatches: 6
 Query Match: 67.33% Indels: 6
 DB: 3 Gaps: 1
 US-09-674-716B-1 (1-415) x US-08-767-128-28 (1-120)
 QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGAGGCTTGGTCAACCTGGAGGATCCATGAACCTC 146
 Db 1 GluValIleThrGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
 QY 147 TCCTGTAGCCTCTGAGTTACTTTCAGTGGGTACTGATGCTTGGTCCGCCAGTCT 206
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
 QY 207 CCAGAGAAGGGCTTGAGTGGTCTGCTGAAATAGATTGAAATCTGATAATTATGCAACA 266
 Db 41 ProGluLysGlyLeuGluTrpValAlaGluIleArgLeuLysSerAsnAsnTyrAlaThr 60
 QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCCCATCTCAAGAGATGATCCAAAAGTCGT 326
 Db 61 HisTyrAlaGluSerValLysGlyA:GpheThrIleSerArgAspAspSerLysSerSer 80
 QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGTGGAGTGGAGTTTATTACTGTACA--- 383
 Db 81 ValTyrLeuGlnMetAsnAsnLeuA:GalaGluAspThrGlyIleTyrTrpCysThrArg 100
 QY 384 -----GATTTCATAGACTGGGGCCCAAGGACACTA 413
 Db 101 TyrGlyArgGluGlyGlyPheAlaTyrTrpGlyGluGlyThrLeu 115

RESULT 6
 US-09-318-661-4
 ; Sequence 4, Application US/09318661
 ; Patent No. 6268488
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbas III, Carlos F.
 ; APPLICANT: Shabat, Doron
 ; APPLICANT: Rader, Christoph
 ; APPLICANT: List, Benjamin
 ; APPLICANT: Lerner, Richard A.
 ; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
 ; FILE REFERENCE: PLF00115
 ; CURRENT APPLICATION NUMBER: US/09/318,661
 ; CURRENT FILING DATE: 1999-05-25
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 285
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
 ; OTHER INFORMATION: residue sequence of catalytic fragment
 ; US-09-318-661-4

Alignment Scores:
 Pred. No.: 4.01e-53 Length: 285
 Score: 500.00 Matches: 96
 Percent Similarity: 87.61% Conservative: 3
 Best Local Similarity: 84.96% Mismatches: 10
 Query Match: 66.40% Indels: 4
 DB: 3 Gaps: 1
 US-09-674-716B-1 (1-415) x US-09-318-661-4 (1-285)
 QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGAGGCTTGGTCAACCTGGAGGATCCATGAACCTC 146
 Db 154 GluValMetLeuValGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 173
 QY 147 TCCTGTAGCCTCTGAGTTACTTTCAGTGGGTACTGATGCTTGGTCCGCCAGTCT 206

Db 174 SerCysValValSerGlyLeuThrPheSerArgPheTrpMetSerTrpValArgGlnSer 193
QY 207 CCAGAGAGGGGCTTCAGTGGCTGCTGAAATAGATTGAATCTGATAATATATCAACA 266
Db 194 ProGluLysGlyLeuGluTrpValAlaGluLeuLysSerAspAsnTyrAlaThr 213
QY 267 CATTATGCGGAGTCTGTGAAGGGAGTTCACCATCTCAAGAGATGATCCAAAAGTCGT 326
Db 214 HisTyrAlaGluSerValLysGlyLysPheThrIleSerArgAspSerLysSerArg 233
QY 327 CTCCTACTCCAAATGAACAGCTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA--- 383
Db 234 LeuTyrLeuGlnMetAsnSerLeuArgThrGluAspThrGlyIleTyrCysLysile 253
QY 384 -----GATTTCATAGACTGGGCCCAAGGACACTA 413
Db 254 TyrPheTyrSerPheSerTyrTrpGlyGlnGlyThrLeu 266
RESULT 7
US-09-893-758-4
; Sequence 4, Application US/09883758
; Patent No. 6677435
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/893,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1993-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment
US-09-893-758-4
Alignment Scores:
Pred. No.: 4,01e-53 Length: 285
Score: 500.00 Matches: 96
Percent Similarity: 87.61% Conservative: 3
Best Local Similarity: 84.96% Mismatches: 10
Query Match: 66.40% Indels: 4
DB: 4 Gaps: 1
US-09-674-716b-1 (1-415) x US-09-893-758-4 (1-285)
QY 87 GAAGTGAAGCTTGAGGAGTCTGAGGAGGCTTGGTCAACCTGGAGGATCCATGAACCTC 146
Db 154 GluValMetLeuValGluSerGlyGlyLeuValGlnProGlySerMetLysLeu 173
QY 147 TCCTGTGTAGCTCGGATTTACTTTCAGTGCTACTGAGTCTTGGTCCGCCAGTCT 206
Db 174 SerCysValValSerGlyLeuThrPheSerArgPheTrpMetSerTrpValArgGlnSer 193
QY 207 CCAGAGAGGGGCTTCAGTGGGTTGCTGAAATAGATTGAATCTGATAATATATCAACA 266
Db 194 ProGluLysGlyLeuGluTrpValAlaGluLeuLysSerAspAsnTyrAlaThr 213
QY 267 CATTATGCGGAGTCTGTGAAGGGAGTTCACCATCTCAAGAGATGATCCAAAAGTCGT 326
Db 214 HisTyrAlaGluSerValLysGlyLysPheThrIleSerArgAspSerLysSerArg 233
QY 327 CTCCTACTCCAAATGAACAGCTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACA--- 383

Db 234 LeuTyrLeuGlnMetAsnSerLeuArgThrGluAspThrGlyIleTyrCysLysile 253
QY 384 -----GATTTCATAGACTGGGCCCAAGGACACTA 413
Db 254 TyrPheTyrSerPheSerTyrTrpGlyGlnGlyThrLeu 266
RESULT 8
US-08-767-128-26
; Sequence 26, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-26
Alignment Scores:
Pred. NO.: 4.43e-53 Length: 119
Score: 498.50 Matches: 95
Percent Similarity: 89.57% Conservative: 8
Best Local Similarity: 82.61% Mismatches: 5

| | | | |
|---|--------|--|-----|
| Query Match: | 66.20% | Indels: | 7 |
| DB: | 3 | Gaps: | 2 |
| US-09-674-716B-1 (1-415) x US-08-767-128-26 (1-119) | | | |
| Qy | 87 | GAAGTCAGCTCGAGAGCTCTGGAGGAGCGCTTGTCGCAACTCGGAGGATC | |
| Db | 1 | GlualValysLeuGluGluSer-GlyGlyLeuValGlnProGlyGlySer | |
| Qy | 147 | TCTGTGTAGCCTCGGATTTACTTTCAGTGGCTACTCGATGCTCTGGG | |
| Db | 21 | SerCysValAlaSer-GlyPheThr-PheSerAsnYrTrpMetAsnTrpVal | |
| Qy | 207 | CCAGAGAGGGCGCTGAGTGGTTCCTGAAATTAGATTGAAATCTGATAA | |
| Db | 41 | ProGluLysGlyLeuGluTrpValAlaGluValargLeuLysSer---Asn | |
| Qy | 267 | CATTATGGGAGCTCTGTCAAAGGGAAGTTCACCATCTCAAGAGATGATT | |
| Db | 60 | HisTyAlaGluSerValLysGlyArgPheThrIleSerArgAspAspSer | |
| Qy | 327 | CNCTACCTCGAAATCAACAGCTTAAAGCTCAAGACAGTGGAGTTATTAT | |
| Db | 80 | ValTyLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyTrp | |
| Qy | 387 | TTCT-----ATAGATGGGGCCAAAGGACACTA | 413 |
| Db | 100 | TyrGivArgGluGlyGlyValAlaIleTyTrpGlyGlnGlyThrLeu | 114 |

RESULT 'S
 US-08-483-749A-10
 ; Sequence 10, Application US/08483749A
 ; Patent No. 6054561
 ; GENERAL INFORMATION:
 ; APPLICANT: RING, DAVID B.
 ; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
 ; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CHIRON CORPORATION
 ; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
 ; CITY: EMERYVILLE
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94682-8097
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,749A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SAVEREIDE, PAUL B.
 ; REGISTRATION NUMBER: 36,914
 ; REFERENCE/DOCKET NUMBER: 0508.008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (510) 601-2585
 ; TELEFAX: (510) 655-3542
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 114 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-483-749A-10

```

Best Local Similarity: 82.41% Mismatches: 8
Query Match: 65.21% Indels: 0
DB: 3 Gaps: 0

US-09-674-716B-1 (1-415) x US-08-483-749A-10 (1-114):

QY 87 GAAGTGAAGCTTACGAGCTCTGGAGGGGCTTGGTGCACACTGGAGGATCCATGAACCTC 116
Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTGTAGCCTCTGGATTTTACTTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGTCT 206
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAAGGGCTTGAGTGGTTCCTGAAATTAGATTGAAATCTCGATTAATTATGCAACA 266
Db 41 ProGluLysGlyLeuGluTrpValAlaGluTrileLysLeuLysSerAsnAsnTyPrThr 60
QY 267 CATTATGCGGAGCTCTGTGAAGGGAAGCTTCACCATCTCAAGAGATGATTCCTAAAAGTCGT 326
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrAlaSerArgAspSerLysSerSer 50
QY 327 CTCCTACCTGCAAAATCAAACAGCTTAAAGAGCTGAAGACACAGCTGGAGTTATTACTGTACAGAT 386
Db 81 IleTyLeuGlnMetAsnAsnLeuArgThrGluAspThrGlyIleTyPheCysThrPhe 100
QY 387 TTCATAGACTGGGGCCAAAGGGACA 410
Db 101 TrpAspTyTrpGlyArgGlyThr 108

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```

RESULT 10
US-08-483-749A-2
; Sequence 2, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483.749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-749A-2

Alignment Scores:
Pred. No.: 5e-52
Score: 490.00
Length: 122
Matches: 93

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US-08-192-102-5
 ; Sequence 5, Application US/08192102
 ; Patent No. 5656272
 ; GENERAL INFORMATION:
 ; APPLICANT: Le, Junming
 ; APPLICANT: Vilcek, Jan
 ; APPLICANT: Daddona, Peter E.
 ; APPLICANT: Grayeb, John
 ; APPLICANT: Knight, David M.
 ; APPLICANT: Siegel, Scott A.
 ; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND ASSAYS EMPLOYING
 ; TITLE OF INVENTION: ANTI-TNF ANTIBODIES
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/192,102
 ; FILING DATE: 04-FEB-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/192,093
 ; FILING DATE: 04-FEB-1994
 ; APPLICATION NUMBER: US 08/013,413
 ; FILING DATE: 02-FEB-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/010,406
 ; FILING DATE: 29-JAN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/943,852
 ; FILING DATE: 11-SEP-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/853,606
 ; FILING DATE: 18-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/670,827
 ; FILING DATE: 18-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brook, David E.
 ; REGISTRATION NUMBER: 22,592
 ; REFERENCE/DOCKET NUMBER: NY093-01M3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 861-6240
 ; TELEFAX: (617) 861-9540
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 119 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-192-102-5

Alignment Scores:
 Pred. No.: 1,07e-48 Length: 119
 Score: 463.00 Matches: 90
 Percent Similarity: 83.62% Conservative: 7
 Best Local Similarity: 77.59% Mismatches: 9
 Query Match: 61.49% Indels: 10
 DB: 1 Gaps: 2

US-09-674-716B-1 (1-415) x US-08-192-102-5 (1-119)
 QY 87 GAAGTGAAGCTTGAGGAGTCTGGTGCACCACTGGAGGATCCATGAATCTC 146
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Db . 1 GluVallylsLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
 QY 147 TCCTGTGTAGCCTCTGATTTACTTTCAGTGGTACTGATGCTCTGGTCCGCCAGTCT 206
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 21 SerCysValAlaSerGlyPheIlePheSerAsnHisTrpMetAsnTrpValArgGlnSer 40
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 207 CCAGAGAAGGGCTTGAGTGGTGTGAAATAGATTGAATCTGATTAATTATGCAACA 266
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 41 ProGlnlysglyLeuGlnTrpValAlaGluIleArgSerlysserIleasnSerAlaThr 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 267 CATTATCGGAGTCTGTGAAAGGGAAGTTCAACATCTCAAGAGATGATTCCTCAAAAGTCGT 326
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 HistyAlaGluSerVallysGlyA:GpheThrIleSerArgAspSerlysserAla 80
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGTGGAGTGTATTACTGTACA--- 383
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
 Db 81 ValTyrLeuGlnMetThrAspLeuA:GThrGluAspThrGlyValTyrTyrCysSerArg 100
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 384 -----GATTTTCATAGACTGGGGCCCAAGGACA 410
 |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
 Db 101 AsnTyrTyrGlySerThrTyrAspTyr-----TipGlyGlnGlyThr 114
 |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 14
 US-08-324-799-5
 ; Sequence 5, Application US/08324799
 ; Patent No. 5698195
 ; GENERAL INFORMATION:
 ; APPLICANT: Le, Junming
 ; APPLICANT: Vilcek, Jan
 ; APPLICANT: Daddona, Peter E.
 ; APPLICANT: Grayeb, John
 ; APPLICANT: Knight, David M.
 ; APPLICANT: Siegel, Scott A.
 ; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND PEPTIDES
 ; TITLE OF INVENTION: OF HUMAN TUMOR NECROSIS FACTOR
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/324,799
 ; FILING DATE: 18-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/192,093
 ; FILING DATE: 04-FEB-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/192,102
 ; FILING DATE: 04-FEB-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/192,861
 ; FILING DATE: 04-FEB-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/013,413
 ; FILING DATE: 02-FEB-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/010,406
 ; FILING DATE: 29-JAN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/943,852
 ; FILING DATE: 11-SEP-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/853,606
 ; FILING DATE: 18-MAR-1992
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: NYU93-01M4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-324-799-5

Alignment Scores:
Pred. No.: 1,07e-48 Length: 119
Score: 463.00 Matches: 90
Percent Similarity: 83.62% Conservative: 7
Best Local Similarity: 77.59% Mismatches: 9
Query Match: 61.49% Indels: 10
DB: 1 Gaps: 2

US-09-674-716B-1 (1-415) x US-08-324-799-5 (1-119)

QY 87 GAAGTGAAGCTTGAAGAGCTTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAATC 146
Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTGAGCTCTGGATTACTTTCAGTGCTACTGCTGCTGCTGCTGCTGCTGCTGCT 206
Db 21 SerCysValAlaSerGlyPheIlePheSerAsnHisTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAAGGGCTTGAAGGAGTTCACCATCTCAAGAGATGATTGAAATCTGATTAATGCAACA 266
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgSerLysSerIleAsnSerAlaThr 60
QY 267 CATTATCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTGAAATCTGATTAATGCAACA 326
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerAla 80
QY 327 CTCTACTGCTCAATGAACAGCTTAAGAGCTGACAGACAGCTGAGTTTATTACTGTACA--- 383
Db 81 ValTyrLeuGlnMetThrAspLeuArgThrGluAspThrGlyValTyrCysSerArg 100
QY 384 -----GATTTCATAGACTGGGCCCAAGGACA 410
Db 101 AsnTyrTyrGlySerThrTyrAspTyr-----TrpGlyGlnGlyThr 114

Search completed: September 30, 2004, 09:31:33

APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: NYU93-01M4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-324-799-5

Alignment Scores:
Pred. No.: 1,07e-48 Length: 119
Score: 463.00 Matches: 90
Percent Similarity: 83.62% Conservative: 7
Best Local Similarity: 77.59% Mismatches: 9
Query Match: 61.49% Indels: 10
DB: 1 Gaps: 2

US-09-674-716B-1 (1-415) x US-08-324-799-5 (1-119)

QY 87 GAAGTGAAGCTTGAAGAGCTTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAATC 146
Db 1 GluValLysLeuGluGluSerGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 147 TCCTGTGAGCTCTGGATTACTTTCAGTGCTACTGCTGCTGCTGCTGCTGCTGCTGCT 206
Db 21 SerCysValAlaSerGlyPheIlePheSerAsnHisTrpMetAsnTrpValArgGlnSer 40
QY 207 CCAGAGAAGGGCTTGAAGGAGTTCACCATCTCAAGAGATGATTGAAATCTGATTAATGCAACA 266
Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgSerLysSerIleAsnSerAlaThr 60
QY 267 CATTATCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTGAAATCTGATTAATGCAACA 326
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerAla 80
QY 327 CTCTACTGCTCAATGAACAGCTTAAGAGCTGACAGACAGCTGAGTTTATTACTGTACA--- 383
Db 81 ValTyrLeuGlnMetThrAspLeuArgThrGluAspThrGlyValTyrCysSerArg 100
QY 384 -----GATTTCATAGACTGGGCCCAAGGACA 410
Db 101 AsnTyrTyrGlySerThrTyrAspTyr-----TrpGlyGlnGlyThr 114

RESULT 15
US-08-192-861A-5
Sequence 5, Application US/0819286:1A
Patent No. 5919452
GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter E.
APPLICANT: Grayeb, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: METHODS OF TREATING TNF- α -MEDIATED DISEASE USING
NUMBER OF INVENTION: CHIMERIC ANTI-TNF ANTIBODIES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:

Thu Sep 30 13:18:40 2004

us-09-674-716b-1.ra1

Page 10

Job time : 13.1499 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:29:27 ; Search time 17.3249 Seconds
(without alignments)
4852.647 Million cell updates/sec

Title: US-09-674-716B-2

Perfect score: 785

Sequence: 1 aagctttacgttactcagc.....agttggaataaaacgtacg 437

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cnp2.1/USPTO.spool.p/US09674716/runat.30092004.070259.25882/app.query.fasta_1.3164
-DB=PIR_78 -QPMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEXT=0
-UNITS=BITS -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MIN=100 -THR MAX=15 -ALIGN=15 -MODES=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09674716 @CNP 1.1 152 @runat.30092004.070259.25882 -NCPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=5 -DELEXT=7

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 601 | 76.6 | 120 | 1 KVM567 | Ig kappa chain pre |
| 2 | 558 | 71.1 | 120 | 2 A29775 | Ig kappa chain pre |
| 3 | 542 | 69.0 | 112 | 1 KVM516 | Ig kappa chain v r |
| 4 | 539 | 68.7 | 113 | 1 KVM551 | Ig kappa chain v r |
| 5 | 522 | 66.5 | 120 | 2 B29775 | Ig kappa chain pre |
| 6 | 503 | 64.1 | 136 | 2 S40357 | Ig kappa chain v-j |
| 7 | 492 | 62.7 | 131 | 2 S40372 | Ig kappa chain v-j |
| 8 | 489 | 62.3 | 132 | 2 S26882 | Ig kappa chain v r |
| 9 | 487 | 62.0 | 133 | 2 S23230 | Ig kappa chain pre |
| 10 | 486 | 61.9 | 142 | 2 S22902 | Ig kappa chain v r |
| 11 | 485 | 61.8 | 135 | 2 S40342 | Ig kappa chain - h |
| 12 | 483 | 61.5 | 197 | 2 S29593 | Ig kappa chain (WM |
| 13 | 479 | 61.0 | 133 | 1 K2HURP | Ig kappa chain pre |
| 14 | 479 | 61.0 | 133 | 2 S40324 | Ig kappa chain v r |

ALIGNMENTS

RESULT 1

KVM567

Ig kappa chain precursor V region (VK167) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000

C:Accession: A01909

R:Selsing, E.; Storb, U.

Cell 25, 47-58, 1981

A>Title: Somatic mutation of immunoglobulin light-chain variable-region genes.

A:Reference number: A01909; MUID:82002223; PMID:6791832

A:Accession: A01909

A:Molecule type: DNA

A:Residues: 1-120 <SEL>

A>Note: the sequence was determined from the germline gene

C:Genetics: 17/1

A:introns: 17/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>

F:136-115/Domain: immunoglobulin homology <IMM>

F:143-113/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 1,31e-51 Length: 120
Score: 601.00 Matches: 117
Percent Similarity: 99.17% Conservative: 2
Best Local Similarity: 97.50% Mismatches: 1
Query Match: 76.56% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KVM567 (1-120)

Qy 36 ATGAGGTCTCTGTTTCAGTTCTGGGGTCTTATGTTCTGATCTCTGGAGTCAGTGGG 95

Db 1 MetArgCysSerLeuGlnPheLeuGlyValIleuMetPheIrrIleSerGlyValSerCly 20

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QY 96 GATATTGTGATACCCAGGATGAACCTCAATCCTGTCTCACTCTCTGAGAAATCAGTTTCC 155
DB 21 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 40

QY 156 ATCTCTGCGAGTCTAGTAAGATCTCCTGTATAGATGGGAAGACATACCTGTAATGG 215
DB 41 IleSerCysArgSerSerLysLeuLeuTyLysAspGlyLysThrTyLysLeuAsnTrp 60

QY 216 TTCTCTCAGAGACCCAGACATCTCTCAGCTCCTCATGATGATTGATGTCACCCGTGCA 275
DB 61 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuLeuIleTyLysMetSerThrArgala 80

QY 276 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGTCCAGGACAGATTCACCTCGAAATC 335
DB 81 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluile 100

QY 336 ACTAGAGTGAAGCTGAGGATGGGTGTGTTACTGTCAACACTTGTAGAGTATCCA 395
DB 101 SerArgValLysAlaGluAspValGlyValTyLysCysGlnGlnLeuValGluTyPro 120

RESULT 2
A29775
Ig kappa chain precursor V region (mouse 24.2) - shrew mouse
C:Species: Mus pahari
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C:Accession: A29775
R:Jouvin-Marche, E.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A:Title: Evolution of a V-kappa gene family.
A:Reference number: A91751; MUID:87006895; PMID:3093373
A:Accession: A29775
A:Molecule type: DNA
A:Residues: 1-120 <JOU>
A:Cross-references: GB:M15552; NID:g197468; PIDN:AAA39036.1; PID:g197469
A:Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region 24.2 #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2,45e-47 Length: 120
Score: 558.00 Matches: 107
Percent Similarity: 96.67% Conservative: 9
Best Local Similarity: 89.17% Mismatches: 4
Query Match: 71.08% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x A29775 (1-120)

QY 36 ATGAGTCTCTCTTCTCAGTTCTCTGGGGTCTTATGTTCTGAGTCTCTGAGTCTGAGTGG 95
DB 1 MetArgHisSerLeuGlnPheLeuGlyLeuLeuLeuPheCysIleSerGlyValSerGly 20

QY 96 GATATTGTGATACCCAGGATGAACCTCAATCCTGTCTCACTCTCTGAGAAATCAGTTTCC 155
DB 21 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 40

QY 156 ATCTCTGCGAGTCTAGTAAGATCTCCTGTATAGATGGGAAGACATACCTGTAATGG 215
DB 61 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuLeuIleTyLysMetSerThrArgala 80

QY 216 TTCTCTCAGAGACCCAGACATCTCCTCAGCTCCTCATGATGATTGATGTCCACCCGTGCA 275
DB 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuLeuIleSerLeuMetSerThrArgala 60

QY 276 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGTCCAGGACAGATTCACCTCGAAATC 335
DB 61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluile 80

QY 336 AGTAGTGAAGCTGAGGATGGGTGTGTTACTGTCAACACTTGTAGAGTATCCA 395
DB 81 SerArgValLysAlaGluAspValGlyValTyLysCysGlnGlnLeuValGluTyPro 100

QY 396 TTCACGTCGCGCTCGGGGACAAAAGTTGGAAATAAAA 431
DB 101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuLys 112

RESULT 4
KVMS16
Ig kappa chain V region (M511) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C:Accession: A01910
R:Appella, E.
Mol. Immunol. 17, 711-718, 1980
A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine
A:Reference number: A01910; MUID:81052016; PMID:6776396
A:Accession: A01910
A:Molecule type: protein
A:Residues: 1-113 <APP>
```

```
QY 336 AGTAGTGAAGCTGAGGATGGGTGTGTTACTGTCAACACTTGTAGAGTATCCA 395
DB 101 SerArgValGluAlaGluAspValGlyValTyLysCysGlnGlnLeuValGluTyPro 120

RESULT 3
KVMS16
Ig kappa chain V region (M167) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
C:Accession: A01908
R:Rudikoff, S.; Potter, M.
Biochemistry 17, 2703-2707, 1978
A:Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prote
A:Reference number: A01908; MUID:79000273; PMID:99160
A:Accession: A01908
A:Molecule type: protein
A:Residues: 1-112 <RUD>
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine. J
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 9.5e-46 Length: 112
Score: 542.00 Matches: 106
Percent Similarity: 97.32% Conservative: 3
Best Local Similarity: 94.64% Mismatches: 3
Query Match: 69.04% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KVMS16 (1-112)

QY 96 GATATTGTGATACCCAGGATGAACCTCAATCCTGTCTCACTCTCTGAGAAATCAGTTTCC 155
DB 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20

QY 156 ATCTCTGCGAGTCTAGTAAGATCTCCTGTATAGATGGGAAGACATACCTGTAATGG 215
DB 21 IleSerCysArgSerSerLysLeuLeuTyLysAspGlyLysThrTyLysLeuAsnTrp 40

QY 216 TTCTCTCAGAGACCCAGACATCTCCTCAGCTCCTCATGATGATTGATGTCCACCCGTGCA 275
DB 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuLeuIleSerLeuMetSerThrArgala 60

QY 276 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGTCCAGGACAGATTCACCTCGAAATC 335
DB 61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluile 80

QY 336 AGTAGTGAAGCTGAGGATGGGTGTGTTACTGTCAACACTTGTAGAGTATCCA 395
DB 81 SerArgValLysAlaGluAspValGlyValTyLysCysGlnGlnLeuValGluTyPro 100

QY 396 TTCACGTCGCGCTCGGGGACAAAAGTTGGAAATAAAA 431
DB 101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuLys 112

RESULT 4
KVMS11
Ig kappa chain V region (M511) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C:Accession: A01910
R:Appella, E.
Mol. Immunol. 17, 711-718, 1980
A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine
A:Reference number: A01910; MUID:81052016; PMID:6776396
A:Accession: A01910
A:Molecule type: protein
A:Residues: 1-113 <APP>
```

US-09-674-716B-2 (1-437) x B29775 (1-120)

QY 36 ATGAGTCTCTCGTTCACTTCCTGGGGGTCTATGTTCTGGATCTCTGGAGTCACGTGG 95

 : :: :: :: :

Db 1 MetArgHisSerLeuGlnPheLeuGlyLeuLeuIleCysPheSerArgValSerGly 20

 : :: :: :: :

QV 96 GATATTGTGAATACCAGAGTGAACTTCCAAATCCTGTCAACTTCTGGAGAATCAGATTCCC 155

| | | | |
|----|-----|--|-----|
| Db | 21 | AspValValIleThrGlnAspGluSerAsnProValThrSerGlyGluSerValSer | 40 |
| | | | |
| QY | 156 | ATCTCTCGAGCTCTAGTAGAGTCTCTGTATAAGATGGGAAGACATCTGAATCG | 215 |
| Db | 41 | IleSerCysArgSerSerLysSerLeuLeuTyrLysAspGlyLysThrTyrLeuAsnTrp | 60 |
| QY | 216 | TTTCTGCAGACACAGGACAACTCTCTCAGCTCTGATGTATTTGATGCCACCCGTGCA | 275 |
| | | | |
| Db | 61 | PheLeuGlnArgProGluGlnSerProGlnLeuLeuIleCysLeuMetSerThrHisAla | 80 |

| | | | |
|---|-----|--|-----|
| QY | 276 | TCAGAGTCTCAGACCGGCTTTAGTGGCAGTGCGGTCAGGCACAGATTTCACCTCGGAATC | 335 |
| Db | 81 | LeuGIyValSerAspArgpheSerGIySerGIySerGIyThrAspPheThrLeuLySile | 100 |
| QY | 336 | AGTAGAGTGAAGCGTCGAGGAGTGCGGTGTATTACTGTCAACAACCTGTAGAGATATCCA | 395 |
| Db | 101 | SerArgValGluAaGluValGlyValTyTyTyCysGlnGlnIleValGluTyPPro | 120 |
| RESULT 6 | | | |
| S40357 | | | |
| Ig kappa chain V-J-C region - human | | | |
| C:Species: Homo sapiens (man) | | | |
| C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 | | | |
| C:Accession: S40357 | | | |
| R:Klein, R.; Jaenichen, R.; Zachau, H.G. | | | |
| Eur J Immunol 23, 3248-3271, 1993 | | | |
| A:Title: Expressed human immunoglobulin chi genes and their hypermutation. | | | |
| A:Reference number: S40312; MUID:94080891; PMID:8258341 | | | |
| A:Accession: S40357 | | | |
| A>Status: preliminary; translation not shown | | | |
| A:Molecule type: mRNA | | | |
| A:Residues: 1-136 <KLE> | | | |
| A:Cross-references: EMBL:X72467 | | | |

```

C;superfamily: immunoglobulin V region; immunoglobulin Homology
C;keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:          7,278-42      Length:          136
Score:              503.00        Matches:       96
Percent Similarity: 83.58%        Conservative:  16
Best Local Similarity: 71.64%      Mismatches:    22
Query Match:        64.08%        Indels:        0
DB:                  2              Gaps:          0

US-09-674-716B-2 (1-437) x S40357 (1-136)

Qy      36  ATGAGGTTCTCTGTTTCAGTTTCTGGGGGTCCTTATGTTCTGGATCTCTGGAGTCAGTGGG  95
Db      1  MetArgLeuProAlaGlnLeuLeuGlyLeuLeuMetLeuTrpValSerGlySerSerGly  20
Qy      96  GATATTGTGATACCAGGATGAACCTCCAACTCTGTCTACCTCTCGGAGAACTCAGTTTCC  155
Db      21  AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer    40
Qy     156  ATCTCTCTGCAGGTCCTAGTAAAGAGTCTCCTCTGTATAAGGATGGGAAGACATACCTTGAATTCG  215

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| | | |
|----|-----|---|
| Db | 41 | lleSerCyArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp |
| Qy | 216 | TTTTCGAGAGACACGAGCAATCTCCTCAGCTCCTGATGTTGATGCCACCGTGCA |
| Db | 61 | TyrLeuGlnLysProGlyYglnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla |
| Qy | 276 | TCAGGAGTCTCAGACCGGTTTTAGTGGCAGATGGGGTCAGGCACAGATTTCACCGTGAAGATC |

Db 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 100
 QY 336 AGTAGAGTGAAGCTGAGATGGGTGTGTTACTCTCAACACTGTGAGAGTATCCA 395
 Db 101 SerArgValGluAlaGluAspValGlyValTyTyCysMetGlnAlaLeuGlnThrPro 120
 QY 396 TTCACGTTCCGCTCGGGGCAAGTTGGAAATAAAACGTAACG 437
 Db 121 TrpThrPheGlyGlnGlyThrLysValGluLeuLysArgThr 134

RESULT 7
 S40372
 Ig kappa chain V-J region - human
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40372
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40372
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-131 <KDE>
 A/Cross-references: EMBL:X72482; NID:g441432; PIDN:CAA51150.1; PID:g441433
 C/Superfamily: immunoglobulin V region; immunoglobulin
 C/Keywords: heterotetramer; immunoglobulin
 F/36-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 8,98e-41 Length: 131
 Score: 492.00 Matches: 93
 Percent Similarity: 83.97% Conservative: 17
 Best Local Similarity: 70.99% Mismatches: 21
 Query Match: 62.68% Indels: 0
 Gaps: 0

US-09-674-716B-2 (1-437) X S40372 (1-131)

QY 36 ATGAGGTTCTCTGTTCTGAGTTCTGGGGTGCTTATGTTCTGATCTCTGAGTCAGTGG 95
 Db 1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuMetLeuTrpValSerGlySerGly 20
 QY 96 GATATTGTGATACCCAGGATGACTCTCCATCTCTGCTCAGTCTGGAGAACAGTTCC 155
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluSerAla 40
 QY 156 ATCTCTGCTGATACCCAGGATGACTCTCCATCTCTGCTCAGTCTGGAGAACAGTTCC 155
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluSerAla 40
 QY 156 ATCTCTGCTGATACCCAGGATGACTCTCCATCTCTGCTCAGTCTGGAGAACAGTTCC 215
 Db 41 PheSerCysIysThrSerGlnSerLeuLeuHisSerAsnGlyHisAsnTyLeuAspTrp 60
 QY 216 TTCTCGCAGACAGACAAATCTCTCAGTCTCTGATGATTTGATGTCCACCCGTGCA 275
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
 QY 276 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTCAAGGACAGATTTCCACCTGGAATC 335
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100
 QY 336 AGTAGAGTGAAGCTGAGATGGGTGTGTTACTCTCAACACTGTGAGAGTATCCA 395
 Db 101 SerArgValGluAlaGluAspValGlyValTyTyCysMetGlnProLeuGlnThrPro 120
 QY 396 TTCACGTTCCGCTCGGGGCAAGTTGGAAATA 428
 Db 121 TyrThrPheGlyGlnGlyThrLysValGluLeuLysile 131

RESULT 8
 S26882
 Ig kappa chain V region (V607) - human
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
 C/Accession: S26882

R/Weichhold, G.M.; Klobbeck, H.G.; Ohnheiser, R.; Combriato, G.; Zachau, H.G.
 Nature 347, 90-92, 1990
 A/Title: Megabase inversions in the human genome as physiological events.
 A/Reference number: S26882; MUID:90370099; PMID:2118596
 A/Accession: S26882
 A/Status: preliminary; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-132 <MEI>
 A/Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367
 C/Genetics: 17/1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/36-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 1,79e-40 Length: 132
 Score: 489.00 Matches: 94
 Percent Similarity: 82.58% Conservative: 15
 Best Local Similarity: 71.21% Mismatches: 23
 Query Match: 62.29% Indels: 0
 Gaps: 0

US-09-674-716B-2 (1-437) X S26882 (1-132)

QY 36 ATGAGGTTCTCTGTTCTGAGTTCTGGGGTGCTTATGTTCTGATCTCTGAGTCAGTGG 95
 Db 1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuMetLeuTrpValSerGlySerGly 20
 QY 96 GATATTGTGATACCCAGGATGACTCTCCAACTCTGCTCAGTCTGGAGAACAGTTCC 155
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
 QY 156 ATCTCTGCTGATACCCAGGATGACTCTCCATCTCTGCTCAGTCTGGAGAACAGTTCC 215
 Db 41 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyLeuAspTrp 60
 QY 216 TTCTCGCAGACAGACAAATCTCTCAGTCTCTGATGATTTGATGTCCACCCGTGCA 275
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
 QY 276 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTCAAGGACAGATTTCCACCTGGAATC 335
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100
 QY 336 AGTAGAGTGAAGCTGAGATGGGTGTGTTACTCTCAACACTGTGAGAGTATCCA 395
 Db 101 SerArgValGluAlaGluAspValGlyValTyTyCysMetGlnAlaLeuGlnThrPro 120
 QY 396 TTCACGTTCCGCTCGGGGCAAGTTGGAAATAAAA 431
 Db 121 GlnThrPheGlyGlnGlyThrLysValGluLeuLys 132

RESULT 9

S23230
 Ig kappa chain precursor V-J region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S23230

R/Kennedy, M.A.
 J. Exp. Med. 173, 1033-1036, 1991
 A/Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and light
 A/Reference number: S23230; MUID:91178439; PMID:1840606
 A/Accession: S23230
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-133 <KEN>
 A/Cross-references: EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:g34000
 C/Genetics: 17/1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/36-115/Domain: immunoglobulin homology <IMM>

| Alignment Scores: | 2.82e-40 | Length: 133 |
|---|---|---|
| Pred. No.: | 487.00 | Matches: 92 |
| Score: | 80.45% | Conservative: 15 |
| Percent Similarity: | 69.17% | Mismatches: 26 |
| Best Local Similarity: | 62.04% | Indels: 0 |
| Query Match: | 2 | Gaps: 0 |
| DB: | | |
| US-09-674-716B-2 (1-437) x S23230 (1-133) | | |
| Qy | 36 | ATGAGGTTCTCTGTTTCAGTTTCGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95 |
| Db | 1 | MetArgLeuProAlaGlnLeuLeuGlyLeuMetLeuTrpValProGlySerSerGly 20 |
| Qy | 96 | GATATTGTGATACCCAGGATGAACCTCTCAATCTCTGTCACCTTCGGAGAAATCACTTTCC 155 |
| Db | 21 | AspValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40 |
| Qy | 156 | ATCTCTCGAGGCTAGTAAGTCTCCGTGATGATGAGGATGGGAAGACATACCTTGAATTGG 215 |
| Db | 41 | ILSerCysArgSerGlnSerLeuValTyrSerAspGlyAsnThrHisLeuAsnTrp 60 |
| Qy | 216 | TTTCTCGAGACACGAGCAATCTCTCAGCTCTCTGATGATATTGATGTCACCCGTCGA 275 |
| Db | 61 | PheGlnArgProGlyGlnSerProArgLeuLeuLeuValSerAsnArgAsp 80 |
| Qy | 276 | TCAGGAGTCTCAGCCGTTTAGTGGCAGTGGTTCAGGCACAGATTTTCACTCGGAATC 335 |
| Db | 81 | SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100 |
| Qy | 336 | AGTAGAGTGAAGCTCAGGATGTGGGTGTGTTACTGTCAACAACCTTCAGAGATCCA 395 |
| Db | 101 | SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpPro 120 |
| Qy | 396 | TTACAGTTCGGTCTGGGGGACAAAGTTGGAAATTAACGT 434 |
| Db | 121 | TyrThrPheGlyGlnGlyThrLysLeuGluIleLysArg 133 |
| RESULT 10 | | |
| S22902 | | |
| Ig kappa chain V region - human | | |
| C;Species: | Homo sapiens (man) | |
| C;Date: | 19-Feb-1994 | #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 |
| C;Accession: | S22902 | |
| Gene | 101, 305-306, 1991 | |
| A;Title: | Cloning of a gene encoding a lupus-associated human autoantibody V(K) region us | |
| A;Reference number: | S22902, PMID:91276289, PMID:1905262 | |
| A;Accession: | S22902 | |
| A;Status: | preliminary; translation not shown | |
| A;Molecule type: | mrna | |
| A;Residues: | 1-142 <CHA> | |
| A;Cross-references: | EMBL:X56510 | |
| C;Superfamily: | immunoglobulin V region; immunoglobulin homology | |
| C;Keywords: | heterotetramer; immunoglobulin | |
| F;47-126/Domain: | immunoglobulin homology <IMM> | |
| Alignment Scores: | | |
| Pred. No.: | 3.57e-40 | Length: 142 |
| Score: | 486.00 | Matches: 92 |
| Percent Similarity: | 80.45% | Conservative: 15 |
| Best Local Similarity: | 69.17% | Mismatches: 26 |
| Query Match: | 61.91% | Indels: 0 |
| DB: | 2 | Gaps: 0 |
| US-09-674-716B-2 (1-437) x S22902 (1-142) | | |
| Qy | 30 | CTCACCATGAGGTTCTCTGTTTCAGTTTCGGGGTCTTATGTTCTGGATCTCTGGAGTC 89 |
| Db | 10 | LeuThrMetArgLeuProAlaGlnLeuLeuGlyLeuMetLeuTrpValProGlySer 29 |
| Qy | 90 | AGTGGGGATATTGTGATAACCCAGGATGAACCTCTCAACTCTCTGTCACCTCTCTGGAGATCA 149 |

| | | | |
|----|-----|--|-----|
| Db | 101 | ValGlyValTyrTy-CysMetGlnAlaLeuGlnThrProArgThrPheGlyGlnGlyThr | 120 |
| Qy | 417 | RAGTTGGAAATAAACCCTACG | 437 |
| Dδ | 121 | LysvalGluIleLysArgThr | 127 |

RESULT 12

S29593
IG kappa chain (WG65) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S29593
R:Seymour, R.
submitted to the EMBL Data Library, February 1991
A:Reference number: S29593
A:Accession: S29593
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197 <EX>
A:Cross-references: EMBL:X57856; NID:g52588; PID:g52589
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

| | | |
|------------------------|----------|------------------|
| Alignment Scores: | | |
| Pred. No.: | 7,296-40 | 197 |
| Score: | 483.00 | Matches: 94 |
| Percent Similarity: | 82.03% | Conservative: 11 |
| Best Local Similarity: | 73.44% | Mismatches: 23 |
| Query Match: | 61.53% | Indels: 0 |
| DR: | 2 | Gaps: 0 |

U.S.-09-674-716B-2 (1-437) x S29593 (1-197)

| | | | |
|-----|----|---|-----|
| 51 | QY | CAGTTTCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTTGTAAC | 110 |
| | | | |
| 1 | Db | GluPheLeuGlyLeuLeuValLeuTrpIleProGlyAlaIleGlyAspIleValMetThr | 20 |
| | | | |
| 111 | QY | CAGGATGAACCTCTCAATCCTGTCACATCTCTGGAGAATCAGTTTCCATCTCCCTGCAGGTC | 170 |
| | | | |
| 21 | Db | GlnAlaAlaProSerIleProValThrProGlyGluSerAlaSerIleSerCysArgSer | 40 |
| | | | |
| 171 | QY | AGTAGAGATCTCCTGTATTAAGATCTGGGAAGACATCTGAATTGGTTTCTGCAGAGACCA | 230 |
| | | | |
| 41 | Db | SerLysSerLeuLeuHisSerAsnGlyAspThrTyrlLeuTyrlTrpPheLeuGlnArgPro | 60 |
| | | | |
| 231 | QY | GGACAATCTCTCAGCTCCTGATGTTATTTGATGTCACCCGTGCATCAGAGGTCACAG | 290 |
| | | | |
| 61 | Db | GlyGlnSerProGlnLeuLeuIleTyrlArgMetSerAsnLeuAlaSerGlyValProAsp | 80 |
| | | | |
| 291 | QY | CGGTTTAGTCGAGTGGGTCAGGCACAGATTTCACCCCTGGAAATCAGTAGAGTGAAGGT | 350 |
| | | | |
| 81 | Db | ArgPheSerGlySerGlySerGlyThrSerPheThrLeuArgIleSerArgValGluAla | 100 |
| | | | |
| 351 | QY | GAGGATGTGGGTGCTATTACTGTCAACAACCTCTAGAGTATCCATTTCAGCTTCGGCTCG | 410 |
| | | | |
| 101 | Db | GluAspValGlyPheTyrlPheCysMetGlnHisLeuGlnTyrlProTyrlThrPheGlyGly | 120 |
| | | | |
| 411 | QY | GGACAAAGTTGGAATAAAACGT | 434 |
| | | | |
| 121 | Db | GlyThrLysLeuGluIleIleValArg | 128 |

RESULT 13

K2HURP
 Ig kappa chain precursor V-II region (RPMI) - human
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997
 C;Accession: A01890
 R;Klobeck, H.G.; Meindl, A.; Combratio, G.; Solomon, A.; Zachau, H.G.
 Nucleic Acids Res. 13, 6499-6513, 1985
 A;Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
 A;Reference number: A93588; MUID:86041852; PMID:2997711
 A;Accession: A01890

A, Molecule type: DNA
A, Residues: 1-133 <MO>
A, Note: the sequence was determined from the differentiated gene
C, Genetics:
A, Gene: GDB:ICKV2
A, Cross-references: GDB:136265
A, Map position: 2p12-2p12
A, Introns: 17/1
C, Complex: An immunoglobulin heterotetramer subunit consists of 4 heavy chain disulfide bonds. In some cases, such as IGA and IGM, the subunit is also associated with a light chain disulfide bond. The subunit family: immunoglobulin V region; immunoglobulin homology C; Superfamily: heterotetramer; immunoglobulin
C, Keywords: heterotetramer; immunoglobulin
F, 1-20/Domain: signal sequence #status predicted <SIG>
F, 21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted
F, 21-43/Region: framework 1
F, 36-115/Domain: immunoglobulin homology <IMM>
F, 44-59/Region: complementarity-determining 1
F, 60-74/Region: framework 2
F, 75-81/Region: complementarity-determining 2
F, 82-113/Region: framework 3
F, 114-122/Region: complementarity-determining 3
F, 123-133/Region: framework 4
F, 43-113/Disulfide bonds: #status predicted

| | | |
|------------------------|----------|------------------|
| Alignment Scores: | | |
| Pred. No.: | 1.76s-39 | Length: 133 |
| Score: | 499.00 | Matches: 91 |
| Percent Similarity: | 79.70% | Conservative: 27 |
| Best Local Similarity: | 68.42% | Mismatches: 25 |
| Query Match: | 61.03% | Indels: 0 |
| DB: | 1 | Gaps: 0 |

U.S.-09-674-716B-2 (1-437) x K2HURP (1-133)

```

36  ATGAGGTTCTCTGTTCAGTTTCTGGGGGTCCTTATGTTCTCGATCTCTCGAGTCAGTGG 95
    |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1  MetArgLeuProAlaGlnLeuLeuLeuGlyLeuLeuMetLeuTrpValProGlySerSerGly 20
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
96  GNTATTGTGTAACCCAGGATGAACCTCCAATCCCTGTCACTTCTCGAGAAATCAGTTCC 155
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
21  AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
156  ATCTCCTCGAGTCTAGTAAAGAGTCTCCTGTATAAGGATGGGAAGACATCTGAATTGG 215
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
41  IleSerCysArgSerSerGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
216  TTTTTCAGAGACACGAGCAATCTCTCAAGTCTCTGATGTTGATTTGATGTCACCCCTGCA 275
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
61  PheGlnGlnArgProGlyGlnSerProArgGluLeuIleTyrLysValSerAsnArgAsp 80
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
276  TCAGAGTCTCAGACCCGGTTTAGGCGAGTGGGTTCAGGCACAGATTCACCTCGGAAATC 335
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
81  SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
336  AGTAGAGTGAAGGCTGAGGATGTCGGGTGCTATTACTGTCAACAACCTGTAGAGTATCCA 395
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
101  SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnGlyThrHisTrpSer 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
396  TTCAGTTCTGGCTCGGGACAAAGTTCCGAATAAACGT 434
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
121  TrpThrPheGlyGlnGlyThrLysValGluIleLysArg 133
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 14
S40324
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40324
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:5408091; PMID:8258341
A:Accession: S40324

```

RESULT 14

S40324
I9 kappa chain V region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40324
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3249-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference: S40312; MUID:94080891; PMID:18256341
A/Accession: S40324

A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-133 <KLE>
A:Cross-references: EMBL:X72434
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-112/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1.76e-39 Length: 133
Score: 479.00 Matches: 90
Percent Similarity: 81.40% Conservative: 15
Best Local Similarity: 69.77% Mismatches: 24
Query Match: 61.02% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x S40324 (1-133)

| | | | |
|----|-----|---|-----|
| QY | 51 | CAGTTTCTGGGGTCTCTATGTTCTGGATCTCTGAGTCAGTGGGATATTGTGATAACC | 110 |
| Db | 3 | GlnLeuLeuGlyLeuLeuMetLeuTrpValProGlySerSerGlyAspValValLeuThr | 22 |
| QY | 111 | CAGGATGAACCTCCAACTCTGCTCACTCTGAGAAATCAGTTTCCATCTCTGCAAGTCT | 170 |
| Db | 23 | GlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSerIleSerCysArgSer | 42 |
| QY | 171 | AGTAAGAGTCTCCTCTATAGGATGGAGACATCTTGAATTTGTTCTGCAGAGCCA | 230 |
| Db | 43 | AspGlnSerLeuValtyrSerAspGlyThrLeuAsnTrpValGlnGlnArgPro | 62 |
| QY | 231 | GGACAACTCTCTCAGCTCCTGATGTTTATTTGATGTCACCCCTGCATCAGGAGTCTCAGAC | 290 |
| Db | 63 | GlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAspSerGlyValProAsp | 82 |
| QY | 291 | CGTTTAGTGGAGTGGTCCAGCAGATTTCCACCTGGAAATCAGTAGAGTGAAGCT | 350 |
| Db | 83 | ArgPheThrGlySerGlySerGlyThrAspPheThrLeuGluIleSerArgValGluAla | 102 |
| QY | 351 | GAGGATGGGGTGTATTACTGTCACAACTGTAGAGTATCCATTCACGTTGGGCTCG | 410 |
| Db | 103 | GluAspValGlyValtyrTyrCysMetGlnGlyThrHisTrpProGlyThrPheGlyGln | 122 |
| QY | 411 | GGGACAAAGTTGGAAATAAACGTACG | 437 |
| Db | 123 | GlyThrLysValGluIleLysArgThr | 131 |

RESULT 15

S40321
ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40321
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; PMID:94080891; PMID:8258341
A:Accession: S40321
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-130 <KLE>
A:Cross-references: EMBL:X72431
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2.48e-39 Length: 130
Score: 477.50 Matches: 93
Percent Similarity: 83.08% Conservative: 15
Best Local Similarity: 71.54% Mismatches: 21
Query Match: 60.83% Indels: 1
DB: 2 Gaps: 1

US-09-674-716B-2 (1-437) x S40321 (1-130)

| | | | |
|----|-----|--|-----|
| QY | 51 | CAGTTTCTGGGGTCTCTATGTTCTGGATCTCTGAGTCAGTGGGATATTGTGATAACC | 110 |
| Db | 1 | GlnLeuLeuGlyLeuLeuMetLeuTrpValProGlySerSerGlyAspValValMetThr | 20 |
| QY | 111 | CAGGATGAACCTCTCCAACTCTGCTCACTCTGAGAAATCAGTTTCCATCTCTGCAAGTCT | 170 |
| Db | 21 | GlnThrProLeuSerLeuProValThrProGlyGluProAlaSerIleSerCysArgSer | 40 |
| QY | 171 | AGTAAGAGTCTCCTG---TATAAGGATGGGAACACATCTTGAATTTGTTCTGCAGAGA | 227 |
| Db | 41 | SerGlnSerLeuLeuAspSerAspGlyAsnThrTyrLeuAspTrpTyrLeuGlnLys | 60 |
| QY | 228 | CCAGGACAAATCTCCTCAGCTCCTGATGATGATTTGATGTCACCCGTCATCAGAGTCTCA | 287 |
| Db | 61 | ProGlyGlnSerProGlnLeuLeuIleTyrThrLeuSerTyrArgAlaSerGlyValPro | 80 |
| QY | 288 | GACCGGTTTAGTGGCAGTGGGTCCAGCACACAGATTTCCACCTGGAAATCAGTAGAGTGAAG | 347 |
| Db | 81 | AspArgPheSerGlySerGlyThrAlaPheThrLeuLysIleSerArgValGlu | 100 |
| QY | 348 | GCTGAGAGATGGGTGTGTTACTGTCTCAACAACTTGTAGAGTATCCATTCAGTTTCGGC | 407 |
| Db | 101 | AlaGluAspValGlyLeuTyrTyrCysMetGlnArgIleGluPheProTyrThrPheGly | 120 |
| QY | 408 | TCGGGGACAAAGTTGGAAATAAACGTACG | 437 |
| Db | 121 | GlnGlyThrLysLeuGluIleLysArgThr | 130 |

Search completed: September 30, 2004, 08:57:01
Job time : 19.3249 secs

Blank sheet

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:20:22 ; Search time 9.48126 Seconds
(without alignments)
4799.922 Million cell updates/sec

Title: US-09-674-716B-2
Perfect score: 785
Sequence: 1 aagttttacagttactacgc.....agttggaaataaaacgtacg 437

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xl
-O=/cgn2_1/USPTO_spool_p/US09674716/runat_30092004_070257_25855/app_query.fasta_1.3164
-DB=SwissProt_42 -QFMT=fastan -SUFFIX=rs -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=sct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -WINLEN=0 -MAXLEN=200000000
-USER=US09674716 @CGN 1.1.82 @runat_30092004_070257_25855 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|--------------|--------------------|
| 1 | 601 | 76.6 | 120 | 1 KV2B_MOUSE | P01627 mus musculu |
| 2 | 542 | 69.0 | 112 | 1 KV2A_MOUSE | P01626 mus musculu |
| 3 | 539 | 68.7 | 113 | 1 KV2C_MOUSE | P01628 mus musculu |
| 4 | 479 | 61.0 | 133 | 1 KV2P_HUMAN | P06310 homo sapien |
| 5 | 435 | 55.4 | 113 | 1 KV2D_HUMAN | P01617 homo sapien |
| 6 | 431 | 54.9 | 113 | 1 KV2F_MOUSE | P01630 mus musculu |
| 7 | 431 | 54.9 | 117 | 1 KV2E_HUMAN | P08309 homo sapien |
| 8 | 427.5 | 54.5 | 115 | 1 KV2A_HUMAN | P01614 homo sapien |
| 9 | 427 | 54.4 | 113 | 1 KV2E_MOUSE | P03976 mus musculu |
| 10 | 422 | 53.8 | 113 | 1 KV2B_HUMAN | P01615 homo sapien |
| 11 | 417 | 53.1 | 112 | 1 KV2D_MOUSE | P01629 mus musculu |
| 12 | 400 | 51.0 | 113 | 1 KV2G_MOUSE | P01631 mus musculu |
| 13 | 398.5 | 50.8 | 112 | 1 KV2C_HUMAN | P01616 homo sapien |
| 14 | 398.5 | 50.8 | 134 | 1 KV4C_HUMAN | P06313 homo sapien |
| 15 | 378 | 48.2 | 133 | 1 KV4B_HUMAN | P06313 homo sapien |
| 16 | 357.5 | 45.5 | 114 | 1 KV4A_HUMAN | P01625 homo sapien |
| 17 | 353.5 | 45.0 | 108 | 1 KV1_CANFA | P01618 canis famil |
| 18 | 351 | 44.7 | 129 | 1 KV3L_HUMAN | P18135 homo sapien |

ALIGNMENTS

```

RESULT 1
KV2B_MOUSE
ID_KV2B_MOUSE STANDARD; PRT; 120 AA.
AC P01627;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region vkappa167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82002223; PubMed=6791832;
RA Selsing E., Storb U.;
RT "Somatic mutation of immunoglobulin light-chain variable-region
   genes.";
RL Cell 25:47-58(1981).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00562; AAA39032.1; -
DR EMBL; K02415; AAA39051.1; -
DR PIR; A01909; KWS67.
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IGLIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 120 IG KAPPA CHAIN V-II REGION VKAPPA167.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.

```

P18136 homo sapien
P01637 mus musculu
P06311 homo sapien
P06312 homo sapien
P04431 homo sapien
P01661 mus musculu
P01658 mus musculu
P01665 mus musculu
P01633 mus musculu
P04207 homo sapien
P01667 mus musculu
P01664 mus musculu
P01666 mus musculu
P83593 homo sapien
P01669 mus musculu
P01673 mus musculu
P01668 mus musculu
P01619 homo sapien
P01622 homo sapien
P01671 mus musculu
P01634 mus musculu
P01670 mus musculu
P01620 homo sapien
P01623 homo sapien
P04206 homo sapien
P01656 mus musculu
P01672 mus musculu

FT DOMAIN 60 74 FRAMEWORK-2.
 FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 82 113 FRAMEWORK-3.
 FT DOMAIN 114 120 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 113 BY SIMILARITY.
 SQ SEQUENCE 120 AA; 13280 MW; 63BB571F084D3E8 CRC64;

Alignment Scores:
 Pred. No.: 6,95e-57 Length: 120
 Score: 601.00 Matches: 117
 Percent Similarity: 99.17% Conservative: 2
 Best Local Similarity: 97.50% Mismatches: 1
 Query Match: 76.56% Indels: 0
 DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2B_MOUSE (1-120)

QY 36 ATGAGTTCTCTGTTTCAGTTCTGGGGTGCTTATGTTCTGATCTCTGGAGTCAAGTGGG 95
 DB 1 MetArgCysSerLeuGlnPheLeuGlyValLeuMetPheTrpIleSerGlyValSerGly 20
 QY 96 GATATTGTGATACCCAGGATGACTCTCCATCTCTGCTGCTCTGGAGATCAGTTTCC 155
 DB 21 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 40
 QY 156 ATCTCTCGCAGGTCTAGTAAGAGTCTCTGTTATAGGATGGGAGACATACCTGAATTGG 215
 DB 41 IleSerCysArgSerSerLysSerLeuValLysAspGlyValThrTyrLeuAsnTrp 60
 QY 216 TTCTCTCAGACAGCAGCAATCTCTCAGCTCTGATGATTTGATGTCACCCGTGCA 275
 DB 61 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleTyrLeuMetSerThrArgala 80
 QY 276 TCAGGAGTCTCAGCCGTTTACTGTCAGTGGTTCAGGACAGATTCACCTGGAATC 335
 DB 81 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLe 100
 QY 336 AGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 395
 DB 101 SerArgValLysAlaGluAspValGlyValTyrCysGlnGlnLeuValGluTyrPro 120

RESULT 2

KV2A_MOUSE STANDARD; PRT; 112 AA.
 ID KV2A_MOUSE
 AC P01626;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region MOPC 167.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]_TaxID=10090;
 RP SEQUENCE
 RX MEDLINE=79000273; PubMed=99160;
 RA Rudikoff S., Potter M.;
 RT "kappa Chain variable region from M167, a phosphorylcholine binding myeloma protein."
 RL Biochemistry 17:2703-2707(1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN HAS ALSO BEEN DETERMINED.
 CC PIR; A01908; KWS16.
 DR HSSP; P80362; IWL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin v region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 62 93 FRAMEWORK-3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 103 112 BY SIMILARITY.
 FT NON TER 112 112
 SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;

Alignment Scores:
 Pred. No.: 1.63e-50 Length: 112
 Score: 542.00 Matches: 106
 Percent Similarity: 97.32% Conservative: 3
 Best Local Similarity: 94.64% Mismatches: 3
 Query Match: 69.04% Indels: 0
 DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2A_MOUSE (1-112)

QY 96 GATATTGTGATACCCAGGATGAACTCTCCATCTCTGCTGCTCTGGAGATCAGTTTCC 155
 DB 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
 QY 156 ATCTCTCGCAGGTCTAGTAAGAGTCTCTGTTATAGGATGGGAGACATACCTGAATTGG 215
 DB 21 IleSerCysArgSerSerLysSerLeuValLysAspGlyValThrTyrLeuAsnTrp 40
 QY 216 TTCTCTCAGACAGCAGCAATCTCTCAGCTCTGATGATTTGATGTCACCCGTGCA 275
 DB 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleSerLeuMetSerThrArgala 60
 QY 276 TCAGGAGTCTCAGCCGTTTACTGTCAGTGGTTCAGGACAGATTCACCTGGAATC 335
 DB 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLe 80
 QY 336 AGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 395
 DB 81 SerArgValLysAlaGluAspValGlyValTyrCysGlnGlnLeuValGluTyrPro 100
 QY 396 TCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAAA 431
 DB 101 LeuThrPheGlyAlaGlyThrLysLeuGluLys 112

RESULT 3

KV2C_MOUSE STANDARD; PRT; 113 AA.
 ID KV2C_MOUSE
 AC P01628;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region MOPC 511.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]_TaxID=10090;
 RP SEQUENCE
 RX MEDLINE=81052016; PubMed=6776396;
 RA Appella E.;
 RT "Amino acid sequence of the light chain variable region of M511, a phosphorylcholine-binding murine myeloma protein."
 RL Mol. Immunol. 17:711-718(1980).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE.
 CC PIR; A01910; KWS1.
 DR HSSP; P80362; IWL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin v region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 23

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FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Alignment Scores:
Pred. No.: 3 45e-50 Length: 113
Score: 539.00 Matches: 105
Percent Similarity: 96.48% Conservative: 4
Best Local Similarity: 92.92% Mismatches: 0
Query Match: 68.66% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2C_MOUSE (1-113)
QY 96 GATATTGTGATTAACCCAGAGTAACTCTCCATCTCTGTCACCTTCGGAGATCAGTTTCC 155
Db 1 AspIleValIleThrGlnAspGluLeuSerLysProValThrSerGlyLysValSer 20
QY 156 ATCTCTCGAGCTAGTAAGAGTCTCTGTATAGGATGGAGACATATCTGAATTGG 215
Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrLysAspGlyLysThrTyrLeuAsnTrp 40
QY 216 TTCTCTCGAGAGACCAATCTCTCAGCTCTCTGATGTTATTTGATCTCACCGGTGCA 275
Db 41 PheLeuGlnGlyProGlnGlnSerProArgLeuLeuTyrLysMetSerThrArgala 60
QY 276 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTGGCAGCAGATTTCCACCTGGAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLeu 80
QY 336 AGTAGAGTGAAGGCTCAGAGTGGGTGTGTATTAATCTCTCAACACTTGTAGAGTATCCA 395
Db 81 SerA-gValLysAlaGluAspValGlyValTyrCysGlnGlnLeuValGluTyrPro 100
QY 396 TTCACGTTCCGTCGGGACAAAGTTGGAATAAAGCT 434
Db 101 LeuThrPheGlyAlaGlyThrLysLeuGluLeuTyrArg 113

RESULT 4
KV2F_HUMAN STANDARD; PRT; 133 AA.
ID KV2F_HUMAN
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2957711;
RA Klobeck H.G.; Weindl A.; Combrato G.; Solomon A.; Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and III."
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00020; CAA77315.1; -

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DR PIR; A01890; K0HURP.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT CHAIN 21 133 FRAMEWORK-1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 59 FRAMEWORK-2.
FT DOMAIN 60 74 FRAMEWORK-3.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 113 FRAMEWORK-4.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Alignment Scores:
Pred. No.: 1 09e-43 Length: 133
Score: 479.00 Matches: 91
Percent Similarity: 79.70% Conservative: 15
Best Local Similarity: 68.42% Mismatches: 27
Query Match: 61.02% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2F_HUMAN (1-133)
QY 36 ATAGGTTCTCTGTTTCTGATTTCTGGGTCCTATGTTCTGGATCTCTGGAGTCAGTGGG 95
Db 1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuMetLeuTrpValProGlySerSerGly 20
QY 96 GATATTCTGATAACCAGGATGAACCTCCCAATCTCTGCTCACTCTCGAGAAATCAGTTTCC 155
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnGlnProAlaSer 40
QY 156 ATCTCTCGAGGCTAGTAAGAGTCTCTGATGTTATTAAGAGTGGGAGACATCTTGAATTGG 215
Db 41 IleSerCysArgSerSerGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 60
QY 216 TTCTCTGAGAGACCAAGCAATCTCTCAGCTCTCTGATGTTATTTGATCTCACCGGTGCA 275
Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuLeuTyrLysValSerAsnArgAsp 80
QY 276 TCAGGAGTCTCAGACCGGTTTCTGAGTGGTGGTGGCAGCAGATTTCCACCTGGAATC 335
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100
QY 336 AGTAGAGTGAAGGCTCAGAGTGGGTGTGTATTAATCTCTCAACACTTGTAGAGTATCCA 395
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpSer 120
QY 396 TTCACGTTCCGTCGGGACAAAGTTGGAATAAAGCT 434
Db 121 TrpThrPheGlyGlnGlyThrLysValGluLeuLysArg 133

RESULT 5
KV2D_HUMAN STANDARD; PRT; 113 AA.
ID KV2D_HUMAN
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
RL primary amyloidosis."
RN Biochemistry 12:3763-3780(1973).
RN [2]
RN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=7316638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
RL patient with plasma cell dyscrasia and amyloidosis."
RN J. Clin. Invest. 52:1276-1281(1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
DR PIR; A90370; K2HUTW.
DR HSP; P01607; 1REI.
DR GO; G3:0005576; C:extracellular; NAS.
DR GO; G3:0003823; P:antigen binding; NAS.
DR GO; G3:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein; Amyloid.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Alignment Scores:
Pred. No.: 6,02e-39 Length: 113
Score: 435.00 Matches: 82
Percent Similarity: 84.96% Conservative: 14
Best Local Similarity: 72.57% Mismatches: 17
Query Match: 55.41% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2D_HUMAN (1-113)

QY 96 GATATTGTGATACCCAGGATGAACCTCTCAATCTGTCTCACTCTCGGAGATCAGTTTCC 155
Db 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20

QY 156 ATCTCTCGAGGCTCTAGTAAGAGTCTCTGTATTAAGAGTGGGAGACATACCTTGAATTGG 215
Db 21 IleSerCysArgSerGlnSerLeuLeuHisSerAspGlyPheAspTyrLeuAsnTrp 40

QY 216 TTCTCTCAGACACGACAGACTCTCTCAGCTGATGATTTATGATGTCACCCGTGCA 275
Db 41 TyrLeuGlnLysProGlyGlnSerPro***LeuLeuIleTyrAlaLeuSerAsnArgAla 60

QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTCCACCTGGAATC 335
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80

QY 336 AGTAGAGTGAAGCTGAGATGGGTGTGTTACTGTCAACACTGTGATAGATATCCA 395
Db 81 SerArgValGlnAlaGluAspValGlyValTyrCysMet***AlaLeuGlnAlaPro 100

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QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACGT 434
Db 101 IleThrPheGlyGlnGlyThrArgLeuGluIleLysArg 113

RESULT 6
KV2F_MOUSE
ID KV2F_MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 7834.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01913; KVM578.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Monoclonal antibody; Hybridoma.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Alignment Scores:
Pred. No.: 1.63e-38 Length: 113
Score: 431.00 Matches: 87
Percent Similarity: 82.30% Conservative: 6
Best Local Similarity: 76.99% Mismatches: 20
Query Match: 54.90% Indels: 0
DB: 1 Gaps: 0

US-09-674-716B-2 (1-437) x KV2F_MOUSE (1-113)

QY 96 GATATTGTGATACCCAGGATGAACCTCTCAATCTGTCTCACTCTCGGAGATCAGTTTCC 155
Db 1 AspIleValMetThrGlnThrAlaProSerAlaLeuValThrProGlyGluSerValSer 20

QY 156 ATCTCTCGAGGCTCTAGTAAGAGTCTCTGTATTAAGAGTGGGAGACATACCTTGAATTGG 215
Db 21 IleSerCysArgSerGlySerLeuLeuHisSerAsnGlyAsnThrTyrLeuTyrTrp 40

QY 216 TTCTCTCAGACACGACAGACATCTCTCAGCTGATGATTTATGATGTCACCCGTGCA 275
Db 41 PheLeuGlnArgProGlyGlnCysProGlnLeuLeuIleTyrArgMetSerAsnLeuAla 60

QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTCCACCTGGAATC 335
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAlaPheThrLeuArgIle 80

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QY 336 AGTAGAGTGAAGGCTGAGGATGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 395
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlnArgGluTyrPro 100
QY 396 TTCAGTTCGGCTCGGACAAAGTTGGAATAAACCT 434
Db 101 TyrThrPheGlyGlyThrLysLeuGluLeuLysArg 113
RESULT 7
KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Kloeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RL Nature 309:73-76(1984).
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-----
DR EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUCM.
DR HSSP; P80382; LWTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 5 27 FRAMEWORK-1.
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 58 FRAMEWORK-2.
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 66 97 FRAMEWORK-3.
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 FRAMEWORK-4.
FT DISULFID 27 117 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
Alignment Scores:
Pred. No.: 1.64e-38 Length: 117
Score: 431.00 Matches: 85
Percent Similarity: 83.76% Conservative: 13
Best Local Similarity: 72.65% Mismatches: 19
Query Match: 54.90% Indels: 0
DB: 1 Gaps: 0
US-09-674-716B-2 (1-437) x KV2E_HUMAN (1-117)
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QY 84 GGAGTCAGTGGGATATTGTGTATTAACCCAGGATGAACCTCCCAATCTGTCACTTCTGGA 143
Db 1 GlySerSerGlyAspIleValMetThrGlnSerProLeuSerLeuProValThrProGly 20
QY 144 GAATCAGTTTCCATCTCCCTGACGCTCTAGTAAGAGTCTCTGTATATAAGATGGGAAGACA 203
Db 21 GluProAlaSerIleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsn 40
QY 204 TACTTGAATTGGTTTCTGACAGACACCAGGACAACTCTCCAGCTCTCTGATGATTTGATG 263
Db 41 TyrLeuAspTrpTyrLeuGlnLysProGlnGlnSerProGlnLeuLeuIleTyrLeuGly 60
QY 264 TCCACCGCTGCATCAGGAGTCTCAGACCGGTTTGTGGGAGTGGGTCCAGGCACAGATTTC 323
Db 61 SerAsnArgAlaSerGlyValProAspArgPheSerGlySerGlyThrAspPhe 80
QY 324 ACCCTGGAATCAGTAGAGTGAAGGCTGAGGAGTGGGTGTGTATTACTGTCAACAACCT 383
Db 81 ThrLeuLysIleSerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnGly 100
QY 384 GTAGAGTATCCATTCAGCTTCGGCTCGGACAAAGTTGGAATAAACCT 434
Db 101 LeuGlnThrProGlnThrPheGlyGlnGlyThrLysValGluLeuLysArg 117
RESULT 8
KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
[2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
PIR; B91639; K2HUCM.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;
Alignment Scores:
Pred. No.: 3.9e-38 Length: 115
Score: 427.50 Matches: 85
Percent Similarity: 84.21% Conservative: 11
Best Local Similarity: 74.56% Mismatches: 17
Query Match: 54.46% Indels: 1
DB: 1 Gaps: 1
US-09-674-716B-2 (1-437) x KV2A_HUMAN (1-115)
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US-09-674-716B-2 (1-437) x KV2A_HUMAN (1-115)
QY 96 GATATTGTGATTAACCCAGGAGTAACCTCTCAATCTCTGACCTCTGAGAAATCAGTTTCC 155
DB 2 AspileValMetThrGlnThrProLeuSerLeuProValThrProGlyLeuProAlaSer 21
QY 156 ATCTCTCGAGGCTAGTAAGAGTCTCTGTATAAG--GATGGGAGACACTTGAT 212
DB 22 IleserCysargSerGlnSerLeuAaspSerGlyAaspGlyAsnThrTyrLeuAsn 41
QY 213 TGGTTTCTGAGAGACCCAGGACAAATCTCTCAGCTCTCTGATGTATTGTGTCACCCCGT 272
DB 42 TriTy-LeuGlnLysAlaGlyGlnSerProGlnLeuLeuIleTyrThrLeuSerTyrArg 61
QY 273 GCATCAGGAGTCTCAGACCGGTTAGTGCAGTGGTGCAGGACAGATTTCCACCTGGAA 332
DB 62 AlaSerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLys 81
QY 333 ATCAGTAGAGTGAAGCTCAGAGTGGGTGTATTACTGTCAACAACCTGTAGAGTAT 392
DB 82 IleserArgValGlnAlaGluAaspValGlyValTyrTyrCysMetGlnArgLeuGluLeu 101
QY 393 CAAATTCAGCTTCGGCTCGGGGACAAAGTTGGAAATAAAACGT 434
DB 102 ProTyrThrPheGlyGlnGlyThrLysLeuGluLeuArgArg 115

RESULT 9
KV2E_MOUSE STANDARD; PRT; 113 AA.
ID KV2E_MOUSE AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DE IG kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Rodentia; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP TISSUE=Hybridoma;
RC MEDLINE=6441748;
RA "Muller R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide."
RL Hoppe-Sevler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR: A01912; KWS17.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Hybridoma.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Alignment Scores:
Pred. No.: 4,41e-38 Length: 113
Score: 427.00 Matches: 84
Percent Similarity: 82.30% Conservatives: 9
Best Local Similarity: 74.34% Mismatches: 20

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Query Match: 54.39% Indels: 0
DB: 1 Gaps: 0
US-09-674-716B-2 (1-437) x KV2E_MOUSE (1-113)
QY 96 GATATTGTGATTAACCCAGGAGTAACCTCTCAATCTCTGACCTCTGAGAAATCAGTTTCC 155
DB 1 AspileValMetThrGlnAlaValPheSerAsnProValThrLeuGlyThrSerAlaSer 20
QY 156 ATCTCTCGAGGCTAGTAAGAGTCTCTGTATAAGATCGGAGACACTTGATTTGG 215
DB 21 IleserCysargSerGlySerLeuLeuHisSerAsnGlyIleThrTyrLeuTyrTrp 40
QY 216 TTTCTGAGAGACCCAGGACAAATCTCTCAGCTCTCTGATGTATTGTGTCACCCCGTGA 275
DB 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrGlnMetSerAsnLeuAla 60
QY 276 TCAGGAGTCTCAGACCGGTTTGTGTCAGTGGTGCAGGACAGATTTCCACCTGGAAATC 335
DB 61 SerGlyValProAspArgPheSerSerGlySerGlyThrAspPheThrLeuA-gile 80
QY 336 AGTAGAGTGAAGCTCAGAGTGGGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395
DB 81 SerArgValGluAlaGluAaspValGlyValTyrTyrCysAlaHisAsnLeuGluLeuPro 100
QY 396 TTCAGTTTCGGCTCGGGGACAAAGTTGGAAATAAAACGT 434
DB 101 TyrThrPheGlyGlyThrLysLeuGluLeuLysArg 113

RESULT 10
KV2B_HUMAN STANDARD; PRT; 113 AA.
ID KV2B_HUMAN AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG kappa chain V-II region FR.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenstroms IgM
RT with specificity for phosphorylcholine."
RL Biochemistry 15:3829-3833(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR PIR: A01886; KZHUFR.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Alignment Scores:

```

| Alignment Scores: | 5.3e-37 | Length: | 112 |
|---|--|--|--------------|
| YPred. No.: | 417.00 | Matches: | 83 |
| Score: | 79.46% | Conservative: | 6 |
| Percent Similarity: | 74.11% | Mismatches: | 23 |
| Best Local Similarity: | 53.12% | Indels: | 0 |
| Query Match: | 1 | Gaps: | 0 |
| DB: | | | |
| US-09-674-716B-2 (1-437) x KV2D_MOUSE (1-112) | | | |
| QY | 96 | GATATTGTGATACCCAGGATGAATCTCCAAATCCTGTCACATCTGTGAGAAATCAAGTTTCC | 155 |
| DB | 1 | AspileValMetThrGlnIalaAlaPheSerAsnProValThrLeuGlyThrSerAlaSer | 20 |
| QY | 156 | ATCTCTCGAGGCTAGTAGACTCTCCCTGTATAGGATGGGAAGACATACTTCAATGG | 215 |
| DB | 21 | PheSerCysargSerSerLysSerLeuGlnSerLysGlyLeuThrTyLeuTyTrp | 40 |
| QY | 216 | TTTCTGCAGAGACAGACAAATCTCCTACGCTCCTGATGTATTTGATCTCCACCCGTGCA | 275 |
| DB | 41 | TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrGlnMetSerAsnLeuAla | 60 |
| QY | 276 | TCAGAGCTCTCAGACCGGTTTAGTGCAGTGGGTGAGCAGGACAGATTTCAACCTGGAATC | 335 |
| DB | 61 | SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuArgIle | 80 |
| QY | 336 | AGTAGAGTGAAGCTGAGGATGGGTGTATTACTGTCAACAACTTGTAGAGATATCCA | 395 |
| DB | 81 | SerArgValGlnIalagluaspValGlyValTyrCysAlaAsnLeuGlnGluLeuPro | 100 |
| QY | 396 | TTACGTTCCGCTCGGGGCAAAAGTTGGAAATAAAA | 431 |
| DB | 101 | TyrThrPheGlyGlyThrLysLeuGluIleLys | 112 |
| RESULT 12 | | | |
| KV2G_MOUSE | | | |
| ID | KV2G_MOUSE | STANDARD; | PRT; 113 AA. |
| AC | P01631; | | |
| DT | 21-JUL-1986 | (Rel. 01, Created) | |
| DT | 21-JUL-1986 | (Rel. 01, Last sequence update) | |
| DT | 15-JUL-1999 | (Rel. 38, Last annotation update) | |
| DE | I9 kappa chain V-II region 25-10. | | |
| OS | Mus musculus (Mouse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| NCBI | NCBI_TaxID=10090; | | |
| RN | [1] | | |
| RP | SEQUENCE | | |
| RC | STRAIN=A/J; | | |
| RX | MEDLINE=83178921; PubMed=6404298; | | |
| RA | Novotny J., Margolies M.N.; | | |
| RT | "Amino acid sequence of the light chain variable region from a mouse | | |
| RL | anti-digoxin hybridoma antibody." | | |
| RL | Biochemistry 22:1153-1158(1983). | | |
| CC | !- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA | | |
| CC | PROTEIN THAT BINDS DIGOXIN. | | |
| CC | PIR; A01914; KVM26. | | |
| DR | HSSP; P80362; 1WT. | | |
| DR | InterPro; IPR007110; IG-like. | | |
| DR | InterPro; IPR003596; IG_V. | | |
| DR | Pfam; PF00047; ig; 1. | | |
| DR | SMART; SM00406; IGV; 1. | | |
| DR | PROSITE; PS00835; IG_LIKE; 1. | | |
| KW | Immunoglobulin V region; Monoclonal antibody; Hybridoma. | | |
| FT | DOMAIN 1 | | |
| FT | DOMAIN 23 | | |
| FT | DOMAIN 24 | | |
| FT | DOMAIN 39 | | |
| FT | DOMAIN 40 | | |
| FT | DOMAIN 54 | | |
| FT | DOMAIN 55 | | |
| FT | DOMAIN 61 | | |
| FT | DOMAIN 62 | | |
| FT | DOMAIN 93 | | |
| FT | DOMAIN 94 | | |
| FT | DOMAIN 103 | | |
| FT | DOMAIN 112 | | |
| FT | DISULFID 23 | | |
| FT | NON TER 113 | | |
| FT | NON TER 113 | | |

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 1.53e-37 | Length: | 113 |
| Score: | 422.00 | Matches: | 77 |
| Percent Similarity: | 83.19% | Conservative: | 17 |
| Best Local Similarity: | 68.14% | Mismatches: | 19 |
| Query Match: | 53.76% | Indels: | 0 |
| DB: | 1 | Caps: | 0 |

US-09-674-716B-2 (1-437) x KV2B_HUMAN (1-113)

| | | | |
|----|-----|---|-----|
| QY | 96 | GATATTGTGATAAACCAGGATGAACCTCCAAATCCTGTCACTTCTCGAGAAATCAAGTTTCC | 155 |
| DB | 1 | AspValValMetThrGlnSerProLeuPheLeuProValThrLeuGlyGluProAlaSer | 20 |
| QY | 156 | ATTCCTCTGCAGGCTTAGTAGAGTCTCTGTATTAAGGATGGGAAGACATCTTGTAATGG | 215 |
| DB | 21 | IleGlnCysArgSerSerGlnSerLeuValTyrArg***Gly***ThrTyrLeu***Trp | 40 |
| QY | 216 | TTTCTGCAGACACGACGACCAATCTCCTCACCTCCTGTATGTATTGTATGCCACCGTGCA | 275 |
| DB | 41 | TyrLeuGlnIlySerProGlyGlnSerProGluLeuLeuIleTyrLeuSerSerTyrArgasp | 60 |
| QY | 276 | TCAGGAGTCTCAGACCCGGTTTAGTGGCAGTGGGTTCAGGCAGACAGATTACCTCGAAATC | 335 |
| DB | 61 | SerGlyValProAspArgPheSerAspSerGlySerGlyThrAspPheThrLeuLysile | 80 |
| QY | 336 | AGTAGAGTAGAGCTGAGGATCGGGTGTCTATTACTGTGTCAACACTTCTGAGAGTATCCA | 395 |
| DB | 81 | ThrArgValGlnAlaGluAspValGlyValTyrTyrCysMetGlnAlaThr***SerPro | 100 |
| QY | 396 | TTACAGTTCGGCTCGGGACACAAAGTTGGAAATAAAACGT | 434 |
| DB | 101 | TyrThrPheGlyGlnGlyThrLysLeu***IleLysArg | 113 |

RESULT 11

| | | | | |
|------------|---|-----------------------------------|------|---------|
| ID | KV2D MOUSE | STANDARD; | PRT; | 112 AA. |
| AC | P01629; | | | |
| DT | 21-JUL-1986 | (Rel. 01, Created) | | |
| DT | 21-JUL-1986 | (Rel. 01, Last sequence update) | | |
| DT | 15-JUL-1999 | (Rel. 38, Last annotation update) | | |
| DE | Ig kappa chain V-II region 2S1.3. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| NCBI_TaxID | 10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE. | | | |
| RP | MEDLINE=83055101; PubMed=7141411; | | | |
| RT | Herbst H., Chang J.Y., Abersold R., Braun D.G.; | | | |
| RA | "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for | | | |
| RT | the group A streptococcal polysaccharide." | | | |
| RL | Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076 (1982). | | | |
| CC | -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL | | | |
| CC | ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE. | | | |
| DR | PIR; A01911; KVMSS1. | | | |
| DR | HSSP; P01607; IREI. | | | |
| DR | InterPro; IPR007110; Ig-like. | | | |
| DR | InterPro; IPR003596; Ig_v. | | | |
| DR | Pfam; PF00047; ig_1. | | | |
| DR | SMART; SM00406; IGV; 1. | | | |
| DR | PROSITE; PS0835; IG_LIKE; 1. | | | |
| KW | Immunoglobulin V region; Monoclonal antibody. | | | |
| FT | DOMAIN 1 23 | | | |
| FT | DOMAIN 24 39 | | | |
| FT | DOMAIN 40 54 | | | |
| FT | DOMAIN 55 61 | | | |
| FT | DOMAIN 62 93 | | | |
| FT | DOMAIN 94 102 | | | |
| FT | DOMAIN 103 112 | | | |
| FT | DISULFID 23 93 | | | |
| FT | NON TER 112 112 | | | |
| SQ | SEQUENCE 112 AA; 12221 MW; BD5EF5E6D789FBEC CRC64; | | | |

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Alignment Scores:
Pred. No.: 5,48e-35 Length: 134
Score: 398.50 Matches: 78
Percent Similarity: 75.81% Conservative: 16
Best Local Similarity: 62.90% Mismatches: 29
Query Match: 50.76% Indels: 1
DB: 1 Gaps: 1

US-09-674-716B-2 (1-437) x KV4C_HUMAN (1-134)

QY 66 CTTATGTTCTGGATCTCTGGAGTCAGTGGGGATATTGTGATAACCCAGGATGAACCTCTCC 125
Db 11 LeuLeuLeuTrpIleSerGlyAlaTyrGlyAspIleValMetThrGlnSerProAspSer 30
QY 126 AATCCTGTCACCTCTGGAGAACAGTCATCTCCAGTCTAGTAAGAGTCTCTCTG 185
Db 31 LeuAlaValSerLeuGlyGluArgAlaThrIleAsnCysLysSerGlnSerIleLeu 50
QY 186 TAT---AAGATGGGAAGACATACCTTGAATGTTCTTCGACAGACACGAGTCTCTCT 242
Db 51 TyrSerSerAspAsnLysAsnTyrLeuAlaTrpTyrGlnGlnLysProGlyGlnProPro 70
QY 243 CAGCTCCTGATCTATTGATGTCACCGCTGCATCAGGAGTCTCAGCCGGTTAGTGGC 302
Db 71 LysLeuLeuIleTyrTrpAlaSerThrArgLysSerGlyValProAspArgPheSerGly 90
QY 303 AGTGGGTGAGGACAGATTTCCCTCGAATACAGTAGAGTGAAGCTGAGGATGGGT 362
Db 91 SerGlySerGlyThrAspPheThrIleSerSerLeuGlnAlaGluAspValAla 110
QY 363 GTGTATTACTGTCAACAACTTGTAGATATCCATTACGTTTCGGCTCGGGGACAAAGTTG 422
Db 111 ValTyrTyrCysGlnGlnTyrTyrAsnLeuProTrpThrPheGlyGlnGlyThrLysVal 130
QY 423 GAAATAAAACGT 434
Db 131 GluIleLysArg 134

RESULT 15
KV4B_HUMAN
ID KV4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DC 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combrato G., Mocikat R., Pohlenz H.D.,

Zachau H.G.;
RA "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00022; CAA77317.1; -
DR PIR; A01904; K4HUIJ.
DR HSP; P80362; IWTJ.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 133 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AP4 CRC64;

Alignment Scores:
Pred. No.: 8.99e-33 Length: 133
Score: 378.00 Matches: 77
Percent Similarity: 75.00% Conservative: 16
Best Local Similarity: 62.10% Mismatches: 29
Query Match: 48.15% Indels: 2
DB: 1 Gaps: 2

US-09-674-716B-2 (1-437) x KV4B_HUMAN (1-133)

QY 66 CTTATGTTCTGGATCTCTGGAGTCAGTGGGGATATTGTGATAACCCAGGATGAACCTCTCC 125
Db 11 LeuLeuLeuTrpIleSerGlyAlaTyrGlyAspIleValMetThrGlnSerProAspSer 30
QY 126 AATCCTGTCACCTCTGGAGAACAGTCATCTCCAGTCTAGTAAGAGTCTCTCTG 185
Db 31 LeuAlaValSerLeuGlyGluArgAlaThrIleAsnCysLysSerGlnSerValLeu 50
QY 186 TAT---AAGATGGGAAGACATACCTTGAATGTTCTTCGACAGACACGAGTCTCTCT 242
Db 51 TyrSerSerAsnLysAsnTyrLeuAlaTrpTyrGlnGlnLysProGlyGlnProPro 70
QY 243 CAGCTCCTGATCTATTGATGTCACCGCTGCATCAGGAGTCTCAGCCGGTTAGTGGC 302
Db 71 LysLeuLeuIleTyrTrpAlaSerThrArgLysSerGlyValProAspArgPheSerGly 90
QY 303 AGTGGGTGAGGACAGATTTCCCTCGAATACAGTAGAGTGAAGCTGAGGATGGGT 362
Db 91 SerGlySerGlyThrAspPheThrIleSerSerLeuGlnAlaGluAspValAla 110
QY 363 GTGTATTACTGTCAACAACTTGTAGATATCCATTACGTTTCGGCTCGGGGACAAAGTTG 422
Db 111 ValTyrTyrCysGlnGlnTyrTyrAsnLeuProTrpThrPheGlyGlnGlyThrLysVal 129
QY 423 GAAATAAAACGT 434

Thu Sep 30 13:18:44 2004

Page 10

us-09-674-716b-2.rsp

Db 130 GluileLysArg 133
|||||

Search completed: September 30, 2004, 08:42:45
Job time : 11.4813 secs

DR Pfam; PF00047; ig; 2.
 DR SMART; SM00407; IG1; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein_IG_MHC; 1.
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Alignment Scores:
 Pred. No.: 1.35e-48 Length: 239
 Score: 497.00 Matches: 95
 Percent Similarity: 82.84% Conservative: 16
 Best Local Similarity: 70.90% Mismatches: 23
 Query Match: 63.31% Indels: 0
 DB: 4 Gaps: 0

US-09-674-716B-2 (1-437) x Q8NEKO (1-239)

QY 36 ATGAGGTTCTCTGTTCTGAGTTCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
 Db 1 MetArgLeuProAlaGlnLeuLeuGlyLeuMetLeuTrpValSerGlySerGly 20
 QY 96 GATATTGTGATACCCAGGATGAACCTCTCAATCTCTGTCACCTCTGGAGATCAGTTTCC 155
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
 QY 156 ATCTCTGAGGTCCTAGTAAAGATCTCTGTTATAGGATGGGAGACATCTGTAATTGG 215
 Db 41 IleSerCysArgSerGlnSerLeuLeuHisSerAspGlyTyrAsnTyrLeuAspTrp 60
 QY 216 TTCTCTGAGACGACGAGCAATCTCTCAGCTCTGATGTTATGTTCTCAACCGGTGCA 275
 Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 80
 QY 276 TCAGGAGTCACACCGGTTTATGTCAGTGGGTGAGGACACAGATTTACCTCGAAATC 335
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100
 QY 336 AGTAGAGTGAAGCTCAGGATGGGTGTATTACTGTCACAACTGTTAGAGTATCCA 395
 Db 101 SerLysValGluAlaGluAspValGlyIleTyrTyrCysMetGlnGlyLeuGlnThrPro 120
 QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAAACGTACG 437
 Db 121 GlnThrPheGlyGlnGlyThrLysValGluIleLysArgThr 134

RESULT 2

ID Q8TCD0 PRELIMINARY; PRT; 239 AA.
 AC Q8TCD0
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022362; AAH2362.1; -.
 DR PIR; S34095; S34095.
 DR PIR; S42267; S42267.
 DR PIR; S42268; S42268.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 2.

DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Alignment Scores:
 Pred. No.: 7.48e-47 Length: 239
 Score: 482.00 Matches: 91
 Percent Similarity: 79.95% Conservative: 16
 Best Local Similarity: 67.91% Mismatches: 27
 Query Match: 61.40% Indels: 0
 DB: 4 Gaps: 0

US-09-674-716B-2 (1-437) x Q8TCD0 (1-239)

QY 36 ATGAGGTTCTCTGTTCTGAGTTCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
 Db 1 MetArgLeuProAlaGlnLeuLeuGlyLeuMetLeuTrpValSerGlySerGly 20
 QY 96 GATATTGTGATACCCAGGATGAACCTCTCAATCTCTGTCACCTCTGGAGATCAGTTTCC 155
 Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40
 QY 156 ATCTCTGAGGTCCTAGTAAAGATCTCTGTTATAGGATGGGAGACATCTGTAATTGG 215
 Db 41 IleSerCysArgSerThrGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 60
 QY 216 TTCTCTGAGACGACGAGCAATCTCTCAGCTCTGATGTTATGTTCTGACCCGTCGA 275
 Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgSp 80
 QY 276 TCAGGAGTCACACCGGTTTATGTCAGTGGGTGAGGACACAGATTTACCTCGAAATC 335
 Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100
 QY 336 AGTAGAGTGAAGCTCAGGATGGGTGTATTACTGTCACAACTGTTAGAGTATCCA 395
 Db 101 ThrArgValGluAlaGluAspValGlyValTyrPheCysMetGlnGlyThrHisTrpPro 120
 QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAAACGTACG 437
 Db 121 SerThrPheGlyGlnGlyThrLysLeuGluIleLysArgThr 134

RESULT 3

ID Q99M37 PRELIMINARY; PRT; 238 AA.
 AC Q99M37
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002035; AAH02035.1; -.
 DR PIR; A31807; A31807.
 DR PIR; A32248; A32248.
 DR PIR; B32248; B32248.
 DR PIR; C32248; C32248.
 DR PIR; F32530; F32530.
 DR PIR; PH1042; PH1042.
 DR PIR; PH1043; PH1043.
 DR PIR; PH1044; PH1044.
 DR PIR; S07455; S07455.
 DR PIR; S16112; S16112.
 DR PIR; S24500; S24500.
 DR PIR; S24501; S24501.
 DR PIR; S24503; S24503.
 DR PIR; S24504; S24504.


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RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR PIR; S24529; S24529.
DR PIR; S24532; S24532.
DR PIR; S24533; S24533.
DR PIR; S24535; S24535.
DR PIR; S24536; S24536.
DR PIR; S24538; S24538.
DR PDB; 1I91; 25-DEC-02.
DR PDB; 1LO2; 31-JUL-02.
DR PDB; 1LO4; 31-JUL-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB206A0B801330A CRC64;

Alignment Scores:
Pred. No.: 7,628-43 Length: 238
Score: 447.50 Matches: 87
Percent Similarity: 80.45% Conservativeness: 20
Best Local Similarity: 65.41% Mismatches: 25
Query Match: 57.01% Indels: 1
DB: 11 Gaps: 1

US-09-674-716B-2 (1-437) x Q99M37 (1-238)
QY 36 ATGAGTCTCTGTTTCAGTTCTGGGGTGTCTATGTTCTGGATCTCTGGAGTCAGTGGG 95
DB 1 MetLysLeuProValArgLeuLeu---ValLeuMetPheTrpIleProAlaSerSerSer 19
QY 96 GATATTGTGATTAACCCAGATGAATCTCCCAATCTCTGCTCACTCTGGAGATCATGTTCC 155
DB 20 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 39
QY 156 ANCTCTGAGGTCTAGTAGAGTCTCCGTATAGGATGGAAGACATATCTGAATTGG 215
DB 40 IleSerCysArgSerGlnSerIleValHisSerAsnGlyAsnThrTyLeuHisTrp 59
QY 216 TTTCTGCAGACACCCAGGACAACTCTCCTCAGTCTCTGATGTATTTGATCTCCACCGTCCA 275
DB 60 TyrLeuGlnLysProGlyGlnSerProLysLeuLeuLeuTyLysValSerAsnArgPhe 79
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCCACCTGGAATC 335
DB 80 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 99
QY 336 AGTAGAGTGAAGGTGAGGATGTGGTGTGTATCTACTGTCAACAACTTGTAGAGTATCCA 395
DB 100 SerArgValGluAlaGluAspLeuGlyValTyPheCysSerGlnSerThrHisValPro 119

Alignment Scores:
Pred. No.: 2,98-42 Length: 238
Score: 442.50 Matches: 86
Percent Similarity: 79.70% Conservativeness: 20
Best Local Similarity: 64.66% Mismatches: 26
Query Match: 56.37% Indels: 1
DB: 11 Gaps: 1

US-09-674-716B-2 (1-437) x Q8VC16 (1-238)
QY 36 ATGAGTCTCTGTTTCAGTTCTGGGGTGTCTATGTTCTGGATCTCTGGAGTCAGTGGG 95
DB 1 MetLysLeuProValArgLeuLeu---ValLeuMetPheTrpIleProAlaSerSerSer 19
QY 96 GATATTGTGATTAACCCAGATGAATCTCCCAATCTCTGCTCACTCTGGAGATCATGTTCC 155
DB 20 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 39
QY 156 ATCTCTGTCAGTCTCTGATAGAGTCTCTGTATAGGATGGAAGACATATCTGAATTGG 215
DB 40 IleSerCysArgSerGlnSerLeuValHisSerAsnGlyAsnThrTyLeuHisTrp 59
QY 216 TTTCTGCAGACACCCAGGACAACTCTCCTCAGTCTCTGATGTATTTGATCTCCACCGTCCA 275
DB 60 TyrLeuGlnLysProGlyGlnSerProLysLeuLeuLeuTyLysValSerAsnArgPhe 79
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCACAGATTTCCACCTGGAATC 335
DB 80 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 99
QY 336 AGTAGAGTGAAGGTGAGGATGTGGTGTGTATTTACTGTCAACAACTTGTAGAGTATCCA 395
DB 100 SerArgValGluAlaGluAspLeuGlyValTyTyPheCysPheGlnGlySerHisValPro 119

RESULT 4
Q8VC16 PRELIMINARY; PRT; 238 AA.
ID Q8VC16
AC Q8VC16;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;

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Qy 396 TTACAGTTCGGCTCGGGGCAAAAGTTGGAATAAACGT 434
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Db 121 TyrThrPheGlyGlyThrLysLeuGluIleLysArg 133

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| RESULT 6 | |
| QSKOF8 | |
| ID QSKOF8 | PRELIMINARY; PRT: 239 AA. |
| AC QSKOF8; | |
| DT 01-OCT-2002 | (TRENBIrel. 22, Created) |
| DT 01-OCT-2002 | (TRENBIrel. 22, Last sequence update) |
| DT 01-OCT-2003 | (TRENBIrel. 25, Last annotation update) |
| DE | Hypothetical protein. |
| OS | Mus musculus (Mouse). |
| OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | |
| OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; | |
| NCBI_TaxID=10090; | [1] |
| RN | SEQUENCE FROM N A |
| DD | |

RC TISSUE=Breast tumor;
RA Strausberg J.;
RL Submitted (Jun-2002) to the EMBL/GenBank/DBJ databases
DR EMBL; EC031498; AAI31498.1; -

PIR; A33933; A33933
 PDB; 1KN2; 13-MAR-02
 GO; GO:001491; F:oxidoreductase activity; IEA
 GO; GO:0008152; F:metabolism; IEA
 InterPro; IPR002198; ADH short.
 InterPro; IPR003599; IG.
 InterPro; IPR007110; IG-like.
 InterPro; IPR003597; IG cl.
 InterPro; IPR003006; IG MHC.
 InterPro; IPR003596; IG v.
 Pfam; PF00047; IG; 2.
 SMART; SM00409; IG; 2.
 SMART; SM00407; IGcl; 1.
 SMART; SM00406; IGv; 1.
 PROSITE; PS00061; ADH SHORT; 1.
 PROSITE; PS50815; IG LIKE; 2.

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|------------------------|--|---------------|-----|--|--|
| DR | PROSITE; PS00290; IG_NHC; 1. | | | | |
| KW | Hypothetical protein. | | | | |
| SQ | SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CFC64; | | | | |
| Alignment Scores: | | | | | |
| Pred. No.: | 2,048-39 | Length: | 239 | | |
| Score: | 418.00 | Matches: | 82 | | |
| Percent Similarity: | 76.69% | Conservative: | 20 | | |
| Best Local Similarity: | 61.65% | Mismatches: | 31 | | |
| Query Match: | 93.25% | Indels: | 0 | | |
| DB: | 11 | Gaps: | 0 | | |

| DB: | II | Gaps: | 0 |
|---|----|-------|---|
| US-09-674-716B-2 (1-437) x Q8K0F8 (1-239) | | | |

[illegible]

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96 GATATTGTGATAACCCAGGATGAACCTTCCAATCCTGTGCACTTTCTGGAGAAATCAGTTTCC
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Db
21 AspValValMetThrGlnThnProLeuHyrLeuSerValThrIleGluVGIProLlaSer
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156 ATCTCTGCAGGTCTAGTAAGAGTCTCCTGTATTAAGGATGGGAAGACATATCTGAATGG 215

Db 41 IleSerCysLysSerSerGlnSerLeuPheTyThrAsnGlyLysMetTyLeuSerTrp 60
41
QY 216 TTTTCTGCAGAGACCAGACAAATCTCTCCTCAGCTCCTGATGTATTTGATGTCACCCCGTGA 275

61 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleSerLeuValSerLysLeuAsp 80 Db
276 TCAGGAGTCTCAGACC GGTTTACTGGCAGTGGGTTCAGGCACAGATTTCA CCTCGGAATC 335 Oy

81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 1000
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336 AGTAGAGTGAAGGCTGAGGATGCTGGCTGCTATATTACTGTCAACACACTCTGACACTATCCA 395

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|---|--|--|--------------|
| Qy | 393 | CAVTTACGTTTCGGCTCGGGACAAAGTTTGGAAATAAAGCT | 434 |
| | | : | : |
| Db | 101 | ProTrpThrPheGlyGlnGlyThrLysValGluIleLysArg | 114 |
| | | : | : |
| RESULT 6 | | | |
| Q8K122 | | PRELIMINARY; | PRT; 148 AA. |
| ID | Q8K122 | | |
| AC | Q8K122; 2002 (TrEMBLrel. 22, Created) | | |
| DT | 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) | | |
| DT | 01-OCT-2002 (TrEMBLrel. 25, Last annotation update) | | |
| DE | Hypothetical protein. | | |
| OS | Mus musculus (Mouse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| OX | NCBI_TaxID=10090; | | |
| RN | [1] | | |
| RC | SEQUENCE FROM N.A. | | |
| RP | TISSUE=Salivary gland; | | |
| RA | Strausberg R.; | | |
| RL | Submitted (May-2002) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; BC028925; AAH28925.1; -. | | |
| DR | InterPro; IPR003599; IG. | | |
| DR | InterPro; IPR007110; IG-like. | | |
| DR | InterPro; IPR003596; IG_v. | | |
| DR | Pfam; PF00047; IG; 1. | | |
| DR | SMART; SM00409; IG; 1. | | |
| DR | SMART; SM00406; IGv; 1. | | |
| DR | PROSITE; PS00835; IG_LIKE; 1. | | |
| DR | Hypothetical protein. | | |
| SK | PROSITE; 148 AA; 16345 MW; 193920BBD9F3B521 CRC64; | | |
| QW | SEQUENCE | | |
| Alignment Scores: | | | |
| Pred. No.: | 2,22e-37 | Length: | 148 |
| Score: | 400.00 | Matches: | 80 |
| Percent Similarity: | 75.78% | Conservative: | 17 |
| Best Local Similarity: | 62.50% | Mismatches: | 30 |
| Query Match: | 50.96% | Indels: | 1 |
| DB: | 11 | Gaps: | 0 |
| US-09-674-716B-2 (1-437) x Q8K122 (1-148) | | | |
| Qy | 51 | CAGTTTCGGGGTGCTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAACC | 110 |
| | | | |
| Db | 5 | GlnPheLeuPheLeuLeuValLeuTrpIleargGluThrAenGlyAspValValMetThr | 24 |
| | | | |
| Qy | 111 | CAGGATGAACCTCCCAATCCGTGCACATCTCGAGAATCAGTTTCCATCTCCTGCAGGTCT | 170 |
| | | | |
| Db | 25 | GlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSerIleSerCysLysSer | 44 |
| | | | |
| Qy | 171 | AGTAAGAGTCTCTGTATAAGATGGGAAGACATACCTTGAATTTGGTTTCTGCAGAGACA | 230 |
| | | | |
| Db | 45 | SerGlnSerLeuLeuAspSerAspGlyLysThrYrLeuAenTrpLeuLeuGlnArgPro | 64 |
| | | | |
| Qy | 231 | GGACAAATCTCTCAGTCCCTGATCTATGATGTCACCCCGTCATCAGGAGTCTCAGAC | 290 |
| | | | |
| Db | 65 | GlyGlnSerProLysArgLeuIleYrLeuValSerLysLeuAspSerGlyValProAsp | 84 |
| | | | |
| Qy | 291 | CGGTTTAGTGGCAGTGGGTCAAGCAGATTTCCCTCGAAATCAGTAGAGTGAAGGCT | 350 |
| | | | |
| Db | 85 | ArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIleSerArgValGluAla | 104 |
| | | | |
| Qy | 351 | GAGATGGGTGGTGTATTACTGTCAACACTTGTAGNGTATCCATTACGTTCCGGCTCG | 410 |
| | | | |
| Db | 105 | GluAspLeuGlyValTyTyCysTrpGlnGlyThrHisPhePro-GlyArgSerValGl | 124 |
| | | | |
| Qy | 411 | GGGCACAAAGTTGGAAATAAAAC | 432 |
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| Db | 124 | uAlaprosertPlyssSerAen | 131 |
| | | | |
| RESULT 9 | | | |
| Q9JL82 | | PRELIMINARY; | PRT; 104 AA. |
| ID | Q9JL82 | | |

Db 116 TrpThrPheGlyGlnGlyThrLysValGluIleLysArgThr 129
RESULT 11
Q7TS98 PRELIMINARY; PRT; 236 AA.
AC Q7TS98;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-colorectal carcinoma light chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=9338497; PubMed=8372513;
RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of 116N9.9 heavy and light chain
cDNAs and expression of antibody fragments in *Escherichia coli*."
RL Year Immunol. 7:56-62(1993).
DR EMBL; S65921; AAB28160.1; -;
SQ SEQUENCE 236 AA; 26454 MW; 2C586BFBF5EA10F4C CRC64;

Alignment Scores:
Pred. No.: 2,686-30 Length: 236
Score: 339.50 Matches: 66
Percent Similarity: 67.41% Conservative: 25
Best Local Similarity: 48.89% Mismatches: 39
Query Match: 43.25% Indels: 5
DB: 11 Gaps: 1

US-09-674-716B-2 (1-437) x Q7TS98 (1-236)

QY 30 CTCACATGAGTCTCTCTCTCAGTTCTGGGGGCTTATGTTCTGGATCTCTGGAGTC 89
Db 1 MetAspMetArgThrProIaGlnPheLeuGlyIleLeuLeuLeuTrpPheProGlyMet 20
QY 90 AGTGGGATATTGTGATAACCCAGATGAATCTTCAATCTGTCACTCTGGAGAAATCA 149
Db 21 LysCysAspIleLeuMetThrGlnSerProSerMetTyrAlaSerLeuGlyGluArg 40
QY 150 GTTTCATCTCTCAGGCTAGTAAAGTCTCTCTATAGGATGAGGAGACATCTTG 209
Db 41 ValThrIleThrCysLysAlaSer-----GlnAspIleAsnSerTyrLeu 55
QY 210 AATTGTTTCTCAGACAGACAGACAAATCTCCTCAGCTCTGATGATTTGATGCCACC 269
Db 56 SerTrpPheGlnGlnLysProGlyLysSerProLysThrLeuIleTyrArgAlaAsnArg 75
QY 270 CGTGCATCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGGCACAGATTTCACCTG 329
Db 76 LeuValAspGlyValProSerArgPheSerGlySerGlySerGlyGlnAspTyrSerLeu 95
QY 330 GAAATCAGTAGAGTGAAGCTCAGGATGGGTGTATTACTGTCAACAACTTGTAGAG 389
Db 96 ThrIleSerSerLeuGluTyrGluAspMetGlyIleTyrTyrCysLeuGlnTyrAspGlu 115
QY 390 TATCCATTACGTTCCGGTCGGGACAAAGTTGGAAATAAAACGT 434
Db 116 PheProArgThrPheGlyGlyThrLysLeuGluIleLysArg 130

RESULT 12
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AA05332.1; -;
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Alignment Scores:
Pred. No.: 1,756-29 Length: 236
Score: 332.50 Matches: 68
Percent Similarity: 64.71% Conservative: 20
Best Local Similarity: 50.00% Mismatches: 43
Query Match: 42.36% Indels: 5
DB: 4 Gaps: 1

US-09-674-716B-2 (1-437) x Q7Z3Y4 (1-236)

QY 30 CTCACATGAGTCTCTCTCTCAGTTCTGGGGGCTTATGTTCTGGATCTCTGGAGTC 89
Db 1 MetAspMetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuLeuLeuLeuLeuLeu 20
QY 90 AGTGGGATATTGTGATAACCCAGATGAATCTTCAATCTCTCACTCTGGAGAAATCA 149
Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspThr 40
QY 150 GTTTCATCTCTCAGGCTAGTAAAGTCTCTCTATAGGATGAGGAGACATCTTG 209
Db 41 ValThrIleThrCysArgAlaSer-----GlnAspIleSerAsnTyrLeu 55
QY 210 AATTGTTTCTCAGACAGACAGACAAATCTCCTCAGCTCTGATGATTTGATGCCACC 269
Db 56 AlaTrpPheGlnGlnLysProGlyLysAlaProLysSerLeuIleTyrGlyAlaSerSer 75
QY 270 CGTGCATCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGGCACAGATTTCACCTG 329
Db 76 LeuGlnSerGlyValGlnSerLysPheSerGlySerGlySerGlyThrAspPheThrLeu 95
QY 330 GAAATCAGTAGAGTGAAGCTCAGGATGGGTGTATTACTGTCAACAACTTGTAGAG 389
Db 96 ThrIleSerSerLeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrLysSer 115
QY 390 TATCCATTACGTTCCGGTCGGGACAAAGTTGGAAATAAAACGTACG 437
Db 116 TyrProValThrPheGlyGlnGlyThrLysLeuGluIleLysArgThr 131

RESULT 13

330 GAAATCATGATGAGTGAAGCTGAGGATGTGGGTGTGTATTACTGTGTCAACAACCTGTGTAGAG 389
||||| :|||||
Db 96 ThrIleSerSerLeuGluSerAspThrAlaThrTyrTyrCysLeuGlnHisGlyGlu 115
||||| :|||||
Qy 390 TATCCATTACAGTTCGCTCGGGACAAAGTTGGAATAAAACGT 434
||||| :|||||
Db 116 SerProTyrThrPheGlySerGlyThrLysLeuGluLeuLysArg 130
||||| :|||||
RESULT 14
Q75Z36 PRELIMINARY; PRT; 237 AA.
ID Q75Z36 AC Q75Z36;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8335;
RN [1]
RN PP SEQUENCE FROM N.A.
RN RX TISSUE=Whole;
RN RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RN PP SEQUENCE FROM N.A.
RN RX TISSUE=Whole;
RN RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.D., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [3]
RN PP SEQUENCE FROM N.A.
RN RX TISSUE=Whole;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
KW EMBL: BC054155; AAHS4155.1;
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 26300 MW; 47BD0D2639CB436 CRC64;
Alignment Scores:
Prid. No.: 8.7e-29 Length: 237
Score: 326.50 Matches: 65
Percent Similarity: 70.08% Conservative: 24
Best Local Similarity: 51.18% Mismatches: 35
Query Match: 41.59% Indels: 3
DB: 13 Gaps: 2
US-09-674-716B-2 (1-437) x Q75Z36 (1-237)

Blank Sheet

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:19:42; Search time 52.0607 Seconds
(without alignments)
4743.430 Million cell updates/sec

Title: US-09-674-716B-2

Perfect score: 785
Sequence: 1 aggtttacagttactcagc.....agttggaaataaaacgtacg 437

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2_1/USPTO_spool_p/US0674716/runat_30092004_070257_25848/app_query.fasta_1.3164
-DB=A Geneseq 29Jan04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0674716 @CGN 1 1 475 @runat_30092004_070257_25848 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq 29Jan04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 737 | 93.9 | 145 | 3 | AAY32261 |
| 2 | 631 | 80.4 | 132 | 2 | AAR12354 |
| 3 | 626 | 79.7 | 131 | 2 | AAR12232 |
| 4 | 555 | 70.7 | 113 | 2 | AAW39804 |
| 5 | 549 | 69.9 | 113 | 2 | AAW39882 |
| 6 | 547 | 69.7 | 113 | 2 | AAW39803 |
| 7 | 547 | 69.7 | 113 | 2 | AAW39801 |
| 8 | 542 | 69.0 | 122 | 3 | AAW70790 |
| 9 | 541 | 68.9 | 113 | 2 | AAW39802 |
| 10 | 530 | 67.5 | 113 | 2 | AAW39886 |

ALIGNMENTS

RESULT 1

RAY32261
ID AAY32261 standard; protein; 145 AA.

XX AC AAY32261;

XX DT 15-FEB-2000 (first entry)

XX DE Mouse anti-CD23 MAb C11 light chain variable region.

XX KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
KW therapy.

XX OS Mus musculus.

XX FH Key Location/Qualifiers
FT Region 55..70
FT /note= "CDR L1"

FT Region 83..92
FT /note= "CDR L2"

FT Region 125..134
FT /note= "CDR L3"

XX WO9958679-A1.

XX PD 18-NOV-1999.

| | | | | | | |
|----|-------|------|-----|---|----------|--------------------|
| 11 | 516 | 65.7 | 116 | 3 | AAY32262 | AAY32262 Humanised |
| 12 | 509 | 64.8 | 100 | 4 | AAE06989 | AAE06989 Mouse ger |
| 13 | 508 | 64.7 | 239 | 7 | ADE28461 | ADE28461 Human ant |
| 14 | 505 | 64.3 | 239 | 3 | AAY82617 | AAY82617 Human PTH |
| 15 | 505 | 64.3 | 239 | 3 | AAW82615 | AAW82615 Human PTH |
| 16 | 505 | 64.3 | 274 | 2 | AAW39899 | AAW39899 Single ch |
| 17 | 504 | 64.2 | 239 | 3 | AAY82611 | AAY82611 Human PTH |
| 18 | 504 | 64.2 | 239 | 5 | ABG70338 | ABG70338 Human MDD |
| 19 | 500 | 63.7 | 239 | 7 | ADE28405 | ADE28405 Human ant |
| 20 | 499 | 63.6 | 239 | 3 | AAY82616 | AAY82616 Human PTH |
| 21 | 499 | 63.6 | 239 | 7 | ADE28421 | ADE28421 Human ant |
| 22 | 499 | 63.6 | 239 | 7 | ADE28465 | ADE28465 Human ant |
| 23 | 498 | 63.4 | 239 | 7 | ADE28397 | ADE28397 Human ant |
| 24 | 497 | 63.3 | 142 | 7 | ABR82929 | ABR82929 Anti-huma |
| 25 | 495.5 | 63.1 | 170 | 5 | ABP64972 | ABP64972 Human pro |
| 26 | 495 | 63.1 | 141 | 2 | AAR30454 | AAR30454 C242.11 M |
| 27 | 495 | 63.1 | 141 | 2 | AAR32541 | AAR32541 C242 kapp |
| 28 | 495 | 63.1 | 239 | 3 | AAY82614 | AAY82614 Human PTH |
| 29 | 495 | 63.1 | 239 | 3 | AAY82610 | AAY82610 Human PTH |
| 30 | 494 | 62.9 | 133 | 2 | AAR33951 | AAR33951 CTMO1 VL |
| 31 | 494 | 62.9 | 133 | 3 | AAV56874 | AAV56874 MAb CT-M- |
| 32 | 493 | 62.8 | 242 | 6 | ABU09337 | ABU09337 Feline Ig |
| 33 | 492 | 62.7 | 239 | 7 | ADE28469 | ADE28469 Human ant |
| 34 | 491 | 62.5 | 239 | 7 | ADE28521 | ADE28521 Human ant |
| 35 | 491 | 62.5 | 239 | 7 | ADE28477 | ADE28477 Human ant |
| 36 | 490 | 62.4 | 239 | 3 | AAY82618 | AAY82618 Human PTH |
| 37 | 489 | 62.3 | 139 | 4 | AAB99117 | AAB99117 Human pro |
| 38 | 488 | 62.2 | 133 | 7 | ADD25800 | ADD25800 Binding d |
| 39 | 488 | 62.2 | 271 | 7 | ADD25801 | ADD25801 Binding d |
| 40 | 488 | 62.2 | 505 | 7 | ADD25802 | ADD25802 Binding d |
| 41 | 488 | 62.2 | 556 | 7 | ADD25803 | ADD25803 Binding d |
| 42 | 488 | 62.2 | 556 | 7 | ADE86040 | ADE86040 Anti-4-1B |
| 43 | 487 | 62.0 | 239 | 6 | ABR48456 | ABR48456 Human Cal |
| 44 | 483 | 61.5 | 134 | 2 | AAR09420 | AAR09420 B38.1 Lig |
| 45 | 483 | 61.5 | 134 | 2 | AAW06209 | AAW06209 MAb B38-1 |

XX 07-MAY-1999; 99WO-GB001434.
 XX 09-MAY-1998; 98GB-00009839.
 XX (GLAX) GLAXO GROUP LTD.
 XX Bonnafoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPI; 2000-053101/04.
 XX N-PSDB; AA234746.
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 XX diabetes, multiple sclerosis and psoriasis.
 XX Claim 8; Fig 2; 81pp; English.
 XX This sequence represents the light chain variable region (VL) of murine
 CC anti-CD23 (pCERII) monoclonal antibody C11. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies (see
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid
 CC sequences of the C11 light and heavy chain complementarity determining
 CC regions (see AAY32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies are
 CC used to block soluble CD23 formation in human therapy, for the treatment
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX
 XX Sequence 145 AA;
 SQ

Alignment Scores:
 Pred. No.: 2,76e-72 Length: 145
 Score: 737.00 Matches: 145
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.89% Indels: 0
 DB: 3 Gaps: 0

US-09-674-716B-2 (1-437) x AAY32261 (1-145)

QY 3 GCTTTACGTTACTCAGCACACAGACCTCACCAGGTTCTCTGTTTCAGTTCTGGG 62
 Db 1 AlaLeuGlnLeuSerThrGlnAspLeuThrMetArgPheSerValGlnPheLeuGly 20
 QY 63 GTGCTTATCTTCGATCTCTGGAGTCAGTGGGGATTTGTGATAACCCAGGATGAATC 122
 Db 21 ValLeuMetPheTrpIleSerGlyValSerGlyAspIleValIleThrGlnAspGluLeu 40
 QY 123 TCCATCTCTGTCACCTCTCGAATCAGTTTCATCTCTCGAGTCTAGTAAGTCTC 182
 Db 41 SerAsnProValThrSerGlyGluSerValSerIleSerCysArgSerSerIleSerLeu 60
 QY 183 CTGTATAAGGATGGAAGACATCTTGAATGTTTCTGCAGACACAGGACAAATCTCCT 242
 Db 61 LeuTyrLysAspGlyLysThrThrLeuAsnTrpPheLeuGlnArgProGlyGlnSerPro 80
 QY 243 CAGCTCTCTGATGTTTGTATGTCACCCCGTGCATCAGAGTCTCAGACGGTTTAGTGGC 302
 Db 81 GlnLeuLeuMetTyrLeuMetSerThrArgAlaSerGlyValSerAspArgPheSerGly 100
 QY 303 AGTGGGTTCAGGCACAGATTTTACCCTGGAAATCAGTAGTGAAGGCTGAGAGTGTGGGT 362
 Db 101 SerGlySerGlyThrAspPheThrLeuGluIleSerArgValLysAlaGluAspValGly 120
 QY 363 GTGTATTACTGTCAACAATCTGTAGAGTATCCATTCAGTTCGGCTCGGGGACAAAGTTG 422

Db 121 ValTyrTyrCysGlnGlnLeuValGluTyrProPheThrPheGlySerGlyThrLysLeu 140
 QY 423 GAAATAAACGTACG 437
 Db 141 GluileLysArgThr 145
 RESULT 2
 AAR12354
 ID AAR12354 standard; protein; 132 AA.
 XX AC AAR12354;
 XX 25-MAR-2003 (revised)
 DT 15-AUG-1991 (first entry)
 XX Light (kappa) chain variable region of murine 2E12 immunoglobulin.
 XX Chimeric antibodies; immunoconjugates; HIV; AIDS.
 XX Mus musculus.
 XX W09107493-A.
 XX 30-MAY-1991.
 XX 13-NOV-1989; 89US-00433730.
 XX 13-NOV-1989; 89US-00433730.
 XX (XOMA) XOMA CORP.
 XX (GREC) GREEN CROSS CORP.
 XX Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
 XX WPI; 1991-178105/24.
 XX N-PSDB; AAQ12056.
 XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV
 PT -1 antigen from sample.
 PS Disclosure; Fig 1; 107pp; English.
 XX This is the light (kappa)- chain variable (V) region of a mouse
 CC monoclonal antibody (MAB), 2E12, and is specific for an HIV-1 viral
 CC antigen. It is used in the construction of a chimeric MAB comprising
 CC heavy and light chains having murine V regions and human C regions. The
 CC chimeric MABs are more effective than murine MAB 2E12 since they have an
 CC increased compatibility in humans. The heavy and light chain V-regions
 CC are joined by manipulating their respective joining (J) regions, to
 CC generate restriction enzyme recognition sites. The chimeric MABs can be
 CC used as immuno- conjugates, in association with e.g. toxins for HIV
 CC treatment. They can also be used in diagnosis of HIV. See also AAQ12057-
 CC 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003
 CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)
 XX
 XX Sequence 132 AA;
 SQ

Alignment Scores:
 Pred. No.: 1,29e-60 Length: 132
 Score: 631.00 Matches: 122
 Percent Similarity: 96.21% Conservative: 5
 Best Local Similarity: 92.42% Mismatches: 5
 Query Match: 80.38% Indels: 0
 DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x AAR12354 (1-132)

QY 36 ATGAGGTTCTCTCTCAGTTTCGGGGTCTTATCTCTGATCTCTGGAGTCACTGGG 95
 Db 1 MetArgCysSerLeuGlnPheLeuGlyValLeuMetPheTrpIleSerGlyValSerGly 20
 QY 96 GATATTGTGATTAACCCAGGATGAATCTCAATCTCTGTCCTCTGGAGAAATCACTTCC 155

```

Query Match: 79.75% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x AAR12232 (1-131)

QY 36 ATGAGTTCTCTGTTTCAGTTTCTGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
DB 1 MetArgCysSerLeuGlnPheLeuGlyValLeuMetPheTrpIleSerGlyValSerGly 20
QY 96 GATATTGTGATAACCCAGGATGAACCTCCATCCCTGTCACCTTCTGGAGAAATCAGTTTCC 155
DB 21 GluIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 40
QY 156 ATCTCTCGCAGGTCCTAGTAAGAGTCTCTCTGTATTAAGGATGGGAAGACATACTTGAATTGG 215
DB 41 PheSerCysArgSerSerIysSerLeuLeuTyrLysAspGlyIysThrTyrLeuSerTrp 60
QY 216 TTTCTCAGAGACACGAGACAAATCTCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCA 275
DB 61 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleTyrLeuMetSerThrArgVal 80
QY 276 TCAGGAGTCTCAGACCGGTTTAGTCGGCAGTGGGTGAGGCACAGATTTCAACCCTGGAAATC 335
DB 81 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 100
QY 336 AGTAGAGTGAAGCTGAGGATGTGGGTGTCTATTACTGTCAACAACCTGTGAGTATCCA 395
DB 101 SerGlyValIysAlaGluAspValGlyValTyrTyrCysGlnGlnLeuValGluTyrPro 120
QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATA 428
DB 121 TyrThrPheGlyGlyThrLysLeuGluIle 131

RESULT 4
AAW39804
ID AAW39804 standard; protein; 113 AA.
XX
AC AAW39804;
XX
DT 16-JUN-1998 (first entry)
XX
DE Variable domain of the Kappa light chain of catalytic antibody 2A10.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
PN WO9749800-A1.
XX
PD 31-DEC-1997.
XX
PF 25-JUN-1997; 97WO-US010965.
XX
PR 25-JUN-1996; 96US-00672345.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Landry DW;
XX
DR WPI; 1998-077166/07.
XX
PT New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX
PS Claim 16; Page 73-74; 147pp; English.
XX
CC AAW39801-05 represent the amino acid sequences of the variable domain of
CC the Kappa light chain of catalytic antibodies which are able to degrade
CC cocaine. A series of cocaine transition state analogues (TSAs) were

```

CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AAW39809
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state analogue.
 CC Antibody 2A10 has a per minute kcat of 0.011. The antibodies reduce the
 CC concentration of cocaine in a subject, and are used particularly for the
 CC treatment of an overdose. They are also used for treating addiction (by
 CC reducing the in vivo concentration that can be achieved)
 XX
 XX

SQ Sequence 113 AA;

Alignment Scores:
 Pred. No.: 2,95e-52 Length: 113
 Score: 555.00 Matches: 107
 Percent Similarity: 97.35% Conservative: 3
 Best Local Similarity: 94.69% Mismatches: 3
 Query Match: 70.70% Indels: 0
 DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x AAW39804 (1-113)

QY 96 GATATTGTGATACCCAGGATGAATCTCCAACTCTGCTCACTTCTGGAGATCAGTTTC 155
 Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
 QY 156 ATCTCTCGAGGCTAGTAAGAGTCTCCTGTATAGGATGGGAAGACATACCTGAAATTGG 215
 Db 21 IleSerCysArgSerSerLysSerLeuLeuTyGluAspGlyLysThrTyLeuAsnTrp 40
 QY 216 TTTCTGCGAGACAGACAAATCTCTCAGCTCTCTGATGTTTGTATGTCACCCGTCGCA 275
 Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyLeuMetSerThrArgAla 60
 QY 276 TCAGGAGTCTCAGACCGGTTAGTGGTGTTGTTACTGTCAACAACTTGTAGAGTATCCA 335
 Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80
 QY 336 AGTAGAGTGAAGGCTCAGGATGCGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 395
 Db 81 SerArgValLysAlaGluAspValGlyAlaTyTyCysGlnGlnPheValGluTyPro 100
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACGT 434
 Db 101 PheThrPheGlySerGlyThrLysLeuGluIleArgArg 113

RESULT 5

AAW39882
 ID AAW39882 standard; protein; 113 AA.

AC AAW39882;

DT 16-JUN-1998 (first entry)

DE Light chain of the catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX

PI Landry DW;

XX WPI; 1998-077166/07.

DR N-PSDB; AAW09789.

XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX Disclosure; Fig 21; 147pp; English.

XX The present sequence represents the light chain of a catalytic antibody
 CC which is capable of degrading cocaine. A series of cocaine transition
 CC state analogues (TSAs) were prepared and used to immunise mice for
 CC production of hybridomas. Catalytic antibodies were identified by their
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
 CC antibodies reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved)
 XX

SQ Sequence 113 AA;

Alignment Scores:
 Pred. No.: 1,35e-51 Length: 113
 Score: 549.00 Matches: 105
 Percent Similarity: 97.35% Conservative: 5
 Best Local Similarity: 92.92% Mismatches: 3
 Query Match: 69.94% Indels: 0
 DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x AAW39882 (1-113)

QY 96 GATATTGTGATACCCAGGATGAATCTCCAACTCTGCTCACTTCTGGAGATCAGTTTC 155
 Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
 QY 156 ATCTCTCGAGGCTAGTAAGAGTCTCCTGTATAGGATGGGAAGACATACCTGAAATTGG 215
 Db 21 IleSerCysArgSerSerLysSerLeuLeuTyGluAspGlyLysThrTyLeuAsnTrp 40
 QY 216 TTTCTGCGAGACAGACAAATCTCTCAGCTCTCTGATGTTTGTATGTCACCCGTCGCA 275
 Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyLeuMetSerThrArgAla 60
 QY 276 TCAGGAGTCTCAGACCGGTTAGTGGTGTTGTTACTGTCAACAACTTGTAGAGTATCCA 335
 Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80
 QY 336 AGTAGAGTGAAGGCTCAGGATGCGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 395
 Db 81 SerArgValLysAlaGluAspValGlyAlaTyTyCysGlnGlnPheValGluTyPro 100
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACGT 434
 Db 101 PheThrPheGlySerGlyThrLysLeuGluIleArgArg 113

RESULT 6

AAW39803

ID AAW39803 standard; protein; 113 AA.

AC AAW39803;

XX 16-JUN-1998 (first entry)

XX Variable domain of the Kappa light chain of catalytic antibody 12H1.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX Mus sp.

```
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US010965.
XX PR 25-JUN-1996; 96US-00672345.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX DR P-PSDB; AAV09802.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX PS Claim 18; Page 73; 147pp; English.
XX CC AAW39801-05 represent the amino acid sequences of the variable domain of
XX CC the kappa light chain of catalytic antibodies which are able to degrade
XX CC cocaine. A series of cocaine transition state analogues (TSAs) were
XX CC prepared and used to immunise mice for production of hybridomas.
XX CC Catalytic antibodies were identified by their capacity to release 3H-
XX CC benzoic acid from 3H-phenyl cocaine. The 12H antibody (AAW39808
XX CC represents the heavy chain) was identified using TSA2, and has a per
XX CC minute Kcat of 0.016. The antibodies reduce the concentration of cocaine
XX CC in a subject, and are used particularly for the treatment of an overdose.
XX CC They are also used for treating addiction (by reducing the in vivo
XX CC concentration that can be achieved)
XX SQ Sequence 113 AA;

Alignment Scores:
Pred. No.: 2,25e-51 Length: 113
Score: 547.00 Matches: 104
Percent Similarity: 98.23% Conservative: 7
Best Local Similarity: 92.04% Mismatches: 2
Query Match: 69.68% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x AAW39803 (1-113)
QY 96 GATATTGTGATTAACCCAGGATGAATCTCTCAATCTCTGTCACCTCTCGGAGATCAGTTTCC 155
DB 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY 156 ATCTCTCGAGGCTAGTAAGAGTCTCTCTGTATAAGGATGGGAGACATACCTTGAATTGG 215
DB 21 IleSerCysArgSerSerArgSerLeuLeuTyrArgAspGlyThrTyrLeuAsnTrp 40
QY 216 TTCTCTCGAGACCCAGGACAACTCTCTAGCTCTCTGATGATTTGATGTCACCGTGCA 275
DB 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuTyrLeuMetSerThrArgala 60
QY 276 TCAGGAGTCTCGACCGGTTTGTAGTGGCTGAGGTCAGGACAGATTTACCTCGGAATC 335
DB 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile 80
QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTGTTACTGTCAACAACTTGTAGAGATATCA 395
DB 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheValAspTyrPro 100
QY 396 TTCACGTTCCGCTCGGGGCAAGTTGGAAATAAACCGT 434
DB 101 PheThrPheGlySerGlyThrLysLeuGluileLysArg 113

RESULT 7
AAW39801
ID AAW39801 standard; protein; 113 AA.
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XX AC AAW39801;
XX DT 16-JUN-1998 (first entry)
XX DE Variable domain of the kappa light chain of catalytic antibody 3B9.
XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX KW overdose; addiction.
XX OS Mus sp.
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US010965.
XX PR 25-JUN-1996; 96US-00672345.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX DR P-PSDB; AAV09791.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX PS Claim 12; Page 71-72; 147pp; English.
XX CC AAW39801-05 represent the amino acid sequences of the variable domain of
XX CC the kappa light chain of catalytic antibodies which are able to degrade
XX CC cocaine. A series of cocaine transition state analogues (TSAs) were
XX CC prepared and used to immunise mice for production of hybridomas.
XX CC Catalytic antibodies were identified by their capacity to release 3H-
XX CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806
XX CC represents the heavy chain) was identified using TSA1, which is an
XX CC immunogenic conjugate of a phosphate monoester transition state analogue.
XX CC Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the
XX CC concentration of cocaine in a subject, and are used particularly for the
XX CC treatment of an overdose. They are also used for treating addiction (by
XX CC reducing the in vivo concentration that can be achieved)
XX SQ Sequence 113 AA;

Alignment Scores:
Pred. No.: 2,25e-51 Length: 113
Score: 547.00 Matches: 104
Percent Similarity: 98.23% Conservative: 7
Best Local Similarity: 92.04% Mismatches: 2
Query Match: 69.68% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x AAW39801 (1-113)
QY 96 GATATTGTGATTAACCCAGGATGAATCTCTCAATCTCTGTCACCTCTCGGAGATCAGTTTCC 155
DB 1 AspLeuValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY 156 ATCTCTCGAGGCTAGTAAGAGTCTCTCTGTATAAGGATGGGAGACATACCTTGAATTGG 215
DB 21 IleSerCysArgSerSerArgSerLeuLeuTyrArgAspGlyThrTyrLeuAsnTrp 40
QY 216 TTCTCTCGAGACCCAGGACAACTCTCTAGCTCTCTGATGATTTGATGTCACCGTGCA 275
DB 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuTyrLeuMetSerThrArgSer 60
QY 276 TCAGGAGTCTCGACCGGTTTGTAGTGGCTGAGGTCAGGACAGATTTACCTCGGAATC 335
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Db 61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluIle 80
 QY 336 AGTAGAGTGAAGCTGAGGAGTGGGTGTATTACTGTCAACAACTGTAGAGTATCCA 395
 Db 81 SerArgValIysAlaGluAspValGlyValTy-CysGlnHisPheValAspTyPro 100
 QY 396 TTCACGTTCCGCTCGGGGCAAAAGTTGGAATFAAACGT 434
 Db 101 PheThrPheGlySerGlyThrIysLeuGluIleLysArg 113

RESULT 8

AAW70790

ID AAY70790 standard; protein; 122 AA.

XX

AC AAY70790;

XX

31-JUL-2000 (first entry)

XX

Murine anti-PAB-421 IDI-1 mAb light chain variable region.

XX

Murine; p53 protein; PAB-421; monoclonal antibody; mAb; IDI-1;

KW

anti-idiotypic antibody; DNA-binding domain; dermatological;

KW

immunosuppressive; antiinflammatory; autoimmune response; SLE;

KW

systemic lupus erythematosus; diagnosis; treatment; autoantigen;

KW

light chain variable region; VL; complementarity determining region; CDR.

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OS Mus sp.

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FH Key

FT Region

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Alignment Scores:
 Pred. No.: 8.15e-51 Length: 122
 Score: 542.00 Matches: 104
 Percent Similarity: 97.35% Conservative: 6
 Best Local Similarity: 92.04% Mismatches: 3
 Query Match: 69.04% Indels: 0
 DB: 3 Gaps: 0

US-09-674-716B-2 (1-437) x AAY70790 (1-122)

QY 96 CATATTGTGATAACCCAGGATGAACCTCCCAATCCTGCTCACTTCTGGAGAAATCAGTTTCC 155
 Db 4 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 23
 QY 156 ATCTCTGCAGGTCTAGTAAGAGTCTCTCTATTAAGATCGGGAAGACATCTTGAATTGG 215
 Db 24 IleSerCysArgSerArgGlnSerLeuLeuTyLysAsnGlyLysThrTyLeuAsnTrp 43
 QY 216 TTCTCTGCAGAGACAGGACACATCTCTCAGCTCCTGATGATTTGATGTCCACCCGTGCA 275
 Db 44 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuIleTyLeuMetSerIleArgAla 63
 QY 276 TCAGGAGTCTCAGACCCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTCACCCGTGAAATC 335
 Db 64 SerGlyValSerAspA-gPheSerGlyAsnGlySerGlyThrAspPheThrLeuGluIle 83
 QY 336 AGTAGAGTGAAGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCA 395
 Db 84 SerArgValArgAlaGluAspValGlyValTy-CysGlnGlnLeuValGluTyPro 103
 QY 396 TTCACGTTCCGCTCGGGGCAAAAGTTGGAATFAAACGT 434
 Db 104 TyrThrPheGlyGlyGlyThrIysLeuGluIleLysArg 116

RESULT 9

AAW39802

ID AAW39802 standard; protein; 113 AA.

XX

AC AAW39802;

XX

DT 16-JUN-1998 (first entry)

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Db 61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluIle 80
 QY 336 AGTAGAGTGAAGCTGAGGAGTGGGTGTATTACTGTCAACAACTGTAGAGTATCCA 395
 Db 81 SerArgValIysAlaGluAspValGlyValTy-CysGlnHisPheValAspTyPro 100
 QY 396 TTCACGTTCCGCTCGGGGCAAAAGTTGGAATFAAACGT 434
 Db 101 PheThrPheGlySerGlyThrIysLeuGluIleLysArg 113

Location/Qualifiers
 27...42
 /label= CDR
 /note= "Complementarity determining region"
 58...64
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 97...105
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 /note= "Complementarity determining region"

WO200023082-A1.
 27-APR-2000.
 19-OCT-1999; 99WO-US024443.
 19-OCT-1998; 98US-0104816P.
 (VEDA) YEDA RES & DEV CO LTD.
 Cohen IR, Rotter V, Erez-Alon N, Herkel J,
 WPI; 2000-339512/29.
 Treatment of systemic lupus erythematosus by down-regulating the
 autoimmune response to the C-terminal DNA-binding domain of the p53
 protein by an active compound comprising of antibodies to p53 or
 fragments of p53.
 Claim 78; Fig 9; 87pp; English.

The patent discloses a method for the treatment of systemic lupus
 erythematosus (SLE) by down-regulating the autoimmune response to the C-
 terminal DNA-binding domain of p53 protein by an active compound. The
 present sequence is a light chain variable region of IDI-1 an anti-
 idiotypic antibody/Ab2 monoclonal antibody (mAb) specific for PAB-421
 which is an Ab1 mAb specific to the C-terminal DNA-binding domain of
 murine p53 protein. The Ab1 and Ab2 mAbs and peptides based on
 complementarity determining regions of light and heavy chain variable
 regions of these antibodies, are examples of active compounds useful in
 the diagnosis, prevention and treatment of SLE in humans

Sequence 122 AA;

AAW39801-05 represent the amino acid sequences of the variable domain of

KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.
 XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Region 1..23 /note= "framework region 1"
 FT Region 24..39 /note= "CDR 1"
 FT Region 40..54 /note= "framework region 2"
 FT Region 55..61 /note= "CDR 2"
 FT Region 62..93 /note= "framework region 3"
 FT Region 94..102 /note= "CDR 3"
 FT Region 103..113 /note= "framework region 4"
 XX WO955879-A1.
 FN 18-NOV-1999.
 XX 07-MAY-1999; 99WO-GB001434.
 XX 09-MAY-1998; 98GB-00009839.
 XX (GLAX) GLAXO GROUP LTD.
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPI; 2000-053101/04.
 XX N-PSDB; AA234747.

Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.

Claim 9; Fig 3; 81pp; English.

This sequence represents the light chain variable region (VL) of humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human framework (H5IGKVII) and the light chain complementarity determining regions (see AY32254-56) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type 1 diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents

Sequence 116 AA;

Alignment Scores:
 Pred. No.: 5.9e-48 Length: 116
 Score: 516.00 Matches: 99
 Percent Similarity: 92.98% Conservative: 7
 Best Local Similarity: 86.84% Mismatches: 8

Query Match: 65.73% Indels: 0
 DB: 3 Gaps: 0
 US-09-674-716B-2 (1-437) x AAY32262 (1-116)
 QY 96 GATATTGTGATAACCCAGGATGAACCTCCCAACTCTGTCTCTGAGAAATCAGTTTCC 155
 DB 1 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20
 QY 156 ATCTCTGCAGGCTAGTAGAGTCTCTCTATAGATGGGAGACATCTGAAATTGG 215
 DB 21 IleSerCysArgSerSerLeuLeuTyLysAspGlyLysThrTyLeuAsnTrp 40
 QY 216 TTCTGCAGAGACCCAGGACCAATCTCTCAGCTCTCTGATGATTTGATGTCACCCGTGCA 275
 DB 41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuLeuLeuMetSerThrArgAla 60
 QY 276 TCAGGAGTCTCAGACCCGTTTAGTGGCAGTGGGTTCAGGACAGATTTCCCTGGAAATC 335
 DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
 QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTGTATTACTGTCAACAATTTAGAGTATCCA 395
 DB 81 SerArgValGluAlaGluAspValGlyValTyTyCysGlnGlnLeuValGluTyPro 100
 QY 396 TTCAGTTCGGCTCGGGGACAAAGTTGGAAATAAAACGTACG 437
 DB 101 PheThrPheGlyGlnGlyThrLysValGluIleLysArgThr 114

RESULT 12

AAE06969
 ID AAE06969 standard; protein; 100 AA.
 XX AAE06969;
 AC AAE06969;
 DT 16-OCT-2001 (first entry)
 XX Mouse germline kappa light chain variable (VK) region, 167/24.
 KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotonic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angiodysplasia; acquired immune deficiency syndrome; AIDS;
 KW inflammatory glomerulopathy; vascular intervention;
 KW necrotic hyperplasia; VK; kappa light chain variable region.
 XX Mus sp.
 XX WO200157226-A1.
 XX 09-AUG-2001.
 XX 02-FEB-2001; 2001WO-US003537.
 XX 03-FEB-2000; 2000US-00497625.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Larosa GU, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
 WPI; 2001-488888/53.
 XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
 disorder in a patient, comprises a binding specificity for CCR2, and a
 non-human antigen binding region and human immunoglobulin.
 XX Disclosure; Page 151; 183pp; English.
 XX The patent discloses a humanised antibody or its antigen-binding
 fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),

comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherosclerosis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allergy, anaphylaxis, and IgE-mediated allergic reaction, shock, inflammation, histamine and IgE-mediated allergic reaction, inflammatory stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is mouse germline kappa light chain variable (VK) region, 167/24

Sequence 100 AA;

Alignment Scores:
Pred. No.: 3,36e-47 Length: 100
Score: 509.00 Matches: 99
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.00% Mismatches: 0
Query Match: 64.84% Indels: 0
DB: 4 Gaps: 0

US-09-674-716B-2 (1-437) x AAE06969 (1-100)

QY 96 GATATTGTGATTAACCCAGGATCACTCTCCAACTCTGTCAGTCTGGAGATCAAGTTCC 155
Db 1 AspileValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY 156 ATCTCTCGAGTCTAGTAAGAGTCTCTGTATAGGATGGAGACATCTGTAATGG 215
Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrLysAspGlyLysThrTyrLeuAsnTrp 40
QY 216 TTCTGCAGACAGGACCAATCTCTCAGCTCTGATGTTATTCATGTCACCCGTCGA 275
Db 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuLeuIleTyrLeuMetSerThrArgala 60
QY 276 TCAGGAGTCTCAGACCGGTTTATGTCAGTGGGTGAGGACACAGATTTCACCTGGAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile 80
QY 336 AGTAGAGTGAAGCTCAGGATCGGTGTGATTACTGTCAACAACCTGTAGAGTATCCA 395
Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnGlnLeuValGluTyrPro 100

RESULT 13

ADE28461
ID ADE28461 standard; protein; 239 AA.

XX AC ADE28461;
XX 29-JAN-2004 (first entry)
DT Human anti-CD40 antibody 23-28-1 variable region light chain protein.
DE anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW human; variable region light chain; 23-28-1.
XX Homo sapiens.
OS WO2003040170-A2.
XX 15-MAY-2003.

08-NOV-2002; 2002WO-US036107.
09-NOV-2001; 2001US-034980P.
(PFIZ) PFIZER PROD INC.
(ABGE-) ABGENIX INC.
Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
WFI; 2003-441521/41.
N-PSDB; ADE28460.
XX New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.
XX Claim 1; SEQ ID NO 68; 177pp; English.
XX The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody variable region light chain protein of the invention.

Sequence 239 AA;

Alignment Scores:
Pred. No.: 5.39e-47 Length: 239
Score: 508.00 Matches: 96
Percent Similarity: 84.33% Conservative: 17
Best Local Similarity: 71.64% Mismatches: 21
Query Match: 64.71% Indels: 0
DB: 7 Gaps: 0

US-09-674-716B-2 (1-437) x ADE28461 (1-239)

QY 36 ATGAGGTTCTCTGTTCAAGTTTCTGGGGTCTTATGTTCTGGATCTCTGGATCAGTGGG 95
Db 1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuMetLeuTrpValSerGlySerGly 20
QY 96 GATATTGTGATAACCCAGGATGAACCTTCCAATCTCTGTCATCTCTGGAGATCAAGTTCC 155
Db 21 AspileValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
QY 156 ATCTCTCGAGTCTAGTAAGAGTCTCTGTATAGGATGGAGACATCTTGAATGG 215
Db 41 IleSerCysArgSerSerGlnSerValLeuTyrSerAsnGlyTyrAsnTyrLeuAspTrp 60
QY 216 TTCTGCAGACAGGACCAATCTCTCAGCTCTGATGTTATTCATGTCACCCGTCGA 275
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgala 80
QY 276 TCAGAGTCTCAGACCGGTTTATGTCAGTGGGTGAGGACACAGATTTCACCTGGAATC 335
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100
QY 336 AGTAGAGTGAAGCTCAGGATCGGTGTGATTACTGTCAACAACCTGTAGAGTATCCA 395
Db 101 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnValLeuGlnThrPro 120
QY 396 TTCAGTTTCGGCTCGGGACAAAGTTGGAATAAAGCTACG 437
Db 121 PheThrPheGlyProGlyThrLysValAspileLysArgThr 134

RESULT 14

US-09-674-716B-2 (1-437) x AAY82617 (1-239)

CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment of
CC hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingivitis, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a human
CC PTHrP monoclonal antibody clone protein sequence from the present
CC invention
XX
SQ Sequence 239 AA;

Alignment Scores:
Pred. No.: 1.15e-46 Length: 239
Score: 505.00 Matches: 95
Percent Similarity: 83.58% Conservativeness: 17
Best Local Similarity: 70.90% Mismatches: 22
Query Match: 64.33% Indels: 0
DB: 3 Gaps: 0

US-09-674-716B-2 (1-437) x AAY82615 (1-239)

QY 36 ATGAGGTTCTCTGTCAGTTCTGGGGTGTCTTATGTTCTGGATCTTGGAGTCAGTGGG 95
DB 1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuMetLeuTrpValSerGlySerGly 20
QY 96 GATATTGTGATAACCCAGATGAATCTCCATCTCTGTCACCTCTGGAGATCAGTTTC 155
DB 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
QY 156 ATCTCTCTGAGCTTAGTAAGAGTCTCTGTATAGGATGGAGACATACCTTGAATTGG 215
DB 41 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyAsnAsnTyrLeuAspTrp 60
QY 216 TTCTTCAGAGACCGGCAATCTCTCAGCTCTCTGATGTTATTTGATGTCACCGTCCA 275
DB 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 80
QY 276 TCAGGAGTCTCAGACCGTTTATGTCAGTGGGTGAGGACAGATTTCACCTGGAAATC 335
DB 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
QY 336 AGTAGAGTCAAGGCTGAGGATGTTGTTGTTATTTACTGTCAACAACCTGTAGAGTATCCA 395
DB 101 SerArgValGluAlaGluAspValGlyIleTyrTyrCysMetGlnAlaLeuGlnThrPro 120
QY 396 TTCACGTTCCGCTCGGGGCAAGTTGGAATAAAGCTACG 437
DB 121 PheThrPheGlyProGlyThrLysValAspIleLysArgThr 134

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Delop 6.0 , Delext 7.0

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Maximum Match 100%

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pcp:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pcp:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pcp:*
5: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pcp:*
6: /cgn2_6/ptodata/2/iaa/backfiles.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 555 | 70.7 | 113 | 2 | US-08-672-345C-8 |
| 2 | 555 | 70.7 | 113 | 2 | US-08-672-345C-98 |
| 3 | 555 | 70.7 | 113 | 3 | US-09-214-095D-8 |
| 4 | 549 | 69.9 | 113 | 3 | US-09-214-095D-108 |
| 5 | 547 | 69.7 | 113 | 2 | US-08-672-345C-5 |
| 6 | 547 | 69.7 | 113 | 2 | US-08-672-345C-7 |
| 7 | 547 | 69.7 | 113 | 2 | US-08-672-345C-95 |
| 8 | 547 | 69.7 | 113 | 2 | US-08-672-345C-97 |
| 9 | 547 | 69.7 | 113 | 3 | US-09-214-095D-5 |
| 10 | 547 | 69.7 | 113 | 3 | US-09-214-095D-7 |
| 11 | 547 | 69.7 | 113 | 3 | US-09-214-095D-100 |
| 12 | 547 | 69.7 | 113 | 3 | US-09-214-095D-112 |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 13 | 547 | 69.7 | 280 | 3 | US-09-214-095D-119 |
| 14 | 541 | 68.9 | 113 | 2 | US-08-672-345C-6 |
| 15 | 541 | 68.9 | 113 | 2 | US-08-672-345C-96 |
| 16 | 541 | 68.9 | 113 | 3 | US-09-214-095D-6 |
| 17 | 530 | 67.5 | 113 | 3 | US-09-214-095D-104 |
| 18 | 495 | 63.1 | 141 | 1 | US-08-438-123-7 |
| 19 | 494 | 62.9 | 133 | 1 | US-08-253-877C-10 |
| 20 | 494 | 62.9 | 133 | 1 | US-08-452-164A-10 |
| 21 | 494 | 62.9 | 133 | 3 | US-08-603-024-4 |
| 22 | 493 | 62.8 | 142 | 4 | US-09-479-614-20 |
| 23 | 481 | 61.3 | 132 | 1 | US-08-392-419-4 |
| 24 | 477 | 60.8 | 135 | 1 | US-08-259-372A-12 |
| 25 | 477 | 60.8 | 135 | 1 | US-08-468-671-12 |
| 26 | 455 | 57.0 | 113 | 4 | US-09-406-532-14 |
| 27 | 447.5 | 57.0 | 131 | 1 | US-08-129-930B-95 |
| 28 | 447.5 | 57.0 | 131 | 3 | US-08-134-346A-50 |
| 29 | 447.5 | 57.0 | 131 | 4 | US-08-976-288A-95 |
| 30 | 447 | 56.9 | 112 | 3 | US-08-483-749A-4 |
| 31 | 447 | 56.9 | 132 | 1 | US-08-477-877B-91 |
| 32 | 447 | 56.9 | 132 | 2 | US-08-472-281A-91 |
| 33 | 447 | 56.9 | 132 | 3 | US-08-477-989B-91 |
| 34 | 439.5 | 56.0 | 131 | 3 | US-08-589-939-7 |
| 35 | 438.5 | 55.9 | 149 | 4 | US-09-192-838B-2 |
| 36 | 438.5 | 55.9 | 149 | 4 | US-09-324-191-2 |
| 37 | 437 | 55.7 | 113 | 4 | US-09-025-769B-15 |
| 38 | 436.5 | 55.6 | 149 | 2 | US-08-752-844-2 |
| 39 | 436.5 | 55.6 | 149 | 2 | US-08-591-196-2 |
| 40 | 436.5 | 55.6 | 149 | 4 | US-09-293-533-2 |
| 41 | 436.5 | 55.6 | 238 | 3 | US-09-192-545-4 |
| 42 | 435 | 55.4 | 131 | 4 | US-09-647-468-164 |
| 43 | 434.5 | 55.4 | 113 | 1 | US-08-264-093-10 |
| 44 | 434 | 55.3 | 112 | 1 | US-08-053-171-16 |
| 45 | 434 | 55.3 | 131 | 4 | US-09-647-468-163 |

ALIGNMENTS

RESULT 1
US-08-672-345C-8
; Sequence 8, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/672,345C
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

Sequence 119, Appl
Sequence 6, Appl
Sequence 96, Appl
Sequence 6, Appl
Sequence 104, Appl
Sequence 7, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 4, Appl
Sequence 20, Appl
Sequence 4, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 50, Appl
Sequence 4, Appl
Sequence 91, Appl
Sequence 91, Appl
Sequence 7, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 15, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 164, App
Sequence 10, Appl
Sequence 16, Appl
Sequence 163, App

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-8

Alignment Scores:

Pred. No.: 1.49e-59 Length: 113
Score: 555.00 Matches: 107
Percent Similarity: 97.35% Conservative: 3
Best Local Similarity: 94.69% Mismatches: 3
Query Match: 70.70% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x US-08-672-345C-8 (1-113)

QY 96 GATATTGTGATACCCAGGATGAATCTCCAAATCTCTGTCACCTTCTGGAGAATCAGTTTCC 155
Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY 156 ATCTCTGAGGCTAGTAAGAGTCTCTGTAAGGATGGGAAGACATACCTGAATTGG 215
Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrgluAspGlyLysThrTyrLeuAsnTrp 40
QY 216 TTCTCTGAGAGACAGGACAAATCTCTCAGCTCCTGATGATTTGATGTCACCCGTCGA 275
Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyrLeuMetSerThrArgala 60
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTCAGGCACAGATTTCACCTGGAAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80
QY 336 AGTAGAGTGAAGCTCAGGATGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 395
Db 81 SerArgValIysAlaGluAspValGlyAlaTyrTyrCysGlnGlnPheValGluTyrPro 100
QY 396 TTCACGTTCCGGTCGGGACAAAGTTGGAAATAAAACGT 434
Db 101 PheThrPheGlySerGlyThrLysLeuGluIleArgArg 113

RESULT 2

US-08-672-345C-8
Sequence 96, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry, Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-98

Alignment Scores:

Pred. No.: 1.49e-59 Length: 113
Score: 555.00 Matches: 107
Percent Similarity: 97.35% Conservative: 3
Best Local Similarity: 94.69% Mismatches: 3
Query Match: 70.70% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x US-08-672-345C-98 (1-113)

QY 96 GATATTGTGATACCCAGGATGAATCTCCAAATCTCTGTCACCTTCTGGAGAATCAGTTTCC 155
Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY 156 ATCTCTGAGGCTAGTAAGAGTCTCTGTAAGGATGGGAAGACATACCTGAATTGG 215
Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrgluAspGlyLysThrTyrLeuAsnTrp 40
QY 216 TTCTCTGAGAGACAGGACAAATCTCTCAGCTCCTGATGATTTGATGTCACCCGTCGA 275
Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyrLeuMetSerThrArgala 60
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTCAGGCACAGATTTCACCTGGAAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80
QY 336 AGTAGAGTGAAGCTCAGGATGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 395
Db 81 SerArgValIysAlaGluAspValGlyAlaTyrTyrCysGlnGlnPheValGluTyrPro 100
QY 396 TTCACGTTCCGGTCGGGACAAAGTTGGAAATAAAACGT 434
Db 101 PheThrPheGlySerGlyThrLysLeuGluIleArgArg 113

RESULT 3

US-09-214-095D-8
Sequence 8, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patent In version 3.0
SEQ ID NO 8
LENGTH: 113
TYPE: PRI
ORGANISM: Murinae gen. sp.
US-09-214-095D-8
Alignment Scores:
Pred. No.: 1.49e-59 Length: 113
Score: 555.00 Matches: 107
Percent Similarity: 97.35% Conservative: 3
Best Local Similarity: 94.69% Mismatches: 3
Query Match: 70.70% Indels: 0
DB: 3 Gaps: 0
US-09-674-716B-2 (1-437) x US-09-214-095D-8 (1-113)
QY 96 GATATTGTGATACCCAGGATGAATCTCCAAATCTCTGTCACCTTCTGGAGAATCAGTTTCC 155
Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY 156 ATCTCTGAGGCTAGTAAGAGTCTCTGTAAGGATGGGAAGACATACCTGAATTGG 215

Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrGluAspGlyLysThrTyrLeuAsnTrp 40
 QY 216 TTTCTGCAGACACGAGACATCTCTCAGCTCCTGATGATTTGATGATCCACCCGTGCA 275
 Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyrLeuMetSerThrArgala 60
 QY 276 TCAGAGTCTCAGACCCGTTTAGTGGCAGTGGTCCAGGCACAGATTTTCCACCTGGAAATC 335
 Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile 80
 QY 336 AGTAGAGTGAAGCTGAGGATGCTGGGTGTGATTTACTGTCAACAACCTGTAGAGTATCCA 395
 Db 81 SerArgValLysAlaGluAspValGlyAlaTyrTyrCysGlnGlnPheValGluTyrPro 100
 QY 396 TTCAGTTCCGCTCGGGACAAAGTTGGAATAAAACGT 434
 Db 101 PheThrPheGlySerGlyThrLysLeuGluileArgarg 113

RESULT 4

US-09-214-095D-108

; Sequence 108, Application US/09214095D

; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214,095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 108

; LENGTH: 113

; TYPE: PRT

; ORGANISM: Murine

US-09-214-095D-108

Alignment Scores:

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|------------------------|---------|---------------|-----|
| Pred. No.: | 8.1e-59 | Length: | 113 |
| Score: | 549.00 | Matches: | 105 |
| Percent Similarity: | 97.95% | Conservative: | 5 |
| Best Local Similarity: | 92.92% | Mismatches: | 3 |
| Query Match: | 69.94% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-09-674-716B-2 (1-437) x US-09-214-095D-108 (1-113)

QY 96 GATATTGTGATAACCCAGGATGAATCTCCAACTCTGCTCACTTTCTGGAGATCAGTTTCC 155
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 QY 156 ATCTCTGCAGGCTCTAGTAAGAGTCTCCTGTATAGGATGGAGACATACTTGAATTGG 215
 Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrGluAspGlyLysThrTyrLeuAsnTrp 40
 QY 216 TTTCTGCAGACACGAGCAATCTCCTCAGCTCCTGTATTTGATGTCCACCCGTGCA 275
 Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyrLeuMetSerThrArgala 60
 QY 276 TCAGAGTCTCAGACCCGTTTAGTGGCAGTGGTCCAGGCACAGATTTTCCACCTGGAAATC 335
 Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile 80
 QY 336 AGTAGAGTGAAGCTGAGGATGCTGGGTGTGATTTACTGTCAACAACCTGTAGAGTATCCA 395
 Db 81 SerArgValLysAlaGluAspValGlyAlaTyrTyrCysGlnGlnPheValGluTyrPro 100
 QY 396 TTCAGTTCCGCTCGGGACAAAGTTGGAATAAAACGT 434
 Db 101 PheThrPheGlySerGlyThrLysLeuGluileArgarg 113

RESULT 5

US-08-672-345C-5

; Sequence 5, Application US/08672345C

; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper and Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 113 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-672-345C-5

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 1.43e-58 | Length: | 113 |
| Score: | 547.00 | Matches: | 104 |
| Percent Similarity: | 98.23% | Conservative: | 7 |
| Best Local Similarity: | 92.04% | Mismatches: | 2 |
| Query Match: | 69.68% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-09-674-716B-2 (1-437) x US-08-672-345C-5 (1-113)

QY 96 GATATTGTGATAACCCAGGATGAATCTCCAACTCTGCTCACTTTCTGGAGATCAGTTTCC 155
 Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
 QY 156 ATCTCTGCAGGCTCTAGTAAGAGTCTCCTGTATAGGATGGAGACATACTTGAATTGG 215
 Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrGluAspGlyLysThrTyrLeuAsnTrp 40
 QY 216 TTTCTGCAGACACGAGCAATCTCCTCAGCTCCTGTATTTGATGTCCACCCGTGCA 275
 Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuIleTyrLeuMetSerThrArgser 60
 QY 276 TCAGAGTCTCAGACCCGTTTAGTGGCAGTGGTCCAGGCACAGATTTTCCACCTGGAAATC 335
 Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluile 80
 QY 336 AGTAGAGTGAAGCTGAGGATGCTGGGTGTGATTTACTGTCAACAACCTGTAGAGTATCCA 395
 Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheValAspTyrPro 100
 QY 396 TTCAGTTCCGCTCGGGACAAAGTTGGAATAAAACGT 434
 Db 101 PheThrPheGlySerGlyThrLysLeuGluileArgarg 113

RESULT 6

US-08-672-345C-7

Sequence 7, Application US/08672345C
Patent No. 5948659
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
SURETY: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Data
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672.345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-7

| Alignment Scores: | |
|------------------------|-----------------|
| Pred. No.: | 1,438-58 |
| Score: | 547.00 |
| Percent Similarity: | 92.23% |
| Best Local Similarity: | 98.04% |
| Query Match: | 59.68% |
| DB: | 2 |
| | Indels: 0 |
| | Gaps: 0 |
| | Mismatches: 7 |
| | Conservative: 2 |
| | Matches: 104 |
| | Length: 113 |

US-09-674-716B-2 (1-437) x US-08-672-345C-7 (1-113)

| | | | | | | | |
|-----|--------------------------|-----------------------|---------------------|------------------|-----|------|-----|
| 96 | GATATTGTGATAACCCAGGAGTA | CTC | CAATCTCTG | TCTCACTTCTCGAGAA | TCA | GTTC | 155 |
| | | : | : | : | : | : | |
| 1 | AspMetValMetThrGlnAspGlu | LeuSerAsnProValThrSer | GlyGluSerValSer | 20 | | | |
| 156 | ATCTCCTCCAGGCTTAGTAAG | AGCTCTCCTGTATAAGGAT | GGGAAAGACATCTGTAAT | TGG | 215 | | |
| | | : | : | : | : | : | |
| 21 | IleSerCysArgSerSerArgSer | LeuLeuTyrArgAspGlyLys | ThrTyrLeuAsnTrp | 40 | | | |
| | | : | : | : | : | : | |
| 216 | TTTCTGCAGACACAGGACAA | TCTCCTCAGCTCTGTATTT | TGATGTCACCCGTGCA | 275 | | | |
| | | : | : | : | : | : | |
| 41 | PheLeuGlnArgProGlyArgSer | ProGlnLeuLeuIleTyrLeu | MetSerThrArgAla | 60 | | | |
| | | : | : | : | : | : | |
| 276 | TCAGAGTCTCAGACCCGGTT | AGTGGCAGTGGGTTCAGGC | CACGATTCACCTCGAAATC | 335 | | | |
| | | : | : | : | : | : | |
| 61 | SerGlyValSerAspArgPheSer | GlySerGlySerGlyThrAsp | PheThrLeuGluIle | 80 | | | |
| | | : | : | : | : | : | |
| 336 | AGTACAGTAGAGGCTGAGGAT | TGGGTCTATTACTGTACAC | ACTTCTAGAGATGCA | 395 | | | |
| | | : | : | : | : | : | |
| 81 | SerArgValLysAlaGluasp | ValGlyValTyrCysGlnHis | PheValAspTyrPro | 100 | | | |
| | | : | : | : | : | : | |
| 396 | TTACGTTTCGCTCGGGACAA | AGTTGGAAT | AAAAAGT | 434 | | | |
| | | : | : | : | : | : | |
| 101 | PheThrPheGlySerGlyThr | LysLeuGluIleLysArg | 113 | | | | |
| | | : | : | : | : | : | |

RESULT 7

```

US-08-672-345C-95
; Sequence 95, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; Filing Date: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-95

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| | | |
|------------------------|----------|---------------|
| Alignment Scores: | | |
| Pred. No. \ | 1.43e-58 | Length: |
| Score: | 547.00 | Matches: |
| Percent Similarity: | 98.23% | Conservative: |
| Best Local Similarity: | 92.04% | Mismatches: |
| Query Match: | 69.68% | Indels: |
| DB: | 2 | Gaps: |

US-09-674-716B-2 (1-437) X US-08-672-345C-95 (1-113)

| | | | | | | | | | |
|-----|----|--------------|-----------|-----------|---------|-----------|-----------|-----------|-----|
| 96 | QY | GATATGTGATAA | CC | CCAGGATGA | AACTCC | CAATCCTGT | CTACTCTCG | AAGATCCT | 155 |
| | | | | | | | | | |
| 1 | Db | AspIleValMet | ThrGln | AspGlu | LeuSer | AsnPro | ValThr | SerGlyGlu | 20 |
| | | | | | | | | | |
| 156 | QY | ATCTCCTCCAGG | CTAGTAA | GAGTCTCCT | GTATAA | GATGGGA | AGACATCT | GGAATTGG | 215 |
| | | | | | | | | | |
| 21 | Db | IleSerCys | ArgSer | ArgSer | LeuLeu | TyrArg | AspGly | LeuThr | 40 |
| | | | | | | | | | |
| 216 | QY | TTTCTG | GAGAGACAG | GACAAATCT | CTCAGCT | CCTGAT | TATTGAT | TGCTCC | 275 |
| | | | | | | | | | |
| 41 | Db | PheLeuGln | ArgPro | GlyArg | SerPro | GlnLeu | LeuIle | TyrLeu | 60 |
| | | | | | | | | | |
| 276 | QY | TCAGAG | GTCTCAG | ACCGGTTAG | TGGCAG | TGGGTTC | AGGCAC | AGATTC | 335 |
| | | | | | | | | | |
| 61 | Db | SerGlyVal | SerAsp | ArgPhe | SerGly | SerGly | SerGly | ThrAsp | 80 |
| | | | | | | | | | |
| 336 | QY | AGTACAGT | AGGGCT | AGGATG | CGGTG | CTATTACT | GTCTCA | CAACTT | 395 |
| | | | | | | | | | |
| 81 | Db | SerArg | ValLys | AlaGlu | AspVal | GlyVal | TyrCys | GlnHis | 100 |
| | | | | | | | | | |
| 336 | QY | TTACGTT | CTCGCT | CGGGCA | CAAAAGT | TGGAAT | AAAA | ACGT | 434 |
| | | | | | | | | | |
| 101 | Db | PheThr | PheGly | SerGly | ThrLys | LeuGlu | IleLys | Arg | 113 |
| | | | | | | | | | |

| Alignment Scores: | | | |
|--|----------|--|-----|
| Pred. No.: | 1.43e-58 | Length: | 113 |
| Score: | 547.00 | Matches: | 104 |
| Percent Similarity: | 98.23% | Conservative: | 7 |
| Best Local Similarity: | 92.04% | Mismatches: | 2 |
| Query Match: | 69.68% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |
| US-09-674-716B-2 (1-437) x US-08-672-345C-97 (1-113) | | | |
| Qy | 96 | GATATTGTGATAACCCAGATGAATCTTCCAAATCTCTGCACCTTCTGGAGATCATGTTCC | 155 |
| | | | |
| | | | |
| Db | 1 | AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyLeuSerValSer | 20 |
| Qy | 156 | ATTCCTCTCAGCTCTAGTAACAGAGTCTCTGTATATAGGATGGGAAGACACATACTTGAATTGG | 215 |
| | | | |
| | | | |
| Db | 21 | IleSerCysArgSerSerArgSerLeuLeuTyrArgAspGlyLeuThrTyrLeuAsnTrp | 40 |
| Qy | 216 | TTTCTGCAGACACAGGACAAATCTCTCAGCTCCTCATGTATTTGATGTCACCCGTGCA | 275 |
| | | | |
| | | | |
| Db | 41 | PheLeuGlnArgProGlyArgSerProGlnLeuLeuIleTyrLeuMetSerThrArgala | 60 |
| Qy | 276 | TCAGAGAGTCTAGACCGGTTTAGTGGCAGTGGGTGAGGCACAGATTTCACCCGTGAATC | 335 |
| | | | |
| | | | |
| Db | 61 | SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle | 80 |
| Qy | 336 | AGTAGAGTGAAGGCTGAGGATCGGGTGTGTATTACTGTCAACAACTTGTAGAGTAGTCCA | 395 |
| | | | |
| | | | |
| Db | 81 | SerArgGValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheValAspTyrPro | 100 |
| Qy | 336 | TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAACGT | 434 |
| Db | 101 | PheThrPheGlySerGlyThrLysLeuGluIleLysArg | 113 |

RESULT 9
US-09-214-095D-5
; Sequence 5, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. Sp.
US-09-214-095D-5

Alignment Scores:
Pred. No.: 1,43e-58 Length: 113
Score: 547.00 Matches: 104
Percent Similarity: 98.23% Conservative: 7
Best Local Similarity: 92.04% Mismatches: 2
Query Match: 69.68% Indels: 0
DB: Gaps: 3

US-09-674-716B-2 (1-437) x US-09-214-095D-5 (1-113)

| | | | |
|----|-----|--|-----|
| QY | 96 | GATATTGTGATAACCCAGGATGAATCTCCAATCTCTGATCTCTCGAGATCAGTTTCC | 155 |
| Db | 1 | ApplLeValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer | 20 |
| QY | 156 | ACTCTCTGCAGGCTTAGTAAGAGTCTCTGTATAGAGTAGGGAGACATCTGATTGG | 215 |
| Db | 21 | IleSerCysArgSerSerArgSerLeuLeuTyrArgAspGlyLysThrTyrLeuAsnTrp | 40 |
| QY | 216 | TTTTCGCAGAGACAGGACAATCTCCTCAGCTCCTGATGATTGATGCCACCCGTGCA | 275 |
| Db | 41 | PheLeuGlnArgProGlyArgSerProGlnLeuLeuIleTyrLeuMetSerThrArgSer | 60 |
| QY | 276 | TCAGGAGTCTCAGACCGGTTTAGTGGCAGCTGGGTGAGGCACAGATTCACCCCTGGAATC | 335 |
| Db | 61 | SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluIle | 80 |
| QY | 336 | AGTAGAGTCAAGCGTGAGGATGGGTGTGATTACTGTCAACAACCTGTAGAGATATCCA | 395 |
| Db | 81 | SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheValAspTyrPro | 100 |
| QY | 396 | TTACAGTTCGGTCCGGGACAAAGTTGGAATAAAACGT | 434 |
| Db | 101 | PheThrPheGlySerGlyThrIlysLeuGluIleLysArg | 113 |

RESULT 10
US-09-214-095D-7
; Sequence 7, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp
US-09-214-095D-7

Alignment Scores:
Pred. No.: 1,43e-58 Length: 113

| | | | |
|------------------------|--------|---------------|-----|
| Score: | 547.00 | Matches: | 104 |
| Percent Similarity: | 98.23% | Conservative: | 7 |
| Best Local Similarity: | 92.04% | Mismatches: | 2 |
| Query Match: | 69.68% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-09-674-716B-2 (1-437) x US-09-214-095D-7 (1-113)

[illegible]

RESULT 11

US-09-214-095D-100
: Sequence 100. Application US/09214095D

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/ Patent No. 6280967
/
/ GENERAL INFORMATION:
/
/ APPLICANT: Landry, Donald
/
/ TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
/
/ FILE REFERENCE: 51400-A-PCT-US
/
/ CURRENT APPLICATION NUMBER: US/09/214,095D
/
/ CURRENT FILING DATE: 1999-07-19
/
/ NUMBER OF SEQ ID NOS: 121
/
/ SOFTWARE: PatentIn version 3.0
/

```

| | |
|------------------------|----------|
| Alignment Scores: | |
| Pred. No.: | 1,438-58 |
| Score: | 547.00 |
| Percent Similarity: | 98.23% |
| Best Local Similarity: | 92.04% |
| Query Match: | 69.68% |
| DB: | 3 |
| Length: | 113 |
| Matches: | 104 |
| Conservative: | 7 |
| Mismatches: | 2 |
| Indels: | 0 |
| Gaps: | 0 |

US-09-674-716B-2 (1-437) x US-09-214-095D-100 (1-113)

| | | | |
|----|-----|---|-----|
| | 96 | GATATTGTGAFAACCCAGGATGAACCTCCAATCCTCTCACTTCTCGAGAAATCAGTTTC | 155 |
| QY | | ::::: | |
| Db | | | |
| | 1 | AspIleValMetThrGlnAspGluLeuSerAsnProValThrSerglyGluSerValSer | 20 |
| QY | | | |
| | 156 | ATCTCTCCAGGCTTAGTAACAGTCTCCTGTATAAAGATGGGAAGACATACCTGAATTGG | 215 |
| Db | | ::::: | |
| | 21 | IleSerCysArgSerSerArgSerLeuLeuTyArgAspGlyLysThrTyrlauAsnTrp | 40 |
| QY | | | |
| | 216 | TTTCTGCAGACACAGGACAATCTCCTCAGCTCCTGATGTATTGTATGCCACCCTGCA | 275 |
| Db | | ::::: | |
| | 41 | PheLeuGlnArgProGlyArgSerProGluLeuLeuIleTyrlauMetSerThrArgSer | 60 |
| QY | | | |
| | 276 | TCAGGAGTCTCAGACCCGGTTTTAGTGCGGATGGGTCAGGCACAGATTTCACCTCGGAATP | 335 |

61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80
Db
336 ACTAGAGTCAGCGGTGCGGATGCTGATTACTGTCACAACTGTGAGAGTATCCA 395
QY
81 SerArgValLysAlaGluAspValGlyValTyrCysGlnHisPheValAspTyrPro 100
Db
396 TTCACGTCGCGTCGGGACAAAGTTGGAATAAAACGT 434
QY
101 PheThrPheGlySerGlyThrLysLeuGluIleLysArg 113
Db

RESULT 12

US-09-214-095D-112
; Sequence 112, Application US/09214095D

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; Patent NO.: 6280367
; GENERAL INFORMATION:
;
; APPLICANT: Landry, Donald
;
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
;
; FILE REFERENCE: 51400-A-PCT-US
;
; CURRENT APPLICATION NUMBER: US/09/214,095D
;
; CURRENT FILING DATE: 1999-07-19
;
; NUMBER OF SEQ ID NOS: 121
;
; SOFTWARE: PatentIn version 3.0
;
; SEQ ID NO 112
;
; LENGTH: 113
;
; TYPE: PRT
;
; ORGANISM: Murine
;
; US-09-214-095D-112

```

| | |
|------------------------|----------|
| Alignment Scores: | |
| Pred. No.: | 1,438-58 |
| Score: | 547.00 |
| Percent Similarity: | 98.23% |
| Best Local Similarity: | 92.04% |
| Query Match: | 65.68% |
| DB: | 3 |
| Length: | 113 |
| Matches: | 104 |
| Conservative: | 2 |
| Mismatches: | 2 |
| Indels: | 0 |
| Gaps: | 0 |

US-09-674-716B-2 (1-437) X US-09-214-095D-112 (1-113)

| | | | | | | | |
|-----|----|--|---------|--------------------|-----|------|-----|
| 96 | QY | GATATTGTGATACCCAGGATGAAC | TCTCCAA | TCTGTCACTTCTCGAGAA | TCA | GTTC | 155 |
| | | ::: ::: | | | | | |
| 1 | Db | AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer | 20 | | | | |
| 156 | QY | ATCTCTCTCAGGCTCTAGTAAGAGTCTCCTGTATAAGGATGGGAGACATACTTGAATCG | 215 | | | | |
| | | ::: ::: | | | | | |
| 21 | Db | IleSerCysArgSerSerArgSerLeuLeuTyArgAspGlyLysThrTyLeuAsnTrp | 40 | | | | |
| 216 | QY | TTTCTGACAGACACAGACAAATCTCTCAGCTCCTGATGTTATTGATTCACCCGTGA | 275 | | | | |
| | | ::: ::: | | | | | |
| 41 | Db | PheLeuGlnArgProGlyArgSerProGlnLeuLeuIefTyLeuMetSerThrArgAla | 60 | | | | |
| 276 | QY | TCAGAGTCTCAGACCCGCTTTAGTGGCAGTGGGTTCAGGCACAGATTTCACCTCGAAATC | 335 | | | | |
| | | ::: ::: | | | | | |
| 61 | Db | SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluIle | 80 | | | | |
| 336 | QY | AGTAGCTGAAGCTGAGGATGGGTGTGTTACTGTCTCAACAATCTGAGAGTATCCA | 395 | | | | |
| | | ::: ::: | | | | | |
| 81 | Db | SerArgValLysAlaGluAspValGlyValTyTyCysGlnHisPheValAspTyPro | 100 | | | | |
| 336 | QY | TTACGTTCTCGCTCGGGACAAAGTTGGAAATAAAACGT | 434 | | | | |
| 101 | Db | PheThrPheGlySerGlyThrLysLeuGluIleLvsArg | 113 | | | | |

RESULT 13

US-09-214-095D-119
: Sequence 119, Application US/09214095D

; PATENT NO.: 8280987
 ; GENERAL INFORMATION: Donald
 ; APPLICANT: Landry, Donald
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 51400-A-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/214,095D
 ; CURRENT FILING DATE: 1999-07-19

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; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 119
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-119

Alignment Scores:
Pred. No.: 2,1e-58 Length: 280
Score: 547.00 Matches: 105
Percent Similarity: 95.76% Conservaive: 8
Best Local Similarity: 88.98% Mismatches: 5
Query Match: 69.68% Indels: 0
DB: 3 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-214-095D-119 (1-280)
QY 81 TCTGAGTCAGTGGGATATCTGTATACCCAGGATGAACCTCAATCTCTGCTCACTTCT 140
Db 132 SerGlyGlyAlaMetAspIleValMetThrGlnAspGluLeuSerAsnProValThrSer 151
QY 141 GGAGAAATCAGTTCCATCTCTGAGGCTCTAGTAAGCTCTCTGTATAAGGATGGGAAG 200
Db 152 GlyGluSerValSerIleSerCysArgSerSerArgSerLeuLeuTyrArgAspGlyLys 171
QY 201 ACATCTTGAATGTGTTCTTCGAGAGACAGACAACTCTCTAGCTCTCTGATGATTTTG 260
Db 172 ThrTyrLeuAsnTrpPheLeuGlnArgProGlyArgProGlnLeuLeuIleTyrLeu 191
QY 261 ATGTCACCCGTCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGAT 320
Db 192 MetSerThrArgSerSerGlyValSerAspArgPheSerGlySerGlyThrAsp 211
QY 321 TTCACCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAA 380
Db 212 PheThrLeuGluLeuSerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHis 231
QY 381 CTTGTAGATATCCATTACGTTCCGCTCGGGACAAAGTTGGAATAAAGCT 434
Db 232 PheValAspTyrProPheThrPheGlySerGlyThrLysLeuGluIleLysArg 249

RESULT 14
US-08-672-345C-6
; Sequence 6, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-6

Alignment Scores:
Pred. No.: 7,76e-58 Length: 113
Score: 541.00 Matches: 103
Percent Similarity: 97.35% Conservaive: 7
Best Local Similarity: 91.15% Mismatches: 3
Query Match: 68.92% Indels: 0
DB: 2 Gaps: 0

US-09-674-716B-2 (1-437) x US-08-672-345C-6 (1-113)
QY 96 GATATTGTGATACCCAGGATGAACCTCTCAATCTCTGCTCACTTCTGAGAAATCAGTTTCC 155
Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
QY 156 ATCTCTCTGAGGCTCTAGTAAGAGTCTCTCTGTATAAGGATGGGAAGACATACCTTGAATTGG 215
Db 21 IleSerCysArgSerSerArgSerLeuLeuTyrArgAspGlyLysThrTyrLeuAsnTrp 40
QY 216 TTCTCGAGAGACCCAGACAACTCTCTAGCTCTCTGATGATTTGATGTCACCCCTGCA 275
Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuIleTyrLeuMetSerThrArgAla 60
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTCCCTGGAAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80
QY 336 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCA 395
Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnHisPheGluAspTyrPro 100
QY 396 TTCAGTTCGGCTCGGGACAAAGTTGGAATAAAGCT 434
Db 101 PheThrPheGlySerGlyThrLysLeuGluIleLysArg 113

RESULT 15
US-08-672-345C-96
; Sequence 96, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
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; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 113 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-672-345C-96

Alignment Scores:
  Pred. No.:      7.76e-58      Length:      113
  Score:          541.00        Matches:    103
  Percent Similarity: 97.35%    Conservatives: 7
  Best Local Similarity: 91.15% Mismatches: 3
  Query Match:      68.92%     Indels:      0
  DB:                2         Gaps:          0

US-09-674-716B-2 (1-437) x US-08-672-345C-96 (1-113)

QY   96  GATATTGTGATACCCAGGATCAACTCTCCAATCCTGTCACTTCGAGAAATCAGTTTCC 155
Db   1  AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20

QY   156 ATCTCTCGAGGTCTAGTAAGAGTCTCCTGTATAGGATGGGAAGACATACCTGAATTGG 215
Db   21  IleSerCysArgSerSerArgSerLeuLeuTyArgAspGlyLysThrTyrLeuAsnTrp 40

QY   216 TTCTCTCAGAGACGACGACAACTCTCCTCAGCTCCTGATGTTATTTGATGTCACCGGTGCA 275
Db   41  PheLeuGlnArgProGlyArgSerProGlnLeuLeuIleTyrLeuMetSerThrArgala 60

QY   276 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTGAGGACACAGATTTCACCTGGAATC 335
Db   61  SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluile 80

QY   336 AGTAGAGTGAAGGCTCAGGATGCTGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 395
Db   81  SerArgValLysAlaGluAspValGlyValTyrCysGlnHisPheGluAspLysPro 100

QY   396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAATACGT 434
Db   101 PheThrPheGlySerGlyThrLysLeuGluIleLysArg 113
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Search completed: September 30, 2004, 09:31:35
Job time : 12.688 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model
Run on: September 30, 2004, 08:54:09 ; Search time 57.3185 Seconds
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Perfect score: 785
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Delop 6.0 , Delext 7.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTENT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
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11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
12: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
13: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
15: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
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RESULT 1
US-09-940-727B-8
; Sequence 8, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: US75/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-8

ALIGNMENTS

| | | | | | | |
|----|-----|------|-----|----|--------------------|-------------------|
| 1 | 555 | 70.7 | 113 | 10 | US-09-940-727B-8 | Sequence 8, Appli |
| 2 | 549 | 69.9 | 113 | 10 | US-09-940-727B-108 | Sequence 108, App |
| 3 | 547 | 69.7 | 113 | 10 | US-09-940-727B-5 | Sequence 5, Appli |
| 4 | 547 | 69.7 | 113 | 10 | US-09-940-727B-7 | Sequence 7, Appli |
| 5 | 547 | 69.7 | 113 | 10 | US-09-940-727B-100 | Sequence 100, App |
| 6 | 547 | 69.7 | 113 | 10 | US-09-940-727B-112 | Sequence 112, App |
| 7 | 547 | 69.7 | 113 | 10 | US-09-940-727B-119 | Sequence 119, App |
| 8 | 541 | 68.9 | 113 | 10 | US-09-940-727B-6 | Sequence 6, Appli |
| 9 | 530 | 67.5 | 113 | 10 | US-09-940-727B-104 | Sequence 104, App |
| 10 | 509 | 64.8 | 100 | 9 | US-09-840-458-32 | Sequence 32, Appl |
| 11 | 509 | 64.8 | 100 | 16 | US-10-766-773-32 | Sequence 32, Appl |
| 12 | 509 | 64.8 | 100 | 16 | US-10-766-610-32 | Sequence 32, Appl |
| 13 | 509 | 64.8 | 100 | 16 | US-10-733-563-32 | Sequence 40, Appl |
| 14 | 508 | 64.7 | 239 | 12 | US-10-292-088-40 | Sequence 41, Appl |
| 15 | 506 | 64.5 | 239 | 12 | US-10-404-724-41 | Sequence 45, Appl |
| 16 | 506 | 64.5 | 239 | 12 | US-10-404-724-45 | Sequence 45, Appl |
| 17 | 505 | 64.3 | 239 | 12 | US-10-404-724-10 | Sequence 39, Appl |
| 18 | 505 | 64.3 | 239 | 12 | US-10-404-724-39 | Sequence 69, Appl |
| 19 | 504 | 64.2 | 247 | 12 | US-10-466-164-69 | Sequence 49, Appl |
| 20 | 501 | 63.8 | 239 | 12 | US-10-404-724-49 | Sequence 16, Appl |
| 21 | 500 | 63.7 | 239 | 12 | US-10-292-088-16 | Sequence 43, Appl |
| 22 | 500 | 63.7 | 239 | 12 | US-10-404-724-43 | Sequence 47, Appl |
| 23 | 500 | 63.7 | 239 | 12 | US-10-404-724-47 | Sequence 32, Appl |
| 24 | 499 | 63.6 | 239 | 12 | US-10-292-088-56 | Sequence 56, Appl |
| 25 | 499 | 63.6 | 239 | 12 | US-10-292-088-8 | Sequence 1, Appli |
| 26 | 498 | 63.4 | 239 | 12 | US-10-372-719-1 | Sequence 1, Appli |
| 27 | 497 | 63.3 | 142 | 15 | US-09-479-614-20 | Sequence 20, Appl |
| 28 | 493 | 62.8 | 242 | 10 | US-10-409-772-20 | Sequence 64, Appl |
| 29 | 493 | 62.8 | 242 | 15 | US-10-292-088-64 | Sequence 12, Appl |
| 30 | 492 | 62.7 | 239 | 12 | US-10-404-724-12 | Sequence 80, Appl |
| 31 | 492 | 62.7 | 239 | 12 | US-10-292-088-80 | Sequence 102, App |
| 32 | 491 | 62.5 | 239 | 12 | US-10-292-088-102 | Sequence 361, App |
| 33 | 491 | 62.5 | 239 | 14 | US-10-207-655-361 | Sequence 363, App |
| 34 | 488 | 62.2 | 133 | 14 | US-10-207-655-363 | Sequence 364, App |
| 35 | 488 | 62.2 | 271 | 14 | US-10-207-655-364 | Sequence 8, Appli |
| 36 | 488 | 62.2 | 505 | 14 | US-10-107-991B-4 | Sequence 8, Appli |
| 37 | 488 | 62.2 | 556 | 12 | US-09-992-600A-8 | Sequence 8, Appli |
| 38 | 487 | 62.0 | 239 | 10 | US-09-924-340-8 | Sequence 8, Appli |
| 39 | 487 | 62.0 | 239 | 10 | US-09-992-095B-8 | Sequence 8, Appli |
| 40 | 487 | 62.0 | 239 | 10 | US-09-999-570-8 | Sequence 8, Appli |
| 41 | 487 | 62.0 | 239 | 14 | US-10-000-489-8 | Sequence 8, Appli |
| 42 | 487 | 62.0 | 239 | 14 | US-10-000-986-8 | Sequence 8, Appli |
| 43 | 487 | 62.0 | 239 | 14 | US-10-154-678-8 | Sequence 8, Appli |
| 44 | 487 | 62.0 | 239 | 14 | | |
| 45 | 487 | 62.0 | 239 | 14 | | |

Alignment Scores:

Pred. No.: 6.08e-49 Length: 113
 Score: 555.00 Matches: 107
 Percent Similarity: 97.35% Conservative: 3
 Best Local Similarity: 94.69% Mismatches: 3
 Query Match: 70.70% Indels: 0
 DB: 10 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-940-727B-8 (1-113)

QY 96 GATATTGTGATAACCCAGGATGAACCTCCAAATCCTGTGTCACCTCTCGAGAACATGTTCC 155
 Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
 QY 156 ATCTCTCGAGGCTTAGTAAGAGTCTCCTGTATAGAGTGGGAAGACATCTGAAATGG 215
 Db 21 IleSerCysArgSerSerLysSerLeuLeuTyzGluAspGlyLysThrTyrLeuAsnTrp 40
 QY 216 TTCTCTGAGAGACCCAGGACAAATCCTCAGCTCCTCATGTATTTGATGTCACCCCGTGCA 275
 Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyrLeuMetSerThrArgala 60
 QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGCGGTGAGGACACAGATTTCACCTGGAATC 335
 Db 61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluile 80
 QY 336 AGTAGAGTGAAGGCTCAGAGTGGGTGTATTACTGTCAACAACTTGTAGAGTATCCA 395
 Db 81 SerArgValLysAlaGluAspValGlyAlaTyrTyrCysGlnGlnPheValGluTyrPro 100
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACGT 434
 Db 101 PheThrPheGlySerGlyThrLysLeuGluileArgArg 113

RESULT 2

US-09-940-727B-108
 ; Sequence 108, Application US/09940727B
 ; Publication No. US2003007793A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald W
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 0575/51400-B
 ; CURRENT APPLICATION NUMBER: US/09/940, 727B
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR APPLICATION NUMBER: 09/214, 095
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965
 ; PRIOR FILING DATE: 1997-06-25
 ; PRIOR APPLICATION NUMBER: 08/672,345
 ; PRIOR FILING DATE: 1996-06-25
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 108
 ; LENGTH: 113
 ; TYPE: PRT
 ; ORGANISM: mouse
 US-09-940-727B-108

Alignment Scores:

Pred. No.: 2.56e-48 Length: 113
 Score: 549.00 Matches: 105
 Percent Similarity: 97.35% Conservative: 5
 Best Local Similarity: 92.92% Mismatches: 3
 Query Match: 65.94% Indels: 0
 DB: 10 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-940-727B-108 (1-113)

QY 96 GATATTGTGATAACCCAGGATGAACCTCCAAATCCTGTGTCACCTCTCGAGAACATGTTCC 155
 Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
 QY 156 ATCTCTCGAGGCTTAGTAAGAGTCTCCTGTATAGAGTGGGAAGACATCTGAAATGG 215

Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrGluAspGlyLysThrTyrLeuAsnTrp 40
 QY 216 TTCTCTGAGAGACCCAGGACAAATCCTCAGCTCCTCATGTATTTGATGTCACCCCGTGCA 275
 Db 41 PheLeuGlnArgProGlyGlnSerProHisLeuLeuIleTyrLeuMetSerThrArgala 60
 QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGCGGTGAGGACACAGATTTCACCTGGAATC 335
 Db 61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluile 80
 QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTATTACTGTCAACAACTTGTAGAGTATCCA 395
 Db 81 SerArgValLysAlaGluAspValGlyAlaTyrTyrCysGlnGlnPheValGluTyrPro 100
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACGT 434
 Db 101 PheThrPheGlySerGlyThrLysLeuGluileArgArg 113

RESULT 3

US-09-940-727B-5
 ; Sequence 5, Application US/09940727B
 ; Publication No. US2003007793A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald W
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 0575/51400-B
 ; CURRENT APPLICATION NUMBER: US/09/940, 727B
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR APPLICATION NUMBER: 09/214, 095
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965
 ; PRIOR FILING DATE: 1997-06-25
 ; PRIOR APPLICATION NUMBER: 08/672,345
 ; PRIOR FILING DATE: 1996-06-25
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 113
 ; TYPE: PRT
 ; ORGANISM: mouse
 US-09-940-727B-5

Alignment Scores:

Pred. No.: 4.13e-48 Length: 113
 Score: 547.00 Matches: 104
 Percent Similarity: 98.23% Conservative: 7
 Best Local Similarity: 92.04% Mismatches: 2
 Query Match: 69.68% Indels: 0
 DB: 10 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-940-727B-5 (1-113)

QY 96 GATATTGTGATAACCCAGGATGAACCTCCAAATCCTGTGTCACCTCTCGAGAACATGTTCC 155
 Db 1 AspIleValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
 QY 156 ATCTCTCGAGGCTTAGTAAGAGTCTCCTGTATAGAGTGGGAAGACATCTGAAATGG 215
 Db 21 IleSerCysArgSerSerLysSerLeuLeuTyrArgAspGlyLysThrTyrLeuAsnTrp 40
 QY 216 TTCTCTGAGAGACCCAGGACAAATCCTCAGCTCCTCATGTATTTGATGTCACCCCGTGCA 275
 Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuIleTyrLeuMetSerThrArgSer 60
 QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGCGGTGAGGACACAGATTTCACCTGGAATC 335
 Db 61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluile 80
 QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTATTACTGTCAACAACTTGTAGAGTATCCA 395
 Db 81 SerArgValLysAlaGluAspValGlyValTyrTyrCysGlnGlnPheValAspTyrPro 100

Score: 547.00 Matches: 104
 Percent Similarity: 98.23% Conservative: 7
 Best Local Similarity: 92.04% Mismatches: 2
 Query Match: 69.68% Indels: 0
 DB: 10 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-940-727B-112 (1-113)

QY 96 GATATTGTGATACCCAGGATGACTCTCCAAATCCTGTCACCTCTCGAGAAATCAGTTTCC 155
 Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
 QY 156 ATCTCTGCAGGCTCTAGTAAAGATCTCTCTGATAGGATGGGAGACATACCTTGAATGG 215
 Db 21 IleSerCysArgSerSerArgSerLeuLeuTyArgAspGlyLysThrTyLeuAsnTTP 40
 QY 216 TTCTCTGAGAGACAGGACAACTCTCTCAGCTCCTGATGATGATGATGATGATGATGATG 275
 Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
 QY 276 TCAGGAGTCTCAGACCGGTTTACTGCGAGTGGGTGAGGACAGATTTCCACCTGGAAATC 335
 Db 61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluLeu 80
 QY 336 AGTAGAGTGAAGCTGAGGATGCGGTGTGATTAATCTGTCACAACTTGTAGAGTATCCA 395
 Db 81 SerArgValLysAlaGluAspValGlyValTyTyCysGlnHisPheValAspTyPro 100
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACGT 434
 Db 101 PheThrPheGlySerGlyThrLysLeuGluLeuLysArg 113

RESULT 7

US-09-940-727B-119
 ; Sequence 119, Application US/09940727B
 ; Publication No. US2003007793A1

GENERAL INFORMATION:

APPLICANT: Landry, Donald W

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REFERENCE: 0575/51400-B

CURRENT APPLICATION NUMBER: US/09/940,727B

CURRENT FILING DATE: 2002-09-04

PRIOR FILING DATE: 1998-12-28

PRIOR APPLICATION NUMBER: PCT/US97/10965

PRIOR FILING DATE: 1997-06-25

PRIOR APPLICATION NUMBER: 08/672,345

PRIOR FILING DATE: 1996-06-25

NUMBER OF SEQ ID NOS: 121

SOFTWARE: PatentIn version 3.1

SEQ ID NO 119

LENGTH: 280

TYPE: PRT

ORGANISM: mouse

US-09-940-727B-119

Alignment Scores:
 Pred. No.: 4,88e-48 Length: 280
 Score: 547.00 Matches: 105
 Percent Similarity: 95.76% Conservative: 8
 Best Local Similarity: 88.98% Mismatches: 5
 Query Match: 69.68% Indels: 0
 DB: 10 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-940-727B-119 (1-280)

QY 81 TCTGGAGTCAGTGGGATTTGTGATTAACCCAGGATGACTCTCCAAATCCTGTCACCTTCT 140
 Db 132 SerGlyGlyAlaMetAspLeuValMetThrGlnAspGluLeuSerAsnProValThrSer 151
 QY 141 GGAGATCAGTTTCCATCTCTCGAGGCTCTAGTAAAGATCTCTGATTAAGGATGGGGAAG 200
 Db 152 GlyGluSerValSerIleSerCysArgSerArgSerLeuLeuTyArgAspGlyLys 171

QY 201 ACATACTTGATTTGGTTTCTGCAGAGACAGGACAAATCTCTCTCAGCTCCTGATGATTTG 260
 Db 172 ThrTyLeuAsnTrpPheLeuGlnArgProGlyArgProGlnLeuLeuLeuLeuLeuLeu 191
 QY 261 ATGTCACCCCGTGCATCAGGAGTCTCAGACCGGTTTACTGTCAGTGGGTGAGGACAGAT 320
 Db 192 MetSerThrArgSerSerGlyValSerAspArgPheSerGlySerGlySerGlyThrAsp 211
 QY 321 TTACCCCTGGAAATCAGTAGAGTGAAGCTGAGGATGCTGGGTGTGATTAATCTGTCAACA 380
 Db 212 PheThrLeuGluLeuSerArgValLysAlaGluAspValGlyValTyTyCysGlnHis 231
 QY 381 CTCTGAGAGTATCATTTCACTTCAGCTTCGGCTCGGGGACAAAGTTGGAAATAAAACGT 434
 Db 232 PheValAspTyProPheThrPheGlySerGlyThrLysLeuGluLeuLysArg 249

RESULT 8

US-09-940-727B-6

; Sequence 6, Application US/09940727B

; Publication No. US2003007793A1

GENERAL INFORMATION:

APPLICANT: Landry, Donald W

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REFERENCE: 0575/51400-B

CURRENT APPLICATION NUMBER: US/09/940,727B

CURRENT FILING DATE: 2002-09-04

PRIOR APPLICATION NUMBER: 09/214,095

PRIOR FILING DATE: 1998-12-28

PRIOR APPLICATION NUMBER: PCT/US97/10965

PRIOR FILING DATE: 1997-06-25

PRIOR APPLICATION NUMBER: 08/672,345

PRIOR FILING DATE: 1996-06-25

NUMBER OF SEQ ID NOS: 121

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 113

TYPE: PRT

ORGANISM: mouse

US-09-940-727B-6

Alignment Scores:

Pred. No.: 1,74e-47 Length: 113
 Score: 541.00 Matches: 103
 Percent Similarity: 97.35% Conservative: 7
 Best Local Similarity: 91.15% Mismatches: 3
 Query Match: 68.92% Indels: 0
 DB: 10 Gaps: 0

US-09-674-716B-2 (1-437) x US-09-940-727B-6 (1-113)

QY 96 GATATTGTGATTAACCCAGGATGACTCTCCAAATCCTGTCACCTCTCGAGAAATCAGTTTCC 155
 Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20
 QY 156 ATCTCTGAGGCTCTAGTAAAGATCTCTGATTAAGGATGGGAGACATACCTTGAATGG 215
 Db 21 IleSerCysArgSerSerArgSerLeuLeuTyArgAspGlyLysThrTyLeuAsnTTP 40
 QY 216 TTCTCTGAGAGACAGGACAACTCTCTCAGCTCCTGATGATGATGATGATGATGATGATG 275
 Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
 QY 276 TCAGGAGTCTCAGACCGGTTTACTGCGAGTGGGTGAGGACAGATTTCCACCTGGAAATC 335
 Db 61 SerGlyValSerAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuGluLeu 80
 QY 336 AGTAGAGTGAAGCTGAGGATGCGGTGTGATTAATCTGTCACAACTTGTAGAGTATCCA 395
 Db 81 SerArgValLysAlaGluAspValGlyValTyTyCysGlnHisPheValAspTyPro 100
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACGT 434

Db 101 PhetrPheGlySerGlyThrLysLeuGluLeuLysArg 113

RESULT 9

US-09-940-727B-104

Sequence 104, Application US/09940727B

Publication No. US2003007793A1

GENERAL INFORMATION:

APPLICANT: Landry, Donald W

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REFERENCE: 0575/51400-B

CURRENT APPLICATION NUMBER: US/09/940,727B

CURRENT FILING DATE: 2002-09-04

PRIOR APPLICATION NUMBER: 09/214,095

PRIOR FILING DATE: 1998-12-28

PRIOR APPLICATION NUMBER: PCT/US97/10965

PRIOR FILING DATE: 1997-06-25

PRIOR APPLICATION NUMBER: 08/672,345

PRIOR FILING DATE: 1996-06-25

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patent in version 3.1

SEQ ID NO 104

LENGTH: 113

TYPE: PRT

ORGANISM: mouse

US-09-940-727B-104

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 2,43e-46 | Length: | 113 |
| Score: | 530.00 | Matches: | 102 |
| Percent Similarity: | 96.46% | Conservative: | 7 |
| Best Local Similarity: | 90.27% | Mismatches: | 4 |
| Query Match: | 67.52% | Indels: | 0 |
| DB: | 10 | Gaps: | 0 |

US-09-674-716B-2 (1-437) x US-09-940-727B-104 (1-113)

QY 96 GATATTGTGATACCCAGGATGACTCTCCATCTCTGTCACCTTCTGGAGATCAGTTTCC 155

Db 1 AspMetValMetThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20

QY 156 ATCTCTCGAGGTCTAGTAAGAGTCTCTGTATAAGGATGGAGACATCTTGAATTGG 215

Db 21 IleSerCysArgSerSerGlyLeuLeuTyArgAspGlyLysThrTyLeuAsnTrp 40

QY 216 TTCTTCAGACAGGACCAATCTCTCAGCTCTGATCTTATTCGATCCACCGTGCA 275

Db 41 PheLeuGlnArgProGlyArgSerProGlnLeuLeuLeuTyLeuMetSerThrArgala 60

QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGTTCACCCCTGGAATC 335

Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLeu 80

QY 336 AGTAGAGTGAAGGTGAGGATGTGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395

Db 81 SerArgValLysAlaGluAspValGlyValTyTy-CysGlnGlnLeuValGluTy-Pro 100

RESULT 10

US-09-840-459-32

Sequence 32, Application US/09840459

Patent No. US20020150576A1

GENERAL INFORMATION:

APPLICANT: Larosa, Gregory J.

APPLICANT: Horvath, Christopher

APPLICANT: Newman, Walter

APPLICANT: Jones, S. Tarran

APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REFERENCE: 1855.1052-028

CURRENT APPLICATION NUMBER: US/10/766,773

CURRENT FILING DATE: 2004-01-27

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/121,781

PRIOR FILING DATE: 1998-07-23

NUMBER OF SEQ ID NOS: 106

SOFTWARE: FastSeq for Windows Version 3.0

FILE REFERENCE: 1855.1052-012

CURRENT APPLICATION NUMBER: US/09/840,459

CURRENT FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: PCT/US01/03537

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/121,781

PRIOR FILING DATE: 1998-07-23

NUMBER OF SEQ ID NOS: 107

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 32

LENGTH: 100

TYPE: PRT

ORGANISM: Mus musculus

US-09-840-459-32

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 3,63e-44 | Length: | 100 |
| Score: | 509.00 | Matches: | 99 |
| Percent Similarity: | 100.00% | Conservative: | 1 |
| Best Local Similarity: | 99.00% | Mismatches: | 0 |
| Query Match: | 64.84% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-09-674-716B-2 (1-437) x US-09-840-459-32 (1-100)

QY 96 GATATTGTGATACCCAGGATGAACTCTCAATCTCTGTCACCTTCTGGAGATCAGTTTCC 155

Db 1 AspIleValIleThrGlnAspGluLeuSerAsnProValThrSerGlyGluSerValSer 20

QY 156 ATCTCTCGAGGTCTAGTAAGAGTCTCTGTATAAGGATGGAGACATCTTGAATTGG 215

Db 21 IleSerCysArgSerSerLysSerLeuLeuTyLysAspGlyLysThrTyLeuAsnTrp 40

QY 216 TTCTTCAGACAGGACCAATCTCTCAGCTCTGATCTTATTCGATCCACCGTGCA 275

Db 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuLeuTyLeuMetSerThrArgala 60

QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGTTCACCCCTGGAATC 335

Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluLeu 80

QY 336 AGTAGAGTGAAGGTGAGGATGTGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395

Db 81 SerArgValLysAlaGluAspValGlyValTyTy-CysGlnGlnLeuValGluTy-Pro 100

RESULT 11

US-10-766-773-32

Sequence 32, Application US/10766773

Publication No. US20040126851A1

GENERAL INFORMATION:

APPLICANT: Larosa, Gregory J.

APPLICANT: Horvath, Christopher

APPLICANT: Newman, Walter

APPLICANT: Jones, S. Tarran

APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REFERENCE: 1855.1052-028

CURRENT APPLICATION NUMBER: US/10/766,773

CURRENT FILING DATE: 2004-01-27

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/121,781

PRIOR FILING DATE: 1998-07-23

NUMBER OF SEQ ID NOS: 106

SOFTWARE: FastSeq for Windows Version 3.0

Db 41 PheLeuGlnArgProGlyGlnSerProGlnLeuLeuLeuTyrLeuMetSerThrArgAla 60
QY 276 TCAGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGGACAGATTTCCACCTGGAATC 335
Db 61 SerGlyValSerAspArgPheSerGlySerGlyThrAspPheThrLeuGluIle 80
QY 336 AGTAGAGTGAAGGCTGAGAGTGGTGTGATTACTGTCAACAACCTGTAGAGTATCCA 395
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysGlnGlnLeuValGluTyrPro 100

RESULT 14

US-10-292-088-40
; Sequence 40, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PP/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-40

Alignment Scores:
Pred. No.: 5,42e-44 Length: 239
Score: 508.00 Matches: 96
Percent Similarity: 84.33% Conservative: 17
Best Local Similarity: 71.64% Mismatches: 21
Query Match: 64.71% Indels: 0
DB: 12 Gaps: 0

US-09-674-716B-2 (1-437) x US-10-292-088-40 (1-239)

QY 36 ATCAGGTTCTCTGTTTCAGTTTCGGGGTGTATGTTCTGGATCTCTGGAGTCAGTGG 95
Db 1 MetArgLeuProAlaGlnLeuLeuGlyLeuLeuMetLeuTrpValSerGlySerGly 20
QY 96 GATATTGTGATACCCAGGATGACCTCCATCTCTGTCACCTCTGGAGAACAGTTC 155
Db 21 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
QY 156 ATCTCTGCGAGGTCTAGTAAAGATCTCTCTGTATAGGATGGGAGACATCTGAA 215
Db 41 IleSerCysArgSerSerGlnSerValLeuTyrSerAsnGlyTyrAsnTyrLeuAspTrp 60
QY 216 TTTCTCAGACGACGACCAATCTCTCAGCTCTGATGTTATGTTGATCCACCGTCCA 275
Db 61 TyrLeuGlnTyrProGlyGlnSerProGlnLeuLeuLeuTyrLeuGlySerAsnArgAla 80
QY 276 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGGACAGATTTCCACCTGGAATC 335
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
QY 336 AGTAGAGTGAAGGCTGAGAGTGGTGTGATTACTGTCAACAACCTGTAGAGTATCCA 395
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnValLeuGlnThrPro 120
QY 396 TTCACGTTCCGCTCGGGACAAAGTTGGAATAAAACGTACG 437
Db 121 PheThrPheGlyProGlyThrLysValAspIleLysArgThr 134

RESULT 15

US-10-404-724-41
; Sequence 41, Application US/10404724
; Publication No. US20030203447A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
; FILE REFERENCE: 13698US01
; CURRENT APPLICATION NUMBER: US/10/404,724
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-404-724-41

Alignment Scores:
Pred. No.: 8,74e-44 Length: 239
Score: 506.00 Matches: 99
Percent Similarity: 83.58% Conservative: 13
Best Local Similarity: 73.88% Mismatches: 22
Query Match: 64.46% Indels: 0
DB: 12 Gaps: 0

US-09-674-716B-2 (1-437) x US-10-404-724-41 (1-239)

QY 36 ATCAGGTTCTCTGTTTCAGTTTCGGGGTGTATGTTCTGGATCTCTGGAGTCAGTGG 95
Db 1 MetArgPheSerAlaGlnLeuLeuGlyLeuLeuValLeuTrpIleProGlySerThrAla 20
QY 96 GATATTGTGATACCCAGGATGAACTCTCCAATCTCTGTCACCTCTGGAGAACAGTTC 155
Db 21 AspIleValMetThrGlnSerAlaLeuSerAsnProValThrProGlyGluSerGlySer 40
QY 156 ATCTCTGCGAGGTCTAGTAAAGATCTCTGTATAGGATGGGAGACATCTGAA 215
Db 41 IleSerCysArgSerSerLysSerLeuLeuHisSerAsnGlyIleThrTyrLeuTyrTrp 60
QY 216 TTTCTCAGACGACGACCAATCTCTCAGCTCTCTGATGTTATGTTGATCCACCGTCCA 275
Db 61 TyrLeuGlnTyrProGlyGlnSerProGlnLeuLeuLeuTyrGlnMetSerAsnArgAla 80
QY 276 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGGACAGATTTCCACCTGGAATC 335
Db 81 SerGlyValProAspArgPheSerSerGlySerGlyThrAspPheThrLeuLysIle 100
QY 336 AGTAGAGTGAAGGCTGAGAGTGGTGTGATTACTGTCAACAACCTGTAGAGTATCCA 395
Db 101 SerArgValGluAlaGluAspValGlyValTyrTyrCysAlaGlnAsnLeuGluLeuPro 120
QY 396 TTCACGTTCCGCTCGGGACAAAGTTGGAATAAAACGTACG 437
Db 121 ArgThrPheGlyGlnGlyThrLysLeuGluMetLysArgThr 134

Search completed: September 30, 2004, 09:48:30
Job time : 59.3185 secs

Blank sheet

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 17.3559 Seconds
(without alignments)
88.677 Million cell updates/sec

Title: US-09-674-716B-3

Perfect score: 81
Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 81 | 100.0 | 112 | 1 KVM516 | Ig kappa chain V r |
| 2 | 81 | 100.0 | 113 | 1 KVM551 | Ig kappa chain V r |
| 3 | 81 | 100.0 | 120 | 1 KVM567 | Ig kappa chain pre |
| 4 | 81 | 100.0 | 120 | 2 A23775 | Ig kappa chain pre |
| 5 | 81 | 100.0 | 120 | 2 B23775 | Ig kappa chain pre |
| 6 | 66 | 81.5 | 112 | 2 PL0273 | Ig kappa chain V r |
| 7 | 65 | 80.2 | 133 | 2 S40324 | Ig kappa chain V r |
| 8 | 64 | 79.0 | 83 | 2 S34095 | Ig kappa chain V r |
| 9 | 64 | 79.0 | 111 | 2 S20709 | Ig kappa chain V r |
| 10 | 64 | 79.0 | 120 | 2 S42267 | Ig kappa chain V r |
| 11 | 64 | 79.0 | 120 | 2 S42268 | Ig kappa chain V r |
| 12 | 64 | 79.0 | 133 | 1 K2HURP | Ig kappa chain pre |
| 13 | 63 | 77.8 | 114 | 2 S49572 | Ig kappa chain pre |
| 14 | 61 | 75.3 | 101 | 2 PH1057 | Ig light chain V r |
| 15 | 61 | 75.3 | 113 | 1 K2HUFH | Ig kappa chain V-I |
| 16 | 61 | 75.3 | 122 | 2 S40338 | Ig kappa chain - h |
| 17 | 60 | 74.1 | 112 | 2 PL0275 | Ig kappa chain V r |
| 18 | 60 | 74.1 | 133 | 2 S42611 | HUNVK protein prec |
| 19 | 60 | 74.1 | 249 | 2 S41374 | single chain Fv an |
| 20 | 59 | 72.8 | 87 | 2 S34094 | Ig kappa chain V r |
| 21 | 59 | 72.8 | 91 | 2 S42186 | Ig kappa chain V r |
| 22 | 59 | 72.8 | 101 | 2 A33730 | Ig kappa chain V r |
| 23 | 59 | 72.8 | 103 | 2 PH1055 | Ig light chain V r |
| 24 | 59 | 72.8 | 103 | 2 PH1056 | Ig light chain V r |
| 25 | 59 | 72.8 | 112 | 2 S42659 | Ig kappa chain V r |
| 26 | 59 | 72.8 | 113 | 2 F30560 | Ig kappa chain V r |
| 27 | 59 | 72.8 | 132 | 2 S32513 | Ig kappa chain pre |
| 28 | 59 | 72.8 | 133 | 2 S23230 | Ig kappa chain pre |
| 29 | 59 | 72.8 | 140 | 2 S23658 | Ig kappa chain pre |

ALIGNMENTS

RESULT 1

KVM516
Ig kappa chain V region (M167) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
C:Accession: A01908
R:Rudikoff, S.; Potter, M.
Biochemistry 17, 2703-2707, 1978
A:Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prote
A:Reference number: A01908; MUID:79000273; PMID:99160
A:Accession: A01908
A:Molecule type: protein
A:Residues: 1-112 <RUD>
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine. J
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 81; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
|||
DB 24 RSSKSLLYKDGKTYLN 39

RESULT 2

KVM51
Ig kappa chain V region (M511) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
R:Appella, E.
Mol. Immunol. 17, 711-718, 1980
A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcho
A:Reference number: A01910; MUID:81052016; PMID:6776396
A:Accession: A01910
A:Molecule type: protein
A:Residues: 1-113 <APP>
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 81; DB 1; Length 113;

```

Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
    |||||
Db 24 RSSKSLLYKDGKTYLN 39

RESULT 3
KVMS67
Ig kappa chain precursor V region (VK167) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000
C:Accession: A01909
R:Seising, E.; Scorb, U.
Cell 25, 47-58, 1981
A:Title: Somatic mutation of immunoglobulin light-chain variable-region genes.
A:Reference number: A01909; MUID:82002223; PMID:6791832
A:Accession: A01909
A:Molecule type: DNA
A:Residues: 1-120 <SEL>
A:Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
F:43-113/Disulfide bonds: #status predicted

Query Match 100.0%; Score 81; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
    |||||
Db 44 RSSKSLLYKDGKTYLN 59

RESULT 4
A29775
Ig kappa chain precursor V region (mouse 24.2) - shrew mouse
C:Species: Mus pahari
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C:Accession: A29775
R:Jouvin-Marche, E.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A:Title: Evolution of a V-kappa gene family.
A:Reference number: A91751; MUID:87006895; PMID:3093373
A:Accession: A29775
A:Molecule type: DNA
A:Residues: 1-120 <TOU>
A:Cross-references: GB:M1552; NID:gl97468; PIDN:AAA39036.1; PID:gl97469
A:Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region 24.2 #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
    |||||
Db 44 RSSKSLLYKDGKTYLN 59

```

```

RESULT 5
B29775
Ig kappa chain precursor V region (mouse 24.1) - shrew mouse
C:Species: Mus pahari
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C:Accession: B29775
R:Jouvin-Marche, E.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A:Title: Evolution of a V-kappa gene family.
A:Reference number: A91751; MUID:87006895; PMID:3093373
A:Accession: B29775
A:Molecule type: DNA
A:Residues: 1-120 <TOU>
A:Cross-references: GB:M1553; NID:gl97470; PIDN:AAA39037.1; PID:gl97471
A:Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region 24.1 #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

```

```

Query Match 100.0%; Score 81; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RSSKSLLYKDGKTYLN 16
    |||||
Db 44 RSSKSLLYKDGKTYLN 59

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RESULT 6
PL0273
Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0273
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation of a V region
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0273
A:Molecule type: mRNA
A:Residues: 1-112 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-95/Domain: immunoglobulin homology <IMM>
F:24-39/Region: complementarity-determining 1
F:40-54/Region: framework 2
F:55-61/Region: complementarity-determining 2
F:62-93/Region: framework 3
F:94-102/Region: complementarity-determining 3
F:103-112/Region: framework 4

```

```

Query Match 81.5%; Score 66; DB 2; Length 112;
Best Local Similarity 75.0%; Pred. No. 0.00037;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RSSKSLLYKDGKTYLN 16
    :|||:
Db 24 RSSKSLLYKDGKTYLN 39

```

```

RESULT 7
S40324
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40324
R:Klein, R.; Jaenichen, R.; Zachau, H.G.

```

Eur. J. Immunol. 23, 3248-3271, 1993
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A;Reference number: S40312; MUID:9408091; PMID:8258341
 A;Accession: S40324
 A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-133 <KLE>
 A;Cross-references: EMBL:X72434
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;133-112/Domain: immunoglobulin homology <IMM>
 Query Match 80.2%; Score 65; DB 2; Length 133;
 Best Local Similarity 75.0%; Pred. No. 0.0017; Indels 0; Gaps 0;
 Matches 12; Conservative 2; Mismatches 2;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 41 RSDQSLVYSDGNTYLN 56
 RESULT 8
 S34095
 IG kappa chain V region - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
 C;Accession: S34095
 R;Wagner, S.D.; Luzzatto, L.
 Eur. J. Immunol. 23, 391-397, 1993
 A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
 A;Reference number: S34076; MUID:93170387; PMID:8436174
 A;Accession: S34095
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-83 <WAG>
 A;Cross-references: EMBL:X67179
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-80/Domain: immunoglobulin homology <IMM>
 Query Match 79.0%; Score 64; DB 2; Length 83;
 Best Local Similarity 75.0%; Pred. No. 0.0015; Indels 0; Gaps 0;
 Matches 12; Conservative 2; Mismatches 2;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 9 RSSQSLVYSDGNTYLN 24
 RESULT 9
 S20709
 IG kappa chain V region - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 C;Accession: S20709
 R;Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osh
 submitted to the EMBL Data Library, April 1992
 A;Description: Binding specificity and variable region sequences of two monoclonal antib
 A;Reference number: S20706
 A;Accession: S20709
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-111 <BRE>
 A;Cross-references: EMBL:Z11917; NID:G52655; PIDN:CAA77975.1; PID:G52656
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-95/Domain: immunoglobulin homology <IMM>
 Query Match 79.0%; Score 64; DB 2; Length 111;
 Best Local Similarity 75.0%; Pred. No. 0.0021; Indels 0; Gaps 0;
 Matches 12; Conservative 3; Mismatches 1;
 QY 1 RSSKSLLYKDGKTYLN 16

DB 24 RSSQSLVYSDGNTYLN 39
 RESULT 10
 S42267
 IG kappa chain V region (A1) - human
 C;Species: Homo sapiens (man)
 C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C;Accession: S42267
 R;Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zoc
 Eur. J. Immunol. 22, 1023-1029, 1992
 A;Title: The human immunoglobulin kappa locus. Characterization of the duplicated A reg
 A;Reference number: A49043; MUID:92201291; PMID:1551402
 A;Accession: S42267
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-120 <LAU>
 A;Cross-references: EMBL:X63402
 C;Genetics:
 A;Introns: 17/3
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;36-115/Domain: immunoglobulin homology <IMM>
 Query Match 79.0%; Score 64; DB 2; Length 120;
 Best Local Similarity 75.0%; Pred. No. 0.0022; Indels 0; Gaps 0;
 Matches 12; Conservative 2; Mismatches 2;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 44 RSSQSLVYSDGNTYLN 59
 RESULT 11
 S42268
 IG kappa chain V region (A17) - human
 C;Species: Homo sapiens (man)
 C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jan-2000
 C;Accession: S42268
 R;Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zoc
 Eur. J. Immunol. 22, 1023-1029, 1992
 A;Title: The human immunoglobulin kappa locus. Characterization of the duplicated A reg
 A;Reference number: A49043; MUID:92201291; PMID:1551402
 A;Accession: S42268
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-120 <LAU>
 A;Cross-references: EMBL:X63403
 C;Genetics:
 A;Introns: 17/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;36-115/Domain: immunoglobulin homology <IMM>
 Query Match 79.0%; Score 64; DB 2; Length 120;
 Best Local Similarity 75.0%; Pred. No. 0.0022; Indels 0; Gaps 0;
 Matches 12; Conservative 2; Mismatches 2;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 44 RSSQSLVYSDGNTYLN 59
 RESULT 12
 K2HURP
 IG kappa chain precursor V-II region (RPM1) - human
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997
 C;Accession: A01890
 R;Klobeck, H.G.; Meindl, A.; Combrato, G.; Solomon, A.; Zachau, H.G.
 Nucleic Acids Res. 13, 6499-6513, 1985
 A;Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
 A;Reference number: A93588; MUID:86041852; PMID:2997711
 A;Accession: A01890

A:Molecule type: DNA
A:Residues: 1-133 <KLO>
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-II region (RPM1) #status predicted <MAT>
F:21-43/Region: framework 1
F:36-115/Domain: immunoglobulin homology <IMM>
F:44-59/Region: complementarity-determining 1
F:60-74/Region: framework 2
F:75-81/Region: complementarity-determining 2
F:82-113/Region: framework 3
F:114-122/Region: complementarity-determining 3
F:123-133/Region: framework 4
F:43-113/Disulfide bonds: #status predicted

Query Match 79.0%; Score 64; DB 1; Length 133;
Best Local Similarity 75.0%; Pred. No. 0.0025;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
|||||:|||||
Db 44 RSSQSLVYTDGNTYLN 59

RESULT 13
S49572
IG kappa chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C:Accession: S49572
R:Giachino, C.; Padovan, E.; Lanzavecchia, A.
submitted to the EMBL Data Library, November 1994
A:Description: K-1+ dual receptor B cells are present in the human peripheral repertoire
A:Reference number: S49571
A:Accession: S49572
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114 <GIA>
A:Cross-references: EMBL:246626; NID:g575261; PIDN:CAA6596.1; PID:g575262
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 63; DB 2; Length 114;
Best Local Similarity 75.0%; Pred. No. 0.0031;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
|||||:|||||
Db 24 RSSQSLVYTDGNTYLN 39

RESULT 14
PH1057
IG light chain V region (clone 17s.145) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1057
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1057
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA

A:Residues: 1-101 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 61; DB 2; Length 101;
Best Local Similarity 80.0%; Pred. No. 0.0059;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 15
|||||:|||||
Db 24 RSSQSLVYTDGNTYLN 38

RESULT 15
K2HUPR
IG kappa chain V-II region (Fr) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A01886
R:Rieser, W.F.; Jaton, J.C.
Biochemistry 15, 3829-3833, 1976
A:Title: Variable region sequence of the light chain from a Waldenstrom's IgM with specific
A:Reference number: A01886; MUID:76253627; PMID:821524
A:Accession: A01886
A:Molecule type: protein
A:Residues: 1-113 <RIE>
A:Comment: This chain was isolated from a Waldenstrom's macroglobulin that binds phospho:
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology
C:Superfamily: heterotetramer
C:Keywords: heterotetramer
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Query Match 75.3%; Score 61; DB 1; Length 113;
Best Local Similarity 62.5%; Pred. No. 0.0066;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
|||||:|||||
Db 24 RSSQSLVYRGGTYLB 39

Search completed: September 30, 2004, 06:00:31
Job time : 18.3559 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 52.339 Seconds
(without alignments)
96.454 Million cell updates/sec

Title: US-09-674-716B-3
Perfect score: 81
Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

```
Minimum DB seg length: 0
Maximum DB seg length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*

```

1:  sp_arctea.*
2:  sp_bacteria.*
3:  sp_fungi.*
4:  sp_human.*
5:  sp_invertebrate.*
6:  sp_mammal.*
7:  sp_mhc.*
8:  sp_organella.*
9:  sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query % | | | DB | ID | Description |
|------------|---------|-------|--------|----|--------|---------------------|
| | Score | Match | Length | | | |
| 1 | 64 | 79.0 | 86 | 4 | Q723Y5 | Q723Y5 homo sapien |
| 2 | 61 | 75.3 | 239 | 4 | Q8TCD0 | Q8TCD0 homo sapien |
| 3 | 59 | 72.8 | 148 | 11 | Q8K122 | Q8K122 mus musculus |
| 4 | 57 | 70.4 | 114 | 4 | Q9UL80 | Q9UL80 homo sapien |
| 5 | 50 | 61.7 | 239 | 4 | Q8NEK0 | Q8NEK0 homo sapien |
| 6 | 50 | 61.7 | 758 | 10 | Q9C9P8 | Q9C9P8 arabidopsis |
| 7 | 49 | 60.5 | 238 | 11 | Q8VC16 | Q8VC16 mus musculus |
| 8 | 48 | 59.3 | 104 | 11 | Q9JL82 | Q9JL82 mus musculus |
| 9 | 48 | 59.3 | 239 | 11 | Q8K0P8 | Q8K0P8 mus musculus |
| 10 | 48 | 59.3 | 239 | 11 | Q8VC55 | Q8VC55 mus musculus |
| 11 | 48 | 59.3 | 1561 | 17 | Q26431 | Q26431 methanobact |
| 12 | 46 | 56.8 | 238 | 11 | Q99M37 | Q99M37 mus musculus |
| 13 | 46 | 56.8 | 506 | 16 | Q9L035 | Q9L035 streptomyce |
| 14 | 46 | 56.8 | 573 | 2 | P97179 | P97179 streptomyce |
| 15 | 46 | 56.8 | 574 | 2 | O86876 | O86876 streptomyce |
| 16 | 44 | 54.3 | 419 | 16 | O9CG36 | O9CG36 lactococcus |

ALIGNMENTS

RESULT 1

| | | | | |
|----|--|---|------|--------|
| ID | Q7Z315 | PRELIMINARY; | PRT; | 86 AA. |
| AC | Q7Z3Y5; | | | |
| DT | 01-OCT-2003 | (T=EMBLrel. 25, Created) | | |
| DT | 01-OCT-2003 | (T=EMBLrel. 25, Last sequence update) | | |
| DT | 01-OCT-2003 | (T=EMBLrel. 25, Last annotation update) | | |
| DE | Rearranged VKA17 V gene segment (Fragment). | | | |
| GN | VKA17. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Hodgkin lymphoma; | | | |
| RA | Tingelly M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R., | | | |
| RA | Hansmann M.L., Brauningner A.; | | | |
| RT | "Analysis of a clonally related mantle cell and Hodgkin lymphoma | | | |
| PT | indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg | | | |
| RT | cell precursor in a germinal center."; | | | |
| RL | Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EWBL; AJ564426; CAD9203.1; -. | | | |
| FT | NON TER | | | |
| FT | 1 | | | |
| FT | 86 | | | |
| FT | NON TER | | | |
| FT | 86 | | | |
| SO | SEQUENCE | | | |
| | 86 AA; 9764 MW; D:98FC04EE0C78FD CRC64; | | | |

Query Match 79.0%; Score 64; DB 4; Length 86;

Best Local Similarity 75.0%; Pred. No. 0.0042;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGTKYLN 16
 |||:||:||||
pB 3 RSSOSLVSDGNTYLN 18

RESULT 2

Q8TCD0 PRELIMINARY; PRT; 239 AA.

AC Q8TCD0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Lung;
 RC Strausberg R.;
 RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022362; AAH2362.1; -;
 DR PIR; S34095; S34095.
 DR PIR; S42267; S42267.
 DR PIR; S42268; S42268.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003106; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;
 Query Match 75.3%; Score 61; DB 4; Length 239;
 Best Local Similarity 68.8%; Pred. No. 0.041;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 |||:|||||
 Db 44 RSTQSLVSDGNTYLN 59
 |||:|||||
 RESULT 3
 Q8K122 PRELIMINARY; PRT; 148 AA.
 AC Q8K122;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Salivary gland;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC028925; AAH28925.1; -;
 DR InterPro; IPR003599; Ig-like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 148 AA; 16345 MW; 183920BBD9F3B521 CRC64;
 Query Match 72.8%; Score 59; DB 11; Length 148;
 Best Local Similarity 75.0%; Pred. No. 0.052;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 |||:|||||
 Db 43 KSSQSLVSDGKTYLN 59
 |||:|||||

RESULT 4
 Q9UL80 PRELIMINARY; PRT; 114 AA.
 AC Q9UL80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
 RL EMBL; AF035034; AAD56270.1; -;
 DR PIR; B49002; B49002.
 DR PIR; S23638; S23638.
 DR PIR; S34094; S34094.
 DR PIR; S34095; S34095.
 DR HSP; P80362; IWTL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR NON_TER 1
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12775 MW; 070B31E210D1CB01 CRC64;
 Query Match 70.4%; Score 57; DB 4; Length 114;
 Best Local Similarity 68.8%; Pred. No. 0.085;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 |||:|||||
 Db 24 RSSQSPVSDGNTYLN 39
 |||:|||||
 RESULT 5
 Q8NEKO PRELIMINARY; PRT; 239 AA.
 AC Q8NEKO;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030814; AAH30814.1; -;
 DR PIR; S23638; S23638.
 DR PIR; S34091; S34091.
 DR PIR; S40357; S40357.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00407; IGcl; 1.

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;

Query Match 61.7%; Score 50; DB 4; Length 239;
 Best Local Similarity 62.5%; Pred. No. 2.8;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RSSKSLLYKDGKTYLN 16
 DB 44 RSSQSLHSDGNYLD 59

RESULT 6
 Q9C9E8 PRELIMINARY; PRT; 758 AA.
 AC Q9C9E8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN T10D10.3
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altaki H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway T.H., Dewar K.,
 RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Feng B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,
 RA Miltitscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana."
 RL Nature 408:816-820(2000).
 DR EMBL; AC016529; AGS59586.1; -.
 DR FIR; C96749; C96749.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
 DR GO; GO:0006306; P:DNA methylation; IEA.
 DR InterPro; IPR002052; N6_Mtase.
 DR InterPro; IPR002035; VWFA.
 DR Pfam; PF00092; vwa; 1.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS00092; N6_MTASE; 1.
 DR PROSITE; PS0234; VWFA; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 758 AA; 84789 MW; 8434F219D227036B CRC64;

Query Match 61.7%; Score 50; DB 10; Length 758;
 Best Local Similarity 64.3%; Pred. No. 10;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 SKSLLYKDGKTYLN 16
 DB 194 SQKLYKDGKFLN 207

RESULT 7
 Q8VC16 PRELIMINARY; PRT; 238 AA.
 AC Q8VC16;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019760; AAH19760.1; -.
 DR PIR; A27887; A27887.
 DR PIR; A32248; A32248.
 DR PIR; A33333; A33333.
 DR PIR; B27887; B27887.
 DR PIR; B30577; B30577.
 DR PIR; B31485; B31485.
 DR PIR; B32248; B32248.
 DR PIR; B41340; B41340.
 DR PIR; C27887; C27887.
 DR PIR; C27887; C27887.
 DR PIR; C32248; C32248.
 DR PIR; C34904; C34904.
 DR PIR; D27887; D27887.
 DR PIR; D29380; D29380.
 DR PIR; E28833; E28833.
 DR PIR; F32530; F32530.
 DR PIR; H31485; H31485.
 DR PIR; PH0106; PH0106.
 DR PIR; PH1030; PH1030.
 DR PIR; PH1031; PH1031.
 DR PIR; PH1034; PH1034.
 DR PIR; PL0257; PL0257.
 DR PIR; PT0359; PT0359.
 DR PIR; S07455; S07455.
 DR PIR; S16112; S16112.
 DR PIR; S26334; S26334.
 DR PIR; S53750; S53750.
 DR PIR; S60066; S60066.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
 Query Match 60.5%; Score 49; DB 11; Length 238;
 Best Local Similarity 56.2%; Pred. No. 4.2;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 RSSKSLLYKDGKTYLN 16
 DB 43 RSSQSLVHNSNGTYLN 58

RESULT 8
 Q9JL82 PRELIMINARY; PRT; 104 AA.
 AC Q9JL82;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Anti-myosin immunoglobulin light chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=20448942; PubMed=10992488;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RA "T-Cell-dependent antibody response to the dominant epitope of
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 RT with cardiac myosin";
 RL Infect. Immun. 68:5803-5808 (2000).
 DR EMBL; AF206024; AAF69322.1; -;
 DR PIR; S26334; S26334.
 DR HSP; P01607; IREI.
 DR InterPro; IPR007110; Ig-LIKE.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR NON_TER 1
 FT NON TER 104 104
 FT SEQUENCE 104 AA; 11360 MW; 5DA8BBFDF5FOAALAE CRC64;
 SQ
 Query Match 59.3%; Score 48; DB 11; Length 104;
 Best Local Similarity 56.2%; Pred. No. 2.5;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 16 RSSQSLVHTNGNTYLH 31
 RESULT 9
 Q8KOF8 PRELIMINARY; PRT; 239 AA.
 AC Q8KOF8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC031498; AAH31498.1; -;
 DR PIR; A33933; A33933.
 DR PDB; 1KN2; 13-MAR-02.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002198; ADH_short.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-LIKE.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; IGV; 1.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;

Query Match 59.3%; Score 48; DB 11; Length 239;
 Best Local Similarity 56.2%; Pred. No. 6.1;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 44 KSSQSLFYNGKYYLS 59
 RESULT 10
 Q8VC55 PRELIMINARY; PRT; 239 AA.
 AC Q8VC55;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021781; AAR21781.1; -;
 DR PIR; A33933; A33933.
 DR PDB; 1KC5; 24-JUL-02.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR004214; Conotoxin.
 DR InterPro; IPR007110; Ig-LIKE.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF02950; Conotoxin; 1.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;
 Query Match 59.3%; Score 48; DB 11; Length 239;
 Best Local Similarity 62.5%; Pred. No. 6.1;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 44 KSTKSLNSDGFYLD 59
 RESULT 11
 O26451 PRELIMINARY; PRT; 1561 AA.
 ID O26451
 AC O26451;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Magnesium chelataase subunit.
 GN MR351.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.,
RT "Complete genome sequence of *Mechanobacterium thermoautotrophicum*
RT delCah: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155 (1997).
DR EMBL: AE000820; AAB84857.1; -.
DR PIR: C69145; C69145.
DR GO: GO:0003779; P:actin binding; IEA.
DR GO: GO:0009058; P:biogenesis; IEA.
DR InterPro: IPR001589; Actbind.actnin.
DR InterPro: IPR003672; CbN/Mg_chitase.
DR Pfam: PF02514; CbN-Mg_chel; 1.
DR PROSITE: PS00019; ACTININ_1; 1.
KW Complete proteome.
SQ SEQUENCE 1561 AA; 170574 MW; 764561FA31D719CE CRC64;

Query Match 59.3%; Score 48; DB 17; Length 1561;
Best Local Similarity 64.3%; Pred.No. 47;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0

QY 3 SKSLYKDGKTYLN 16
DQ 224 SRELLYRDGKLYDN 237
DQ :|||||
DQ :|||||

RESULT 12
Q99M37 PRELIMINARY; PRT; 238 AA.
ID 01-JUN-2001 (TrEMBLrel. 17, Created)
AC 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC02035; AAH02035.1; -.
DR PIR: A31807; A31807.
DR PIR: A32248; A32248.
DR PIR: B32248; B32248.
DR PIR: C32248; C32248.
DR PIR: F32530; F32530.
DR PIR: PH042; PH1042.
DR PIR: PH1043; PH1043.
DR PIR: PH1044; PH1044.
DR PIR: S07455; S07455.
DR PIR: S16112; S16112.
DR PIR: S24500; S24500.
DR PIR: S24501; S24501.
DR PIR: S24503; S24503.
DR PIR: S24504; S24504.
DR PIR: S24529; S24529.
DR PIR: S24532; S24532.
DR PIR: S24533; S24533.
DR PIR: S24535; S24535.
DR PIR: S24536; S24536.
DR PIR: S24538; S24538.
DR PDB: 1I91; 25-DEC-02.
DR PDB: 1LO2; 31-JUL-02.
DR PDB: 1LO4; 31-JUL-02.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; Ig; 1.

DR Pfam; PF02806; alpha-amylase_C; 1.
 DR Pfam; PF00686; CBM_20; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR ProDom; PD001568; CBD_4; 1.
 DR SMART; SM00642; Amy; 1.
 DR SMART; SM00632; Amy_C; 1.
 KW Complete proteome.
 SQ SEQUENCE 506 AA; 53868 MW; FCC92A3BED9D2DAE CRC64;
 Query Match 56.8%; Score 46; DB 16; Length 506;
 Best Local Similarity 57.1%; Pred. No. 30;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTY 14
 | : : : : :
 Db 306 RNGETLTYKDGATY 319
 | : : : : :
 RESULT 14
 ID P97179 PRELIMINARY; PRT; 573 AA.
 AC P97179;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Alpha-amylase.
 GN AMLB.
 OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1916;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yin X.H., Gagnat J., Gerbaud C., Guerinneau M., Virolle M.J.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z85949; CAB06622.1; -.
 DR EMBL; Z86113; CAB06815.1; -.
 DR HSSP; P29957; IAQM.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006048; Alpha_amyl_C.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR002044; CBD_4.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR Pfam; PF02806; alpha-amylase_C; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR ProDom; PD001568; CBD_4; 1.
 DR Pfam; PF00686; CBM_20; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR ProDom; PD001568; CBD_4; 1.
 DR SMART; SM00642; Amy; 1.
 DR SMART; SM00632; Amy_C; 1.
 SQ SEQUENCE 573 AA; 61214 MW; E474019661C9D6A2 CRC64;

Query Match 56.8%; Score 46; DB 2; Length 573;
 Best Local Similarity 57.1%; Pred. No. 34;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTY 14
 | : : : : :
 Db 306 RNGETLTYKDGATY 319
 | : : : : :
 RESULT 15
 ID O86876 PRELIMINARY; PRT; 574 AA.
 AC O86876;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Alpha-amylase.
 GN AML.

OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1916;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TK21;
 RA Isiegas C., Parro V., Mellado R.P.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y13601; CAA73926.1; -.
 DR HSSP; P29957; IAQM.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006048; Alpha_amyl_C.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR002044; CBD_4.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR Pfam; PF02806; alpha-amylase_C; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR ProDom; PD001568; CBD_4; 1.
 DR SMART; SM00642; Amy; 1.
 DR SMART; SM00632; Amy_C; 1.
 SQ SEQUENCE 574 AA; 61758 MW; A040AA1092C22270 CRC64;

Query Match 56.8%; Score 46; DB 2; Length 574;
 Best Local Similarity 57.1%; Pred. No. 35;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTY 14
 | : : : : :
 Db 306 RNGETLTYKDGATY 319
 | : : : : :
 Search completed: September 30, 2004, 05:59:22
 Job time : 57.5056 secs

| Result No. | Score | Query | | ID | Description |
|------------|-------|-------|--------|--------------|---------------------|
| | | Match | Length | | |
| 1 | 81 | 100.0 | 112 | 1 KV2A MOUSE | P01626 mus musculus |
| 2 | 81 | 100.0 | 113 | 1 KV2C MOUSE | P01628 mus musculus |
| 3 | 81 | 100.0 | 120 | 1 KV2B MOUSE | P01627 mus musculus |
| 4 | 64 | 79.0 | 133 | 1 KV2F HUMAN | P06310 homo sapien |
| 5 | 61 | 75.3 | 113 | 1 KV2B HUMAN | P01615 homo sapien |
| 6 | 55 | 67.9 | 113 | 1 KV2F MOUSE | P01630 mus musculus |
| 7 | 54 | 66.7 | 113 | 1 KV2G MOUSE | P01631 mus musculus |
| 8 | 53 | 65.4 | 113 | 1 KV2D HUMAN | P01617 homo sapien |
| 9 | 52 | 64.2 | 113 | 1 KV2E MOUSE | P03976 mus musculus |
| 10 | 46.5 | 57.4 | 115 | 1 KV2A HUMAN | P01614 homo sapien |
| 11 | 45 | 55.6 | 117 | 1 KV2E HUMAN | P06309 homo sapien |
| 12 | 43 | 53.1 | 137 | 1 ERR1 YEAST | P42222 saccharomyc |
| 13 | 42 | 51.9 | 343 | 1 Y535 METJA | Q57955 methanococc |
| 14 | 41 | 50.6 | 86 | 1 R31B VIBPA | Q87mc5 vibrio para |
| 15 | 41 | 50.6 | 89 | 1 R31B HAEDU | Q7vk9h haemophilus |
| 16 | 41 | 50.6 | 112 | 1 KV2D MOUSE | P01629 mus musculus |
| 17 | 41 | 50.6 | 891 | 1 ACON LGPN | P37032 legionella |
| 18 | 40 | 49.4 | 87 | 1 R31B RALSO | Q8Y062 raistonia s |
| 19 | 40 | 49.4 | 478 | 1 AMY STRHY | P08486 streptomyces |
| 20 | 40 | 49.4 | 481 | 1 6PGD DROME | P41572 drosophila |
| 21 | 40 | 49.4 | 489 | 1 TRPE SCHPO | O94582 schizosacch |
| 22 | 40 | 49.4 | 521 | 1 SYM URPBA | Q9Pqt6 ureaplasma |
| 23 | 40 | 49.4 | 713 | 1 ETM2 YABAM | Q9q84 yaba monkey |
| 24 | 39.5 | 48.8 | 134 | 1 KV4C HUMAN | P06314 homo sapien |
| 25 | 39 | 48.1 | 213 | 1 ZN80 CERA | P51502 cercopithec |
| 26 | 39 | 48.1 | 214 | 1 LBD7 ARATH | Q9asm9 arabidopsis |
| 27 | 39 | 48.1 | 293 | 1 ZN80 MACMU | P51505 macaca mula |
| 28 | 39 | 48.1 | 473 | 1 SABC BACSU | P05655 bacillus su |
| 29 | 39 | 48.1 | 478 | 1 NIFE METHH | Q27607 methanobact |
| 30 | 39 | 48.1 | 561 | 1 YBJL ECOLI | P75812 escherichia |
| 31 | 39 | 48.1 | 561 | 1 YBJL SALT1 | Q8z851 salmonella |
| 32 | 39 | 48.1 | 561 | 1 YBJL SALT2 | Q8zqk4 salmonella |
| 33 | 39 | 48.1 | 562 | 1 YD26 YERPE | Q8zchl1 versinia pe |

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-II region MOPC 511.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81052016; PubMed=6776396;
 RA Appella E.;
 RT "Amino acid sequence of the light chain variable region of M511, a
 RT phosphorylcholine-binding murine myeloma protein.";
 RL Mol. Immunol. 17:711-718(1980).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS PHOSPHORYLCHOLINE.
 PIR: A01910; KWS51.
 DR HSP; P80362; IWTL.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT SIGNAL 1 23
 FT CHAIN 24 39
 FT DOMAIN 24 39 FRAMEWORK-1.
 FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 FRAMEWORK-3.
 FT DOMAIN 62 93 FRAMEWORK-4.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12496 MW; EFBD0C4DA2B3450 CRC64;

 Query Match 100.0%; Score 81; DB 1; Length 113;
 Best Local Similarity 100.0%; Pred. No. 4.3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 RSSKSLLYKDGKTYLN 16
 DB 24 RSSKSLLYKDGKTYLN 39

 RESULT 3
 KV2B_MOUSE STANDARD; PRT; 120 AA.
 AC P01627;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-II region VKappa167 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82002223; PubMed=6791832;
 RA Selsing E.; Storb U.;
 RT "Somatic mutation of immunoglobulin light-chain variable-region
 RT genes";
 RL Cell 25:47-58(1981).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
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 EMBL; J00562; AAA39032.1; -;
 EMBL; K02415; AAA39051.1; -;

DR PIR: A01909; KWS67.
 DR HSP; P80362; IWTL.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 120
 FT DOMAIN 21 43 IG KAPPA CHAIN V-II REGION VKAPPA167.
 FT DOMAIN 44 59 FRAMEWORK-1.
 FT DOMAIN 60 74 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 75 81 FRAMEWORK-2.
 FT DOMAIN 82 113 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 114 120 FRAMEWORK-3.
 FT DISULFID 43 113
 FT NON_TER 120
 SQ SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;

 Query Match 100.0%; Score 81; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 4.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 RSSKSLLYKDGKTYLN 16
 DB 44 RSSKSLLYKDGKTYLN 59

 RESULT 4
 KV2F_HUMAN STANDARD; PRT; 133 AA.
 AC P06310;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-II region RPMI 6410 precursor.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041852; PubMed=2997711;
 RA Klobbeck H.G.; Meindl A.; Combrato G.; Solomon A.; Zachau H.G.;
 RT "Human immunoglobulin kappa light chain genes of subgroups II and
 RT III";
 RL Nucleic Acids Res. 13:6499-6513(1985).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
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 EMBL; Z00020; CAA77315.1; -;
 PIR: A01890; K2HURP.
 DR HSP; P80362; IWTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 60 74 FRAMEWORK-2.


```

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
DE OS Mus musculus (Mouse).
DE OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DE NCBI_TaxID=10090;
DE [1]
DE RN PIR; A01913; KWS78.
DE RP SEQUENCE.
DE RA MEDLINE=83256427; PubMed=6409088;
DE RX Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
DE "A new isotype sequence (V kappa 27) of the variable region of kappa-
DE RT light chains from a mouse hybridoma-derived anti-(streptococcal group-
DE RT A polysaccharide) antibody containing an additional cysteine residue.
DE RT Application of the dimethylaminobenzene isothiocyanate technique
DE RT for the isolation of peptides.";
DE RL Biochem. J. 211:173-180(1983).
DE CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
DE CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DE CC PIR; A01913; KWS78.
DE DR HSS2; P80362; 1WTL.
DE DR InterPro; IPR007110; Ig-like.
DE DR InterPro; IPR003596; Ig_V.
DE DR Pfam; PF00047; Ig_1.
DE DR SMART; SM00406; IGV; 1.
DE DR PROSITE; PS50835; IG LIKE; 1.
DE KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
DE FT DOMAIN 1 23 FRAMEWORK-1.
DE FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
DE FT DOMAIN 40 54 FRAMEWORK-2.
DE FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
DE FT DOMAIN 62 93 FRAMEWORK-3.
DE FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
DE FT DOMAIN 103 112 FRAMEWORK-4.
DE FT DISULFID 23 93 BY SIMILARITY.
DE FT NON_TER 113 113
DE SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 67.9%; Score 55; DB 1; Length 113;
Best Local Similarity 73.3%; Pred. No. 0.015;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps

QY 1 RSSKSLLYKGGKTYL 15
   |||||: : |||
Db 24 RSSKSLLSHGNTYL 38

RESULT 7
KV2G_MOUSE
ID KV2G_MOUSE STANDARD; PRT; 113 AA.
AC AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
DE OS Mus musculus (Mouse).
DE OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DE NCBI_TaxID=10090;
DE [1]
DE RN PIR; A01914; KWS26.
DE RP SEQUENCE.
DE RA STRAIN=A/J;
DE RX MEDLINE=83178921; PubMed=6404298;
DE RA Novotny J., Margolies M.N.;
DE RT "Amino acid sequence of the light chain variable region from a mouse
DE RT anti-digoxin hybridoma antibody.";
DE RL Biochemistry 22:1153-1158(1983).
DE CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
DE CC PROTEIN THAT BINDS DIGOXIN.
DE DR PIR; A01914; KWS26.
DE DR HSS2; P80362; 1WTL.
DE DR InterPro; IPR007110; Ig-like.

```

DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT DOMAIN 40 54
 FT DOMAIN 55 61
 FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12273 MW; P9F39CB949A84C2A CRC64;

Query Match 66.7%; Score 54; DB 1; Length 113;
 Best Local Similarity 62.5%; Pred. No. 0.022;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
 DB 24 RSSQSLVHSGNTYLN 39

RESULT 8
 KV2D HUMAN STANDARD; PRT; 113 AA.
 AC P01617;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region TEW.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (BENCE-JONES PROTEIN TEW).
 RX MEDLINE=74148480; PubMed=4596149;
 RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
 RT Amino acid sequence of a kappa Bence Jones protein from a case of
 RT primary amyloidosis.;
 RL Biochemistry 12:3763-3780(1973).
 RN [2]
 RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
 RX MEDLINE=73166638; PubMed=4700495;
 RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
 RA Glenner G.G.;
 RT Structural identity of Bence Jones and amyloid fibril proteins in a
 RT patient with plasma cell dyscrasia and amyloidosis.;
 RL J. Clin. Invest. 52:1276-1281(1973).
 CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
 CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
 CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
 CC PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 DR PIR; A90370; K2HTWT.
 DR HSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-Like.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT DOMAIN 40 54
 FT DOMAIN 55 61

FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;
 Query Match 65.4%; Score 53; DB 1; Length 113;
 Best Local Similarity 68.8%; Pred. No. 0.032;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
 DB 24 RSSQSLVHSGNTYLN 39

RESULT 9
 KV2E MOUSE STANDARD; PRT; 113 AA.
 AC P03976;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region 17S29.1.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85128968; PubMed=6441768;
 RA Aehersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
 RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57BL/6
 RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
 RT group A-streptococcal polysaccharide.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
 CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
 DR PIR; A01912; KVM517.
 DR HSP; P01607; IREI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT DOMAIN 40 54
 FT DOMAIN 55 61
 FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12390 MW; 4E93797048F8DB33 CRC64;

Query Match 64.2%; Score 52; DB 1; Length 113;
 Best Local Similarity 73.3%; Pred. No. 0.048;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 15
 DB 24 RSSKSLVHSGNTYLN 38

RESULT 10
 KV2A HUMAN STANDARD; PRT; 115 AA.
 AC P01614;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";
RL Type";
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; B16139; K2HUGM.
DR HSSP; P01407; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95 BY SIMILARITY.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 57.4%; Score 46.5; DB 1; Length 115;
Best Local Similarity 70.6%; Pred. No. 0.45; Mismatches 1; Gaps 1;
Matches 12; Conservative 1; Indels 3; Indels 1; Gaps 1;

OY 1 RSSKSLLYK-DGKTYLN 16
DB 25 RSSQSLSDSGDGTNTYL 41

RESULT 11
KV2E_HUMAN
ID KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain diversity.";
RL Nature 309:73-76(1984).
CC
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CC
CC EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR

DR PIR; A01889; K2HUGM.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117
FT DOMAIN 28 27 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 28 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 65 FRAMEWORK-2.
FT DOMAIN 66 97 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 98 106 FRAMEWORK-3.
FT DOMAIN 107 116 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 FRAMEWORK-4.
FT DISULFID 27 97 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 55.8%; Score 45; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 0.83; Mismatches 4; Indels 3; Indels 0; Gaps 0;
Matches 9; Conservative 4; Mismatches 4; Indels 3; Indels 0; Gaps 0;

OY 1 RSSKSLLYKDGKTYLN 16
DB 28 RSSQSLSHSGNYILD 43

RESULT 12
ERR1_YEAST
ID ERR1_YEAST STANDARD; PRT; 437 AA.
AC P42222;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Enolase related protein 1 (EC 4.2.1.11).
GN ERR1 OR YMR323W OR YMR924.15.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.";
RL Nature 387:90-93(1997).
RN [2]
RP SEQUENCE OF 120-437 FROM N.A.
RX STRAIN=S288C / YP1;
RX MEDLINE=95304851; PubMed=7785338;
RA Pryde F.E., Huckle T.C., Louis E.J.;
RT "Sequencing analysis of the right end of chromosome XV in Saccharomyces cerevisiae: an insight into the structural and functional significance of sub-telomeric repeat sequences.";
RL yeast 11:371-382(1995).
CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2O).
CC -!- SIMILARITY: Belongs to the enolase family.
CC
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CC -----
 CC EMBL; Z54141; CAA90841.1; -;
 CC EMBL; U23472; AAC48992.1; -;
 CC PIR; S69881; S69881.
 CC HSP; P00924; 4ENL.
 CC GERMOnline; 143981; -;
 CC SGD; S0005920; ERL1; -;
 CC InterPro; IPR000941; Enolase.
 CC Pfam; PF00113; enolase; 1.
 CC Pfam; PF03952; enolase_N; 1.
 CC PRINTS; PR00148; ENOLASE.
 CC ProDom; PD000902; Enolase; 1.
 CC TIGR; TIGR01060; eno; 1.
 CC PROSITE; PS00164; ENOLASE; 1.
 CC Lyase; Glycolysis; Magnesium.
 CC ACT_SITE 160 160
 CC FT METAL 247 247
 CC FT METAL 296 296
 CC FT METAL 321 321
 CC SEQUENCE 437 AA; 47312 MW; 143D6EF6FB03D13 CRC64;
 CC BY SIMILARITY.

Query Match 53.1%; Score 43; DB 1; Length 437;
 Best Local Similarity 60.0%; Pred. NO. 7.9;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 SKSKLLYKDGKTYLN 16
 | : : : : :
 Db 248 SAPSVFYKDGKTYLDN 262

RESULT 13
 Y535 METJA STANDARD; PRT; 343 AA.
 AC Q5795;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical protein MJ0535.
 GN MJ0535.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Cocayne J.D.,
 RA Kierlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weisscock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RL Science 273:1058-1073 (1996).

CC -!- FUNCTION: Putative deacetylase (By similarity).
 CC -!- SIMILARITY: Belongs to the histone deacetylase family.
 CC -----
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CC -----
 CC EMBL; U67502; AAB98526.1; -;
 CC PIR; G64366; G64366.
 CC TIGR; MJ0535; -;
 CC InterPro; IPR000286; His_deacetylase.
 CC Pfam; PF00850; Hist_deacetyl; 1.
 CC PRINTS; PR01270; HDASUPER.
 CC KW Hypothetical protein; Hydrolase; Complete proteome.
 CC SEQUENCE 343 AA; 38174 MW; 8848EDB757FDC233 CRC64;

Query Match 51.9%; Score 42; DB 1; Length 343;
 Best Local Similarity 59.2%; Pred. NO. 9;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 SKSKLLYKDGKTYL 15
 | : : : : :
 Db 73 SKSFNYVDGTYL 85

RESULT 14
 R31B VIBPA STANDARD; PRT; 86 AA.
 ID R31B VIBPA
 AC Q87MCS;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE S05 ribosomal protein L31 type B.
 GN RPE2 OR VP2331.
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=670;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RIMD 2210633 / Serotype O3:K6;
 RX MEDLINE=22508454; PubMed=12620739;
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
 RT distinct from that of V. cholerae.";
 RL Lancet 361:743-749 (2003).
 CC -!- SIMILARITY: Belongs to the L31P family of ribosomal proteins.
 CC Subfamily B.

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CC -----
 CC EMBL; AP005081; BAC60594.1; -;
 CC HAMAP; MF_00502; -; 1.
 CC InterPro; IPR002150; Ribosomal_L31.
 CC Pfam; PF01197; Ribosomal_L31; 1.
 CC PRINTS; PR01249; RIBOSOMALL31.
 CC PROSITE; PS01143; RIBOSOMAL_L31; 1.
 CC Ribosomal protein; Complete proteome.
 CC SEQUENCE 86 AA; 9995 MW; 59010EF3786573BF CRC64;

Query Match 50.6%; Score 41; DB 1; Length 86;
 Best Local Similarity 42.9%; Pred. NO. 2.9;
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTY 14
 | : : : : :
 Db 30 KTDRTIEWXDGKTY 43

RESULT 15
 R31B_HAEDU

R31B HAEDU STANDARD; PRT; 89 AA.
AC Q7VKH9;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 50S ribosomal protein L31 type B.
GN RME2 OR HD1927.
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3500HP / ATCC 700724;
RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RT "The complete genome sequence of Haemophilus ducreyi."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the L31P family of ribosomal proteins.
CC Subfamily B.
CC -----
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CC -----
CC EMBL; AB017156; AAP96649.1; -.
DR HAMAP; MF_00502; -; 1.
DR InterPro; IPR002150; Ribosomal_L31.
DR Pfam; PF01197; Ribosomal_L31; 1.
DR PROSITE; PS01143; RIBOSOMAL_L31; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 89 AA; 10187 MW; 4BF9B2435E60530F CRC64;

Query Match 50.6%; Score 41; DB 1; Length 89;
Best Local Similarity 46.2%; Pred. No. 3.1;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSKSLLYKDGKTY 14
Db ::||:::|||
32 TNKSMWEDGKEY 44

Search completed: September 30, 2004, 06:01:14
Job time : 11.7627 secs

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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 78.1017 seconds
(without alignments)
57.883 Million cell updates/sec

Title: US-09-674-716B-3
Perfect score: 81
Sequence: 1 RSSKSLYKDKTYLN 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|------------|--------------------|
| 1 | 81 | 100.0 | 16 | 3 AAY32254 | Aay32254 Light cha |
| 2 | 81 | 100.0 | 100 | 4 AAE06969 | Aae06969 Mouse ger |
| 3 | 81 | 100.0 | 116 | 3 AAY32262 | Aay32262 Humanised |
| 4 | 81 | 100.0 | 145 | 3 AAY32261 | Aay32261 Mouse ant |
| 5 | 77 | 95.1 | 16 | 2 AAW39818 | Aaw39818 Light cha |
| 6 | 77 | 95.1 | 113 | 2 AAW39882 | Aaw39882 Light cha |
| 7 | 77 | 95.1 | 113 | 2 AAW39804 | Aaw39804 Variable |
| 8 | 76 | 93.8 | 131 | 2 AAR12232 | Aar12232 Mouse MAb |
| 9 | 76 | 93.8 | 132 | 2 AAR12354 | Aar12354 Light (ka |
| 10 | 75 | 92.6 | 16 | 2 AAW39824 | Aaw39824 Light cha |
| 11 | 75 | 92.6 | 16 | 2 AAW39815 | Aaw39815 Light cha |
| 12 | 75 | 92.6 | 113 | 2 AAW39803 | Aaw39803 Variable |
| 13 | 75 | 92.6 | 113 | 2 AAW39886 | Aaw39886 Light cha |
| 14 | 75 | 92.6 | 113 | 2 AAW39802 | Aaw39802 Variable |
| 15 | 75 | 92.6 | 113 | 2 AAW39801 | Aaw39801 Variable |
| 16 | 69 | 85.2 | 16 | 2 AAW39875 | Aaw39875 Light cha |
| 17 | 69 | 85.2 | 16 | 2 AAW39839 | Aaw39839 Light cha |
| 18 | 69 | 85.2 | 113 | 2 AAW39897 | Aaw39897 Light cha |
| 19 | 69 | 85.2 | 114 | 2 AAW39805 | Aaw39805 Variable |
| 20 | 67 | 82.7 | 20 | 3 AAY70802 | Aay70802 Murine an |
| 21 | 67 | 82.7 | 122 | 3 AAY70790 | Aay70790 Murine an |
| 22 | 65 | 80.2 | 112 | 4 AAE06992 | Aae06992 Human kap |
| 23 | 64 | 79.0 | 91 | 6 ABR55905 | Abr55905 Human mab |
| 24 | 64 | 79.0 | 91 | 6 ABR55889 | Abr55889 Human mab |
| 25 | 64 | 79.0 | 93 | 3 AAY56670 | Aay56670 Partial p |

| | | | | | |
|----|----|------|-----|------------|---------------------|
| 26 | 64 | 79.0 | 100 | 4 AAE06960 | Aae06960 Mouse ger |
| 27 | 64 | 79.0 | 100 | 4 AAE06961 | Aae06961 Mouse ger |
| 28 | 64 | 79.0 | 100 | 6 AAE35907 | Aae35907 Human A17 |
| 29 | 64 | 79.0 | 100 | 6 ABO27142 | Abo27142 Human ger |
| 30 | 64 | 79.0 | 100 | 6 ABO27143 | Abo27143 Human ger |
| 31 | 64 | 79.0 | 103 | 7 ADC61021 | Adc61021 Human ant |
| 32 | 64 | 79.0 | 112 | 2 AAW53585 | Aaw53585 Light cha |
| 33 | 64 | 79.0 | 112 | 4 AAE07003 | Aae07003 Human kap |
| 34 | 64 | 79.0 | 112 | 4 AAE06993 | Aae06993 Human kap |
| 35 | 64 | 79.0 | 112 | 6 ABB99636 | Abb99636 2A2 monoc |
| 36 | 64 | 79.0 | 112 | 7 ADC61024 | Adc61024 Human ant |
| 37 | 64 | 79.0 | 112 | 7 ADC61023 | Adc61023 Human ant |
| 38 | 64 | 79.0 | 112 | 7 ADE13192 | Adel13192 HZVII 119 |
| 39 | 64 | 79.0 | 112 | 7 ADE13218 | Adel13218 Humanised |
| 40 | 64 | 79.0 | 113 | 2 AAR52057 | Aar52057 Light cha |
| 41 | 64 | 79.0 | 113 | 3 AAU76445 | Aau76445 Mouse mon |
| 42 | 64 | 79.0 | 113 | 3 AAB12170 | Aab12170 Mouse HBV |
| 43 | 64 | 79.0 | 113 | 3 AAB12171 | Aab12171 Humanised |
| 44 | 64 | 79.0 | 113 | 3 AAB12173 | Aab12173 Humanised |
| 45 | 64 | 79.0 | 132 | 2 AAY42306 | Aay42306 Human ant |

ALIGNMENTS

RESULT 1
AAY32254
ID AAY32254 standard; peptide; 16 AA.
XX
AC AAY32254;
XX
DT 15-FEB-2000 (first entry)
XX
DE Light chain CDR L1 of mouse anti-CD23 MAb C11.
XX
KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
KW therapy.
XX
OS Mus musculus.
XX
PN WO958679-A1.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WC-GB001434.
XX
PR 09-MAY-1998; 98GB-00009839.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Bonneyfey JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
XX
DR WPI: 2000-053101/04.
XX
DR N-PSDB; AA234739.
XX
PT Cell receptor specific antibodies useful for treating e.g. arthritis,
XX
PT diabetes, multiple sclerosis and psoriasis.
XX
PS Claim 1; Page 40; 81pp; English.
XX
CC This sequence represents complementarity determining region 1 (CDR L1)
CC of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11
CC (see also AAY32262). The invention provides altered antibodies, such as
CC chimeric or humanised antibodies, which comprise sufficient of the amino
CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble CD23
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
 CC are also useful for studying interactions between CD23 and various
 CC ligands and determining the binding agents
 XX
 XX Sequence 16 AA;
 SQ

Query Match 100.0%; Score 81; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
 |||||
 DB 1 RSSKSLLYKDGKTYLN 16
 |||||

RESULT 2
 AAEE06969
 ID AAE06969 standard; protein; 100 AA.
 AC AAE06969;
 DT 16-OCT-2001 (first entry)
 DE Mouse germline kappa light chain variable (VK) region, 167/24.
 KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherosclerosis; atherosclerosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
 KW inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; VK; kappa light chain variable region.
 OS Mus sp.
 XX WO200157226-A1.
 XX 09-AUG-2001.
 XX
 XX 02-FEB-2001; 2001WO-US003537.
 XX
 XX 03-FEB-2000; 2000US-00497625.
 XX (WILL-) MILLENNIUM PHARM INC.
 XX
 XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
 XX WPI; 2001-48888/53.
 XX
 XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
 PT disorder in a patient, comprises a binding specificity for CCR2, and a
 PT non-human antigen binding region and human immunoglobulin.
 XX
 XX Disclosure; Page 151; 183pp; English.
 XX
 XX The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
 CC comprising an antigen binding region of non-human origin and at least a
 CC portion of an immunoglobulin of human origin. The humanised antibodies
 CC are useful for inhibiting the interaction of a cell expressing CCR2. They
 CC are useful for inhibiting or treating HIV infection. The proteins of the
 CC invention are useful for inhibiting leukocyte trafficking, for treating

CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
 CC disorders such as rheumatoid arthritis and multiple sclerosis,
 CC atherosclerosis and atherosclerosis, and for inhibiting restenosis. They
 CC are useful in therapy or diagnosis, and in the manufacture of a
 CC medicament for treating CCR-2 mediated disease. They are also useful for
 CC treating allergy, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and IGE-mediated allergic reaction, shock,
 CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
 CC associated with vascular intervention, including angioplasty and/or stent
 CC placement in a mammal. Humanised antibodies are also useful for
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated
 CC with vascular intervention. The present sequence is mouse germline kappa
 CC light chain variable (VK) region, 167/24
 XX
 XX Sequence 100 AA;
 SQ

Query Match 100.0%; Score 81; DB 4; Length 100;
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
 |||||
 DB 24 RSSKSLLYKDGKTYLN 39
 |||||

RESULT 3
 AAY32262
 ID AAY32262 standard; protein; 116 AA.
 XX
 AC AAY32262;
 XX
 DT 15-FEB-2000 (first entry)
 DE Humanised anti-CD23 MAb C11 light chain variable region.
 KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Region 1..23
 XX /note= "framework region 1"
 XX Region 24..39
 XX /note= "CDR 1"
 XX Region 40..54
 XX /note= "framework region 2"
 XX Region 55..61
 XX /note= "CDR 2"
 XX Region 62..93
 XX /note= "framework region 3"
 XX Region 94..102
 XX /note= "CDR 3"
 XX Region 103..113
 XX /note= "framework region 4"
 XX
 XX WO9958679-A1.
 XX
 XX 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-GB001434.
 XX

PR 09-MAY-1998; 98GB-00009839.
 XX (GLAX) GLAXO GROUP LTD.
 XX Bonneyfey JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPI; 2000-053101/04.
 DR N-PSDB; AA234747.
 XX
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis.
 XX
 PS Claim 9; Fig 3; 81pp; English.
 XX
 CC This sequence represents the light chain variable region (VL) of
 CC humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human
 CC framework (HSGKVI) and the light chain complementarity determining
 CC regions (see AAY32254-56) of murine antibody C11. The DNA was constructed
 CC by splice overlap PCR. The invention provides altered antibodies, such as
 CC chimeric or humanised antibodies, which comprise sufficient of the amino
 CC acid sequences of the C11 light and heavy chain complementarity
 CC determining regions to render them capable of binding to the CD23 type II
 CC molecule expressed on haematopoietic cells. The antibodies are used to
 CC block soluble CD23 formation in human therapy, for the treatment of
 CC arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX
 SQ Sequence 116 AA;
 Query Match 100.0%; Score 81; DB 3; Length 116;
 Best Local Similarity 100.0%; Pred. No. 7.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 24 RSSKSLLYKDGKTYLN 39
 RESULT 4
 AAY32261
 ID AAY32261 standard; protein; 145 AA.
 XX
 AC AAY32261;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Mouse anti-CD23 MAB C11 light chain variable region.
 XX
 KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
 XX monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.
 XX
 OS Mus musculus.
 XX
 XX Key Location/Qualifiers
 FH 55..70
 Region /note= "CDR L1"
 FT 83..92
 Region /note= "CDR L2"
 FT

FT Region 125..134
 /note= "CDR L3"
 XX
 XX WO9958679-A1.
 XX
 XX 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-GB001434.
 XX
 XX 09-MAY-1998; 98GB-00009839.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 XX
 XX Bonneyfey JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 PI WPI; 2000-053101/04.
 XX N-PSDB; AA234746.
 XX
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis.
 XX
 PS Claim 8; Fig 2; 81pp; English.
 XX
 CC This sequence represents the light chain variable region (VL) of murine
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies (see
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid
 CC sequences of the C11 light and heavy chain complementarity determining
 CC regions (see AAY32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies are
 CC used to block soluble CD23 formation in human therapy, for the treatment
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX
 SQ Sequence 145 AA;
 Query Match 100.0%; Score 81; DB 3; Length 145;
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 55 RSSKSLLYKDGKTYLN 70
 RESULT 5
 AAW39818
 ID AAW39818 standard; peptide; 16 AA.
 XX
 AC AAW39818;
 XX
 XX 16-JUN-1998 (first entry)
 DT
 XX Light chain CDR1 of catalytic antibody 6A12.
 DE
 XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX
 XX WO9749800-A1.
 XX
 XX 31-DEC-1997.
 XX

CC treatment of an overdose. They are also used for treating addiction (by
 CC reducing the in vivo concentration that can be achieved)
 XX
 SQ Sequence 113 AA;
 Query Match 95.1%; Score 77; DB 2; Length 113;
 Best Local Similarity 93.8%; Pred. No. 3.5e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 24 RSSKSLLYKDGKTYLN 39
 RESULT 8
 AAR123232
 ID AAR12232 standard; protein; 131 AA.
 XX AC
 XX AAR12232;
 XX 25-MAR-2003 (revised)
 DT 19-AUG-1991 (first entry)
 XX
 XX Mouse MAb 2E12 L chain V region.
 DE HIV-1; chimera.
 XX
 XX Mus sp.
 OS
 XX WO9107494-A.
 PN 30-MAY-1991.
 PD 13-NOV-1989; 89US-00433703.
 PF 13-NOV-1989; 89US-00433703.
 PR 13-NOV-1989; 89US-00433703.
 XX (XOMA) XOMA CORP.
 PA (GREG) GREEN CROSS CORP.
 PA (ZOMA-) ZOMA CORP.
 XX Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
 PI WPI; 1991-178106/24.
 XX N-PSDB; AAQ12012.
 DR New chimeric mouse human antibodies - used in treatment, diagnosis and
 XX prophylaxis of HIV infections.
 PT Disclosure; Fig 1; 108pp; English.
 PS The mouse VL gene product may be used to produce chimeric mouse- human
 CC Abs against HIV-1 comprising human Ig constant regions and murine
 CC variable regions. These novel sequence are useful in treatment, diagnosis
 CC and prophylaxis of HIV infections, and may be produced by a bacterial,
 CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 131 AA;
 Query Match 93.8%; Score 76; DB 2; Length 131;
 Best Local Similarity 93.8%; Pred. No. 6.1e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 44 RSSKSLLYKDGKTYLS 59
 RESULT 9
 AAR12354
 ID AAR12354 standard; protein; 132 AA.
 XX

AAR12354;
 AC 25-MAR-2003 (revised)
 DT 15-AUG-1991 (first entry)
 XX Light (kappa) chain variable region of murine 2E12 immunoglobulin.
 XX Chimeric antibodies; immunoconjugates; HIV; AIDS.
 KW Mus musculus.
 OS WO9107493-A.
 PN 30-MAY-1991.
 PD 13-NOV-1989; 89US-00433730.
 PF 13-NOV-1989; 89US-00433730.
 PR (XOMA) XOMA CORP.
 XX (GREG) GREEN CROSS CORP.
 PA Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
 PI WPI; 1991-178105/24.
 XX N-PSDB; AAQ12056.
 DR New chimeric mouse-human antibodies - used to detect, kill and remove HIV
 XX -1 antigen from sample.
 PT Disclosure; Fig 1; 107pp; English.
 PS This is the light (kappa)- chain variable (V) region of a mouse
 CC monoclonal antibody (MAB), 2E12, and is specific for an HIV-1 viral
 CC antigen. It is used in the construction of a chimeric MAB comprising
 CC heavy and light chains having murine V regions and human C regions. The
 CC chimeric MABs are more effective than murine MAB 2E12 since they have an
 CC increased compatibility in humans. The heavy and light chain V-regions
 CC are joined by manipulating their respective joining (J) regions, to
 CC generate restriction enzyme recognition sites. The chimeric MABs can be
 CC used as immuno- conjugates, in association with e.g. toxins for HIV
 CC treatment. They can also be used in diagnosis of HIV. See also AAQ12057-
 CC 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003
 CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 132 AA;
 Query Match 93.8%; Score 76; DB 2; Length 132;
 Best Local Similarity 93.8%; Pred. No. 6.1e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 44 RSSKSLLYKDGKTYLS 59
 RESULT 10
 AAR39824
 ID AAR39824 standard; peptide; 16 AA.
 XX AC
 XX AAR39824;
 DT 16-JUN-1998 (first entry)
 XX Light chain CDR1 of catalytic antibody 12H1.
 DE Variable domain; lambda light chain; catalytic antibody; degradation;
 XX cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX Mus sp.
 OS
 XX

PN WO9749800-A1.
 PD 31-DEC-1997.
 XX
 PF 25-JUN-1997; 97WO-US010965.
 XX
 PR 25-JUN-1996; 96US-00672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX
 DR WPI; 1998-077166/07.
 XX
 PF New catalytic antibodies able to decompose cocaine, single-chain
 XX analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 PS Claim 17; Page 83; 147pp; English.
 XX
 CC AAW39824-26 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 12H1, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified
 CC using TSA2, and has a per minute Kcat of 0.16. The antibodies reduce the
 CC concentration of cocaine in a subject, and are used particularly for the
 CC treatment of an overdose. They are also used for treating addiction (by
 CC reducing the in vivo concentration that can be achieved)
 XX
 SQ Sequence 16 AA;
 XX
 Query Match 92.6%; Score 75; DB 2; Length 16;
 Best Local Similarity 87.5%; Pred. No. 8.5e-06;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 RSSKSLLYKDGKTYLN 16
 |||:||||:|||||
 DB 1 RSSRSLLYRDGKTYLN 16
 |||:||||:|||||
 RESULT 11
 AAW39815
 ID AAW39815 standard; peptide; 16 AA.
 XX
 AC AAW39815;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE Light chain CDR1 of catalytic antibody 3B9.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 XX cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 XX overdose; addiction.
 XX
 OS Mus sp.
 XX
 PN WO9749800-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 25-JUN-1997; 97WO-US010965.
 XX
 PR 25-JUN-1996; 96US-00672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX
 DR WPI; 1998-077166/07.
 XX
 PF New catalytic antibodies able to decompose cocaine, single-chain
 XX analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 PS Claim 18; Page 73; 147pp; English.
 XX
 CC AAW39801-05 represent the amino acid sequences of the variable domain of
 CC the kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-

PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 XX Claim 11; Page 80; 147pp; English.
 XX
 CC AAW39815-17 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
 CC transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11.
 CC The antibodies reduce the concentration of cocaine in a subject, and are
 CC used particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can be
 CC achieved)
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 92.6%; Score 75; DB 2; Length 16;
 Best Local Similarity 87.5%; Pred. No. 8.5e-06;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 RSSKSLLYKDGKTYLN 16
 |||:||||:|||||
 DB 1 RSSRSLLYRDGKTYLN 16
 |||:||||:|||||
 RESULT 12
 AAW39803
 ID AAW39803 standard; protein; 113 AA.
 XX
 AC AAW39803;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE Variable domain of the kappa light chain of catalytic antibody 12H1.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX
 PN WO9749800-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 25-JUN-1997; 97WO-US010965.
 XX
 PR 25-JUN-1996; 96US-00672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX
 DR WPI; 1998-077166/07.
 XX
 DR P-PSDB; AAW09802.
 XX
 PF New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 XX Claim 18; Page 73; 147pp; English.
 PS
 CC AAW39801-05 represent the amino acid sequences of the variable domain of
 CC the kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-

CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808
 CC represents the heavy chain) was identified using TSA2, and has a per
 CC minute Kcat of 0.016. The antibodies reduce the concentration of cocaine
 CC in a subject, and are used particularly for the treatment of an overdose.
 CC They are also used for treating addiction (by reducing the in vivo
 CC concentration that can be achieved)
 CC
 XX Sequence 113 AA;
 SQ

Query Match 92.6%; Score 75; DB 2; Length 113;
 Best Local Similarity 87.5%; Pred. No. 7.6e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSSKSLLYKDGKTYLN 16
 |||||:|||||
 Db 24 RSSRSLLYRDGKTYLN 39
 |||||:|||||

RESULT 13
 AAW39886
 ID AAW39886 standard; protein; 113 AA.
 XX
 AC AAW39886;
 XX
 DT 18-JUN-1998 (first entry)
 DE Light chain of the catalytic antibody 6A12.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX
 PN WO9749800-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 25-JUN-1997; 97WO-US010965.
 XX
 PR 25-JUN-1996; 96US-00672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX
 DR WPI; 1998-077166/07.
 XX
 PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 PS Disclosure; Fig 19; 147pp; English.
 XX
 CC The present sequence represents the light chain of a catalytic antibody
 CC which is capable of degrading cocaine. A series of cocaine transition
 CC state analogues (TSAs) were prepared and used to immunise mice for
 CC production of hybridomas. Catalytic antibodies were identified by their
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
 CC antibodies reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved)
 CC
 XX Sequence 113 AA;
 SQ

Query Match 92.6%; Score 75; DB 2; Length 113;
 Best Local Similarity 87.5%; Pred. No. 7.6e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSSKSLLYKDGKTYLN 16
 |||||:|||||

Db 24 RSSRSLLYRDGKTYLN 39
 |||||:|||||

RESULT 14
 AAW39802
 ID AAW39802 standard; protein; 113 AA.
 XX
 AC AAW39802;
 XX
 DT 16-JUN-1998 (first entry)
 DE Variable domain of the Kappa light chain of catalytic antibody 6A12.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX
 PN WO9749800-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 25-JUN-1997; 97WO-US010965.
 XX
 PR 25-JUN-1996; 96US-00672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX
 DR WPI; 1998-077166/07.
 XX
 PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 PS Claim 14; Page 72; 147pp; English.
 XX
 CC AAW39801-05 represent the amino acid sequences of the variable domain of
 CC the Kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 6A12 antibody (AAW39807
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state analogue.
 CC Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the
 CC concentration of cocaine in a subject, and are used particularly for the
 CC treatment of an overdose. They are also used for treating addiction (by
 CC reducing the in vivo concentration that can be achieved)
 CC
 XX Sequence 113 AA;
 SQ

Query Match 92.6%; Score 75; DB 2; Length 113;
 Best Local Similarity 87.5%; Pred. No. 7.6e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSSKSLLYKDGKTYLN 16
 |||||:|||||
 Db 24 RSSRSLLYRDGKTYLN 39
 |||||:|||||

RESULT 15
 AAW39801
 ID AAW39801 standard; protein; 113 AA.
 XX
 AC AAW39801;
 XX
 DT 16-JUN-1998 (first entry)
 DE

| | |
|----|---|
| DE | Variable domain of the Kappa light chain of catalytic antibody 399. |
| XX | |
| XX | Variable domain; lambda light chain; catalytic antibody; degradation; |
| KW | cocaine; cocaine transition state analogue; TSA; benzoic acid; |
| KW | phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; |
| KW | overdose; addiction. |
| XX | |
| OS | Mus sp. |
| XX | |
| XX | WO9749800-A1. |
| FN | |
| XX | |
| PD | 31-DEC-1997. |
| XX | |
| PF | 25-JUN-1997; 97WO-US010965. |
| XX | |
| XX | 25-JUN-1996; 96US-00672345. |
| PR | |
| XX | (UYCO) UNIV COLUMBIA NEW YORK. |
| XX | |
| PA | Landry DW; |
| XX | |
| PI | WPI: 1998-077166/07. |
| XX | |
| DR | P-PSDB; AA09791. |
| DR | |
| XX | |
| XX | New catalytic antibodies able to decompose cocaine, single-chain |
| PT | analogues - used to treat cocaine overdose and addiction, required in far |
| PT | smaller doses than antibodies that antagonise cocaine by simply binding. |
| XX | |
| PS | Claim 12; Page 71-72; 147pp; English. |
| XX | |
| CC | AAW39801-05 represent the amino acid sequences of the variable domain of |
| CC | the Kappa light chain of catalytic antibodies which are able to degrade |
| CC | cocaine. A series of cocaine transition state analogues (TSAs) were |
| CC | prepared and used to immunise mice for production of hybridomas. |
| CC | Catalytic antibodies were identified by their capacity to release 3H- |
| CC | benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806 |
| CC | represents the heavy chain) was identified using TSA1, which is an |
| CC | immunogenic conjugate of a phosphate monoester transition state analogue. |
| CC | Antibody 399 has a per minute Kcat of 0.11. The antibodies reduce the |
| CC | concentration of cocaine in a subject, and are used particularly for the |
| CC | treatment of an overdose. They are also used for treating addiction (by |
| CC | reducing the in vivo concentration that can be achieved) |
| XX | |
| XX | Sequence 113 AA; |
| XX | |
| SQ | |

Query Match 92.6%; Score 75; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 7.6e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 R S S K S L L Y K D G K T Y L N 16
|||:||||:|||||
Db 24 R S S R S L L Y R D G K T Y L N 39

Search completed: September 30, 2004, 06:06:09
Job time : 80.1017 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2004, 06:01:30 ; Search time 268.475 Seconds
(without alignments)
19.178 Million cell updates/sec

Title: US-09-674-716B-3

Perfect score: 81
Sequence: 1 RSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*
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- 10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*
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- 13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 81 | 100.0 | 100 | 9 | US-09-840-459-32 |
| 2 | 81 | 100.0 | 100 | 16 | US-10-766-773-32 |
| 3 | 81 | 100.0 | 100 | 16 | US-10-766-610-32 |
| 4 | 81 | 100.0 | 100 | 16 | US-10-733-563-32 |
| 5 | 77 | 95.1 | 16 | 10 | US-09-940-727B-22 |
| 6 | 77 | 95.1 | 16 | 10 | US-09-940-727B-25 |
| 7 | 77 | 95.1 | 113 | 10 | US-09-940-727B-8 |
| 8 | 77 | 95.1 | 113 | 10 | US-09-940-727B-108 |
| 9 | 75 | 92.6 | 16 | 10 | US-09-940-727B-19 |
| 10 | 75 | 92.6 | 16 | 10 | US-09-940-727B-23 |
| 11 | 75 | 92.6 | 113 | 10 | US-09-940-727B-5 |
| 12 | 75 | 92.6 | 113 | 10 | US-09-940-727B-6 |
| 13 | 75 | 92.6 | 113 | 10 | US-09-940-727B-7 |
| 14 | 75 | 92.6 | 113 | 10 | US-09-940-727B-100 |
| 15 | 75 | 92.6 | 113 | 10 | US-09-940-727B-104 |

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|----|----|------|-----|----|--------------------|-------------------|
| 16 | 75 | 92.6 | 113 | 10 | US-09-940-727B-112 | Sequence 112, App |
| 17 | 75 | 92.6 | 280 | 10 | US-09-940-727B-119 | Sequence 119, App |
| 18 | 69 | 85.2 | 16 | 10 | US-09-940-727B-43 | Sequence 43, App |
| 19 | 69 | 85.2 | 16 | 10 | US-09-940-727B-79 | Sequence 79, App |
| 20 | 69 | 85.2 | 113 | 10 | US-09-940-727B-116 | Sequence 116, App |
| 21 | 69 | 85.2 | 114 | 10 | US-09-940-727B-9 | Sequence 9, Appl |
| 22 | 65 | 80.2 | 112 | 9 | US-09-840-459-55 | Sequence 55, Appl |
| 23 | 65 | 80.2 | 112 | 16 | US-10-766-773-55 | Sequence 55, Appl |
| 24 | 65 | 80.2 | 112 | 16 | US-10-766-610-55 | Sequence 55, Appl |
| 25 | 65 | 80.2 | 112 | 16 | US-10-733-563-55 | Sequence 55, Appl |
| 26 | 64 | 79.0 | 93 | 9 | US-09-905-243-61 | Sequence 61, Appl |
| 27 | 64 | 79.0 | 100 | 9 | US-09-840-459-23 | Sequence 23, Appl |
| 28 | 64 | 79.0 | 100 | 9 | US-09-840-459-24 | Sequence 24, Appl |
| 29 | 64 | 79.0 | 100 | 12 | US-10-453-698-22 | Sequence 22, Appl |
| 30 | 64 | 79.0 | 100 | 12 | US-10-453-698-23 | Sequence 23, Appl |
| 31 | 64 | 79.0 | 100 | 14 | US-10-194-975-75 | Sequence 75, Appl |
| 32 | 64 | 79.0 | 100 | 14 | US-10-194-975-76 | Sequence 76, Appl |
| 33 | 64 | 79.0 | 100 | 14 | US-10-153-382-36 | Sequence 36, Appl |
| 34 | 64 | 79.0 | 100 | 15 | US-10-308-817-22 | Sequence 22, Appl |
| 35 | 64 | 79.0 | 100 | 15 | US-10-308-817-23 | Sequence 23, Appl |
| 36 | 64 | 79.0 | 100 | 16 | US-10-379-392-87 | Sequence 87, Appl |
| 37 | 64 | 79.0 | 100 | 16 | US-10-379-392-88 | Sequence 88, Appl |
| 38 | 64 | 79.0 | 100 | 16 | US-10-766-773-23 | Sequence 23, Appl |
| 39 | 64 | 79.0 | 100 | 16 | US-10-766-773-24 | Sequence 24, Appl |
| 40 | 64 | 79.0 | 100 | 16 | US-10-766-610-23 | Sequence 23, Appl |
| 41 | 64 | 79.0 | 100 | 16 | US-10-766-610-24 | Sequence 24, Appl |
| 42 | 64 | 79.0 | 100 | 16 | US-10-733-563-23 | Sequence 23, Appl |
| 43 | 64 | 79.0 | 100 | 16 | US-10-733-563-24 | Sequence 24, Appl |
| 44 | 64 | 79.0 | 103 | 15 | US-10-309-764-48 | Sequence 48, Appl |
| 45 | 64 | 79.0 | 112 | 9 | US-09-840-459-56 | Sequence 56, Appl |

ALIGNMENTS

RESULT 1
US-09-840-459-32
; Sequence 32, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-32

Query Match 100.0%; Score 81; DB 9; Length 100;

Best Local Similarity 100.0%; Pred. No. 3.2e-06; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSKSLLYKDGKTYLN 16
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Db      24 RSSKSLLYKDGKTYLN 39

RESULT 2
US-10-766-773-32
; Sequence 32, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10766,773
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-773-32

Query Match      100.0%; Score 81; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSKSLLYKDGKTYLN 16
      |||||
Db      24 RSSKSLLYKDGKTYLN 39

RESULT 3
US-10-766-610-32
; Sequence 32, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10766,610
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-610-32

Query Match      100.0%; Score 81; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      24 RSSKSLLYKDGKTYLN 39

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US-10-733-563-32
; Sequence 32, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10733,563
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-733-563-32

Query Match      100.0%; Score 81; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSSKSLLYKDGKTYLN 16
      |||||
Db      24 RSSKSLLYKDGKTYLN 39

RESULT 5
US-09-940-727B-22
; Sequence 22, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 16
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-22

Query Match      95.1%; Score 77; DB 10; Length 16;
Best Local Similarity 93.8%; Pred. No. 2e-06;
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Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RSSKSLLYEDGKTYLN 16

RESULT 6

US-09-940-727B-25
; Sequence 25, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-25.

Query Match 95.1%; Score 77; DB 10; Length 16;
Best Local Similarity 93.8%; Pred. No. 2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16
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Db 1 RSSKSLLYEDGKTYLN 16

RESULT 7

US-09-940-727B-8
; Sequence 8, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
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; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-8

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Best Local Similarity 93.8%; Pred. No. 1.8e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16
|||||:|||||
Db 24 RSSKSLLYEDGKTYLN 39

RESULT 8

US-09-940-727B-108
; Sequence 108, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-108

Query Match 95.1%; Score 77; DB 10; Length 113;
Best Local Similarity 93.8%; Pred. No. 1.8e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16
|||||:|||||
Db 24 RSSKSLLYEDGKTYLN 39

RESULT 9

US-09-940-727B-19
; Sequence 19, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 16
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-19

Query Match 92.6%; Score 75; DB 10; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.3e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16
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Db 1 RSSRSLLYEDGKTYLN 16

RESULT 10

US-09-940-727B-28
; Sequence 28, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 16
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-28

Query Match 92.6%; Score 75; DB 10; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.3e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 11

US-09-940-727B-5
; Sequence 5, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-5

Query Match 92.6%; Score 75; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 4.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 12

US-09-940-727B-6
; Sequence 6, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25

; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-6

Query Match 92.6%; Score 75; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 4.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 13

US-09-940-727B-7
; Sequence 7, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-7

Query Match 92.6%; Score 75; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 4.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 14

US-09-940-727B-100
; Sequence 100, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 113
; TYPE: PRT

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; ORGANISM: mouse
US-09-940-727B-100

Query Match          92.6%; Score 75; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 4.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
   |||:|||||:|||||
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 15
US-09-940-727B-104
; Sequence 104, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-104

Query Match          92.6%; Score 75; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 4.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
   |||:|||||:|||||
Db 24 RSSRSLLYRDGKTYLN 39
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Search completed: September 30, 2004, 06:54:51
Job time : 268.475 secs

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Sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2004, 06:00:45 ; Search time 27.1186 Seconds
(without alignments)
30.459 Million cell updates/sec

Title: US-09-674-716B-3

Perfect score: 81

Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----|--------------------|
| 1 | 77 | 95.1 | 16 | 2 | US-08-672-345C-22 |
| 2 | 77 | 95.1 | 16 | 2 | US-08-672-345C-25 |
| 3 | 77 | 95.1 | 16 | 3 | US-09-214-095D-22 |
| 4 | 77 | 95.1 | 16 | 3 | US-09-214-095D-25 |
| 5 | 77 | 95.1 | 113 | 2 | US-08-672-345C-8 |
| 6 | 77 | 95.1 | 113 | 2 | US-08-672-345C-98 |
| 7 | 77 | 95.1 | 113 | 3 | US-09-214-095D-8 |
| 8 | 77 | 95.1 | 113 | 3 | US-09-214-095D-108 |
| 9 | 75 | 92.6 | 16 | 2 | US-08-672-345C-19 |
| 10 | 75 | 92.6 | 16 | 2 | US-08-672-345C-28 |
| 11 | 75 | 92.6 | 16 | 3 | US-09-214-095D-19 |
| 12 | 75 | 92.6 | 16 | 3 | US-09-214-095D-28 |
| 13 | 75 | 92.6 | 113 | 2 | US-08-672-345C-5 |
| 14 | 75 | 92.6 | 113 | 2 | US-08-672-345C-6 |
| 15 | 75 | 92.6 | 113 | 2 | US-08-672-345C-7 |
| 16 | 75 | 92.6 | 113 | 2 | US-08-672-345C-95 |
| 17 | 75 | 92.6 | 113 | 2 | US-08-672-345C-96 |
| 18 | 75 | 92.6 | 113 | 2 | US-08-672-345C-97 |
| 19 | 75 | 92.6 | 113 | 3 | US-09-214-095D-5 |
| 20 | 75 | 92.6 | 113 | 3 | US-09-214-095D-6 |
| 21 | 75 | 92.6 | 113 | 3 | US-09-214-095D-7 |
| 22 | 75 | 92.6 | 113 | 3 | US-09-214-095D-100 |
| 23 | 75 | 92.6 | 113 | 3 | US-09-214-095D-104 |
| 24 | 75 | 92.6 | 113 | 3 | US-09-214-095D-112 |
| 25 | 75 | 92.6 | 280 | 3 | US-09-214-095D-119 |
| 26 | 69 | 85.2 | 16 | 2 | US-08-672-345C-43 |
| 27 | 69 | 85.2 | 16 | 2 | US-08-672-345C-79 |

28 69 85.2 16 3 US-09-214-095D-43 Sequence 43, Appl
29 69 85.2 16 3 US-09-214-095D-79 Sequence 79, Appl
30 69 85.2 113 3 US-09-214-095D-116 Sequence 116, Appl
31 69 85.2 114 2 US-08-672-345C-9 Sequence 9, Appl
32 69 85.2 114 3 US-09-214-095D-9 Sequence 9, Appl
33 69 85.2 115 2 US-08-672-345C-99 Sequence 99, Appl
34 64 79.0 100 4 US-09-472-087-113 Sequence 113, Appl
35 64 79.0 112 1 US-07-942-245-28 Sequence 28, Appl
36 64 79.0 139 4 US-09-472-087-25 Sequence 25, Appl
37 64 79.0 139 4 US-09-472-087-114 Sequence 114, Appl
38 64 79.0 222 4 US-09-479-614-26 Sequence 26, Appl
39 64 79.0 242 4 US-09-479-614-26 Sequence 20, Appl
40 59 72.8 111 4 US-09-809-739-13 Sequence 13, Appl
41 59 72.8 112 1 US-08-477-877B-89 Sequence 89, Appl
42 59 72.8 112 2 US-08-472-281A-89 Sequence 89, Appl
43 59 72.8 112 2 US-08-678-194-6 Sequence 6, Appl
44 59 72.8 112 2 US-08-477-989B-89 Sequence 89, Appl
45 59 72.8 112 3 US-08-890-011-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-672-345C-22
; Sequence 22, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-22

Query Match 95.1%; Score 77; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2e-06;
Matches 15; Conservative 1; Mismatches 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16

Db 1 RSSKSLLYKDGKTYLN 16

RESULT 2

US-08-672-345C-25
; Sequence 25, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-672-345C-25

Query Match 95.1%; Score 77; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16
| | | | | | | | | | | | | | | |
DB 1 RSSKSLLYEDGKTYLN 16

RESULT 3
US-09-214-095D-22
; Sequence 22, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-22

Query Match 95.1%; Score 77; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16
| | | | | | | | | | | | | | | |
DB 1 RSSKSLLYEDGKTYLN 16

RESULT 4
US-09-214-095D-25
; Sequence 25, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-25

Query Match 95.1%; Score 77; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16
| | | | | | | | | | | | | | | |
DB 1 RSSKSLLYEDGKTYLN 16

RESULT 5
US-08-672-345C-8
; Sequence 8, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/672,345C
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-672-345C-8

Query Match 95.1%; Score 77; DB 2; Length 113;
Best Local Similarity 93.8%; Pred. No. 1.5e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
 Db 24 RSSKSLLYEDGKTYLN 39

RESULT 6
 US-08-672-345C-98
 ; Sequence 98, Application US/08672345C
 ; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper and Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 98:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 113 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-672-345C-98

Query Match 95.1%; Score 77; DB 2; Length 113;
 Best Local Similarity 93.8%; Pred. No. 1.5e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
 Db 24 RSSKSLLYEDGKTYLN 39

RESULT 7
 US-09-214-095D-8
 ; Sequence 8, Application US/09214095D
 ; Patent No. 6280987
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 51400-A-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/214,095D
 ; CURRENT FILING DATE: 1999-07-19
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 113
 ; TYPE: PRT
 ; ORGANISM: Murinae gen. sp.
 ; US-09-214-095D-8

Query Match 95.1%; Score 77; DB 3; Length 113;

Best Local Similarity 93.8%; Pred. No. 1.5e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
 Db 24 RSSKSLLYEDGKTYLN 39

RESULT 8
 US-09-214-095D-108
 ; Sequence 108, Application US/09214095D
 ; Patent No. 6280987
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 51400-A-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/214,095D
 ; CURRENT FILING DATE: 1999-07-19
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 108
 ; LENGTH: 113
 ; TYPE: PRT
 ; ORGANISM: Murine
 ; US-09-214-095D-108

Query Match 95.1%; Score 77; DB 3; Length 113;
 Best Local Similarity 93.8%; Pred. No. 1.5e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
 Db 24 RSSKSLLYEDGKTYLN 39

RESULT 9
 US-08-672-345C-19
 ; Sequence 19, Application US/08672345C
 ; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper and Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

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US-08-672-345C-19
Query Match          92.6%; Score 75; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16
    |||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16
    |||:||||:|||||

RESULT 10
US-08-672-345C-28
; Sequence 28, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-278-0400
; INFORMATION FOR SEQ ID NO: 28:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-28

Query Match          92.6%; Score 75; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16
    |||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16
    |||:||||:|||||

RESULT 11
US-09-214-095D-19
; Sequence 19, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19

US-08-672-345C-19
Query Match          92.6%; Score 75; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16
    |||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16
    |||:||||:|||||

RESULT 12
US-09-214-095D-28
; Sequence 28, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-28

Query Match          92.6%; Score 75; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16
    |||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16
    |||:||||:|||||

RESULT 13
US-08-672-345C-5
; Sequence 5, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-278-0400
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-5

Query Match          92.6%; Score 75; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 4.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYDKGKTYLN 16
    |||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16
    |||:||||:|||||

RESULT 14
US-09-214-095D-19
; Sequence 19, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
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SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-5

Query Match 92.6%; Score 75; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 3.2e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 14

US-08-672-345C-6
Sequence 6 Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-6

Query Match 92.6%; Score 75; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 3.2e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 15

US-08-672-345C-7
Sequence 7, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
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CITY: New York
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-7

Query Match 92.6%; Score 75; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 3.2e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSRSLLYRDGKTYLN 39

Search completed: September 30, 2004, 06:38:15
Job time : 28.1186 secs

Blank sheet

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 7.59322 Seconds
(without alignments)
88.677 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES.

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 31 | 100.0 | 74 | 2 G30538 | Ig kappa chain V r |
| 2 | 31 | 100.0 | 112 | 1 KWS16 | Ig kappa chain V r |
| 3 | 31 | 100.0 | 113 | 1 KWS51 | Ig kappa chain V r |
| 4 | 31 | 100.0 | 120 | 1 KWS67 | Ig kappa chain pre |
| 5 | 27 | 87.1 | 104 | 2 E69832 | conserved hypotet |
| 6 | 27 | 87.1 | 234 | 2 S50468 | hypothetical prote |
| 7 | 27 | 87.1 | 342 | 2 E84451 | flagellar motor sw |
| 8 | 27 | 87.1 | 409 | 2 E86017 | probable beta-keto |
| 9 | 27 | 87.1 | 409 | 2 E91171 | probable beta-keto |
| 10 | 27 | 87.1 | 760 | 2 T39991 | minichromosome mai |
| 11 | 27 | 87.1 | 842 | 2 T16198 | hypothetical prote |
| 12 | 27 | 87.1 | 845 | 1 S34027 | replication licens |
| 13 | 27 | 87.1 | 1401 | 2 T39225 | MAP kinase kinase |
| 14 | 26 | 83.9 | 112 | 2 E95905 | hypothetical prote |
| 15 | 26 | 83.9 | 313 | 2 D96028 | probable transcrip |
| 16 | 26 | 83.9 | 341 | 1 QXFR2Y | NADH2 dehydrogenas |
| 17 | 26 | 83.9 | 810 | 2 C70791 | probable pona, pro |
| 18 | 26 | 83.9 | 1453 | 2 S21626 | collagen alpha 1(I |
| 19 | 26 | 83.9 | 1464 | 1 CGHUIS | collagen alpha 1(I |
| 20 | 25 | 80.6 | 177 | 2 T51460 | hypothetical prote |
| 21 | 25 | 80.6 | 212 | 2 S09623 | agglutinin isolcet |
| 22 | 25 | 80.6 | 212 | 2 T05936 | agglutinin isolcet |
| 23 | 25 | 80.6 | 326 | 2 T26647 | hypothetical prote |
| 24 | 25 | 80.6 | 341 | 2 T39105 | WD repeat protein |
| 25 | 25 | 80.6 | 390 | 2 E88925 | protein T22H9.4 [i |
| 26 | 25 | 80.6 | 511 | 2 C56849 | dopamine receptor |
| 27 | 25 | 80.6 | 532 | 2 AF0453 | malate synthase [E |
| 28 | 25 | 80.6 | 565 | 2 B72660 | probable type II D |
| 29 | 25 | 80.6 | 627 | 2 F95867 | conserved hypotet |

alcohol oxidase (E
probable membrane
probable ATP-depen
rifamycin polyketi
gene MHC DQ-beta 1
hypothetical prote
conserved hypotet
hypothetical prote
hypothetical prote
H1PS-4 protein [i
hypothetical prote
cytolysin II opero
emopamil-binding p
periplasmic immuno
conserved hypotet
Cof family protein

ALIGNMENTS

RESULT 1

G30538 Ig kappa chain V region (253.15E2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996

C:Accession: G30538

R:Clafalin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988

A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum

A:Reference number: A30534; MUID:89035545; PMID:3141511

A:Accession: G30538

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar

A:Molecule type: mRNA

A:Residues: 1-74 <CLA>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 74;

Best Local Similarity 100.0%; Pred. No. 0.75; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7

Db 24 LMSTRAS 30

RESULT 2

KWS16

Ig kappa chain V region (M167) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C:Accession: A01908

R:Rudikoff, S.; Potter, M.

Biochemistry 17, 2703-2707, 1978

A:Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prote

A:Reference number: A01908; MUID:79000273; PMID:99160

A:Accession: A01908

A:Molecule type: protein

A:Residues: 1-112 <RUD>

C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine. 3

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

P:16-95/Domain: immunoglobulin homology <LMM>

P:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 112;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7

Db 55 LMSTRAS 61

RESULT 3

KVMS61

Ig kappa chain V region (MS11) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000

C:Accession: A01910

R:Appella, E.

Mol Immunol. 17, 711-718, 1980

A:Title: Amino acid sequence of the light chain variable region of MS11, a phosphorylcholine

A:Reference number: A01910; MUID:81052016; PMID:6776396

A:Accession: A01910

A:Molecule type: protein

A:Residues: 1-113 <APP>

C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-95/Domain: immunoglobulin homology <IMM>

F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 113;

Best Local Similarity 100.0%; Pred. No. 1.2; 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0;

QY 1 LMSTRAS 7

Db 55 LMSTRAS 61

RESULT 4

KVMS67

Ig kappa chain precursor V region (VK167) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000

C:Accession: A01909

R:Seisang, E.; Storb, U.

Cell 25, 47-58, 1981

A:Title: Somatic mutation of immunoglobulin light-chain variable-region genes.

A:Reference number: A01909; MUID:82002223; PMID:6791832

A:Accession: A01909

A:Molecule type: DNA

A:Residues: 1-120 <SEL>

C:Genetics: the sequence was determined from the germline gene

A:Introns: 17/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>

F:36-115/Domain: immunoglobulin homology <IMM>

F:43-113/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 120;

Best Local Similarity 100.0%; Pred. No. 1.2; 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0;

QY 1 LMSTRAS 7

Db 75 LMSTRAS 81

RESULT 5

E69632

conserved hypothetical protein yhgB - Bacillus subtilis

N:Alternate names: hypothetical protein y (pbpf 5' region)

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999

C:Accession: E69832; C40614

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero

C.; Bron, S.; Brouillet, S.; Bruchi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi

A.; Ehrlich, S.D.; Emmersen, P.T.; Entian, K.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,

Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Segiguchi, J.; Sekowska, A.; Seror,

Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A:Authors: Yoshikawa, H.P.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: E69832

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-104 <KUN>

A:Cross-references: GB:Z99109; GB:AL009126; NID:G2633260; PIDN:CAB12849.1; PID:e1183011;

A:Experimental source: strain 168

R:Popham, D.L.; Setlow, P.

J. Bacteriol. 175, 4870-4876, 1993

A:Title: Cloning, nucleotide sequence, and regulation of the Bacillus subtilis pbpF gene,

A:Reference number: A40614; MUID:93328693; PMID:8335642

A:Accession: C40614

A:Molecule type: DNA

A:Residues: 1-67 <POP>

A:Cross-references: GB:L10630

C:Genetics:

A:Gene: yhgB

Query Match 87.1%; Score 27; DB 2; Length 104;

Best Local Similarity 85.7%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 38 LMSTRAS 44

RESULT 6.

S50468

hypothetical protein YER010c - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002

C:Accession: S50468

R:Dieckrich, F.S.

submitted to the EMBL Data Library, December 1994

A:Description: The sequence of S. cerevisiae cosmid 9537, 9581, 9495, 9867, and lambda c

A:Reference number: S50433

A:Accession: S50468

A:Molecule type: DNA

A:Residues: 1-234 <DIE>

A:Cross-references: EMBL:U18778; NID:G603592; PID:G603602; GSPDB:GN00005; MIPS:YER010C

C:Genetics:

A:Gene: MIPS:YER010C

A:Cross-references: SGD:S0000812

A:Map position: 5R

Query Match 87.1%; Score 27; DB 2; Length 234;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 6

Db 102 LMSTRAS 107

RESULT 7

```

A;Residues: 1-409 <HAY>
A;Cross-references: GB:RA000007; PIDN:BAB37764.1; PID:gl3363815; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs4341
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prote
Query Match      87.1%; Score 27; DB 2; Length 409;
Best Local Similarity 100.0%; Prod.No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 MSTRAS 7
      |||||
Db      77 MSTRAS 82

RESULT 10
T39391
minichromosome maintenance protein mcm7p [imported] - fission yeast (Schizosaccharomyces
N;Alternate names: cell division control protein 47 homolog
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: T39391; T45282
R;Lyne, M.; Rajandream, M.A.; Barrall, B.G.; Whithead, S.; Chillingworth, T.; Churcher,
submitted to the EMBL Data Library, July 1998
A;Reference number: Z21897
A;Accession: T39391
A;Status: preliminary; translated from GB/EMBL/DBJ

```

A;Residues: 1-760 <LYN>
A;Cross-references: EMBL:AL031158; PIDN:CAA20099.1; GSPDB:GN00067; SPDB:SPBC35D12.03C
A;Experimental source: strain 972h-; cosmid C25D12
R;Liang, D.T.; Forsburg, S.L.
submitted to the EMBL Data Library, June 1998
A;Description: Fission yeast mcm7+ is an essential gene required for normal DNA replication
A;Reference number: Z22955
A;Accession: T45282
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-760 <LIA>
A;Cross-references: EMBL:AF070481; PIDN:AAC23693.1
A;Experimental source: strain Sp.011
C;Genetics:
A;Gene: SPBC35D12.03c; mcm7
A;Map position: 2
C;Function:
A;Description: essential replication factor
C;Superfamily: replication licensing factor MCM7; MCM homology
F;170-662/Domain: MCM homology <MCM>

```

Query Match      87.1%; Score 27; DB 2; Length 760;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2 MSTRAS 7
      |||||
Db      243 MSTRAS 248

RESULT 11
TL6198
hypothetical protein F28B4.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Aug-2000
C:Accession: Tl6198
R:Leimbach, D.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid F28B4.
A:Reference number: Z18475
A:Accession: Tl6198
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-842 <LEI>

```

A;Cross-references: EMBL:U42834; NID:g1125756; PID:g1125758; PIDN:AAA83583.1; CESP:F28B4
 C;Genetics:
 A;Gene: CBSP:F28B4.2
 A;Introns: 17/3; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2
 C;Superfamily: CDC25-type guanine nucleotide exchange activator homology
 F;212-481/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

 Query Match 87.1%; Score 27; DB 2; Length 842;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 MSTRAS 7
 |||||
 Db 650 MSTRAS 655

 RESULT 12
 S34027
 replication licensing factor MCM7 [validated] - yeast (Saccharomyces cerevisiae)
 N;Alternate names: cell division control protein CDC47; protein YBR1441; protein YBR202W
 C;Species: Saccharomyces cerevisiae
 C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
 C;Accession: S34027; S46074; S34925; S56049
 submitted to the EMBL Data Library, January 1993
 R;Jacquet, M.
 A;Reference number: S34022
 A;Accession: S34027
 A;Molecule type: DNA
 A;Residues: 1-845 <JAC>
 A;Cross-references: EMBL:Z21487; NID:g311665; PIDN:CAA79689.1; PID:g311678
 R;Bussereau, P.; Demolis, N.; Jacquet, M.; Mallet, L.
 submitted to the Protein Sequence Database, August 1994
 A;Reference number: S46054
 A;Accession: S46074
 A;Molecule type: DNA
 A;Residues: 1-845 <BUS>
 A;Cross-references: EMBL:Z36071; NID:g536576; PIDN:CAA8166.1; PID:g536577; GSPDB:GN0000
 R;Bussereau, P.; Mallet, L.; Gaillon, L.; Jacquet, M.
 Yeast 9, 797-806, 1993
 A;Title: Yeast Sequencing Reports. A 12.8 kb segment, on the right arm of chromosome II
 A;Reference number: S34925; MUID:93377417; PMID:8368014
 A;Accession: S34925
 A;Molecule type: DNA
 A;Residues: 407-620 <BU2>
 A;Cross-references: EMBL:Z21487
 R;Dalton, S.
 submitted to the EMBL Data Library, September 1994
 A;Description: Cdc47 and Cdc54 belong to a family of proteins essential for initiation o
 A;Reference number: S56049
 A;Accession: S56049
 A;Molecule type: DNA
 A;Residues: 1-551, 'G', 553-555, 'TLN', 559-573, 'Y', 575-845 <DAL>
 A;Cross-references: EMBL:U14730; NID:g608168; PIDN:AAA86309.1; PID:g608169
 C;Comment: The complex of six MCM proteins is one of several proteins that must be bound
 phosphorylated and dissociate from the chromatin.
 C;Genetics:
 A;Gene: SGD:CDC47; MIPS:YBR202W
 A;Cross-references: SGD:S0000406; MIPS:YBR202W
 A;Map position: 2R
 C;Complex: The predominant form is a heterohexamer of MCM2 (PIR:S45757), MCM3 (PIR:A3637
 component of replication licensing factor.
 C;Function:
 A;Description: MCM7 is a component of the replication licensing factor that permits DNA
 C;Superfamily: replication licensing factor MCM7; MCM homology
 C;Keywords: cell cycle control; DNA replication initiation; heterohexamer; nucleus; phos
 F;227-719/Domain: MCM homology <MCM>

 Query Match 87.1%; Score 27; DB 1; Length 845;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 MSTRAS 7
 |||||
 Db 650 MSTRAS 655

Db 300 MSTRAS 305

 RESULT 13
 T39225
 MAP kinase kinase - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
 C;Accession: T39225
 R;Churcher, C.M.; Gentles, S.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, August 1997
 A;Reference number: Z21837
 A;Accession: T39225
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1401 <CHU>
 A;Cross-references: EMBL:Z98763; PIDN:CAB11500.1; GSPDB:GN00066; SPDB:SPAC9G1.02
 A;Experimental source: strain 972h-; cosmid c9G1
 C;Genetics:
 A;Gene: SPDB:SPAC9G1.02
 A;Map position: 1
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

 Query Match 87.1%; Score 27; DB 2; Length 1401;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 LMSTRAS 7
 |||||
 Db 81 LMSTRAS 87

 RESULT 14
 E95905
 Hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSymB
 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C;Accession: E95905
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
 A;Reference number: A95842; MUID:2136508; PMID:11481431
 A;Accession: E95905
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-112 <KUR>
 A;Cross-references: GB:AL591985; PIDN:CAC48909.1; PID:g15140382; GSPDB:GN00167
 A;Experimental source: strain 1021, megaplasmid pSymB
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 C;Contents: annotation
 C;Genetics:
 A;Gene: SMB20530
 A;Genome: plasmid

 Query Match 83.9%; Score 26; DB 2; Length 112;
 Best Local Similarity 71.4%; Pred. No. 23;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 1 LMSTRAS 7
 |||||
 Db 5 LMSTRAS 11

 RESULT 15
 D96028
 probable transcription activator of the pca operon, LysR family protein [imported] - Sinc

C:Species: *Sinorhizobium meliloti*
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: D96028
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: D96028
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-313 <KUR>
 A:Cross-references: GB:AL591985; PIDN:CAC49892.1; PID:gl5141380; GSPDB:GN00167
 A:Experimental source: strain 1021, megaplasmid pSymB
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: pcaQ; SMD20580
 A:Genome: plasmid

Query Match 83.9%; Score 26; DB 2; Length 313;
 Best Local Similarity 85.7%; Pred. No. 63;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 |||||
 Db 199 LMPTRAS 205

Search completed: September 30, 2004, 06:00:33
 Job time : 9.59322 secs

Blank sheet

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 4.27119 Seconds
(without alignments)
85.337 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 31 | 100.0 | 112 | 1 KV2A_MOUSE | P01626 mus musculus |
| 2 | 31 | 100.0 | 113 | 1 KV2C_MOUSE | P01628 mus musculus |
| 3 | 31 | 100.0 | 120 | 1 KV2B_MOUSE | P01627 mus musculus |
| 4 | 27 | 87.1 | 104 | 1 YHGB_BACSU | P38048 bacillus su |
| 5 | 27 | 87.1 | 234 | 1 YK00_YEAST | P40011 saccharomyc |
| 6 | 27 | 87.1 | 760 | 1 MCW7_SCHPO | O75001 schizosach |
| 7 | 27 | 87.1 | 845 | 1 CC47_YEAST | P38132 saccharomyc |
| 8 | 27 | 87.1 | 1401 | 1 W164_SCHPO | O14299 schizsacch |
| 9 | 26 | 83.9 | 193 | 1 RS3A_SULTO | Q975f8 sulfolobus |
| 10 | 26 | 83.9 | 341 | 1 NU2M_DROME | P03896 drosophila |
| 11 | 26 | 83.9 | 341 | 1 NU2M_DROYA | P03895 drosophila |
| 12 | 26 | 83.9 | 1453 | 1 C111_MOUSE | P11087 mus musculus |
| 13 | 26 | 83.9 | 1460 | 1 C111_CANFA | Q9xsi7 canis famli |
| 14 | 26 | 83.9 | 1464 | 1 C111_HUMAN | P02452 homo sapien |
| 15 | 25 | 80.6 | 212 | 1 AG11_WHEAT | P10968 triticum ae |
| 16 | 25 | 80.6 | 212 | 1 AG11_HORVU | P15312 hordeum vul |
| 17 | 25 | 80.6 | 463 | 1 D2DR_FUGRU | P53453 fugu rubrip |
| 18 | 25 | 80.6 | 565 | 1 TP6B_AERPE | Q9ye64 aeropyrum p |
| 19 | 25 | 80.6 | 664 | 1 ALOX_PICAN | P04841 pichia angu |
| 20 | 25 | 80.6 | 778 | 1 YFKE_YEAST | P43610 saccharomyc |
| 21 | 25 | 80.6 | 887 | 1 YAV5_SCHPO | O10213 schizosach |
| 22 | 24 | 77.4 | 176 | 1 Y059_NFVOP | O10316 oryza psu |
| 23 | 24 | 77.4 | 228 | 1 EBP_CAVPO | Q60490 cavia porce |
| 24 | 24 | 77.4 | 230 | 1 EBP_MOUSE | P70245 mus musculus |
| 25 | 24 | 77.4 | 250 | 1 PP26_BRUME | Q57099 bruceella me |
| 26 | 24 | 77.4 | 259 | 1 PP26_BRUAB | Q44642 bruceella ab |
| 27 | 24 | 77.4 | 312 | 1 YG37_YEAST | P53275 saccharomyc |
| 28 | 24 | 77.4 | 339 | 1 G3P_MYCTU | O06822 mycobacteri |
| 29 | 24 | 77.4 | 436 | 1 LIP7_CANAL | Q9p4e7 candida alb |
| 30 | 24 | 77.4 | 443 | 1 FBL4_CRIGR | O55058 cricetus |
| 31 | 24 | 77.4 | 443 | 1 FBL4_HUMAN | Q95967 homo sapien |
| 32 | 24 | 77.4 | 443 | 1 FBL4_MOUSE | Q9wvj9 mus musculus |
| 33 | 24 | 77.4 | 463 | 1 SAH1_CAUCR | Q9abn0 caulobacter |

| | | | | | |
|----|----|------|------|--------------|--------------------|
| 34 | 24 | 77.4 | 543 | 1 NFL_HUMAN | P07196 homo sapien |
| 35 | 24 | 77.4 | 548 | 1 NFL_PIG | P02547 sus scrofa |
| 36 | 24 | 77.4 | 584 | 1 PARF_PARTE | F47244 paramecium |
| 37 | 24 | 77.4 | 636 | 1 CAL3_RAT | P13941 rattus norv |
| 38 | 24 | 77.4 | 766 | 1 METE_YEAST | P05694 saccharomyc |
| 39 | 24 | 77.4 | 825 | 1 FTSK_BRAJA | Q89wr2 bradyrhizob |
| 40 | 24 | 77.4 | 859 | 1 ALRI_YEAST | Q08269 saccharomyc |
| 41 | 24 | 77.4 | 892 | 1 CHD3_DROME | O16102 drosophila |
| 42 | 24 | 77.4 | 909 | 1 Y4G1_RHISN | P55465 rhizobium s |
| 43 | 24 | 77.4 | 925 | 1 YBK4_YEAST | P38164 saccharomyc |
| 44 | 24 | 77.4 | 1359 | 1 STH1_YEAST | P32597 saccharomyc |
| 45 | 24 | 77.4 | 1373 | 1 HRPI_SCHPO | Q9ue25 schizosacch |

ALIGNMENTS

RESULT 1
KV2A_MOUSE STANDARD; PRT; 112 AA.
AC P01626; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE IG kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCSI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79000273; PubMed=99160;
RA Rudikoff S., Potter M.;
RT "Kappa Chain variable region from M167, a phosphorylcholine binding
RT myeloma protein."
RL Biochemistry 17:2703-2707(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY
CC CHAIN HAS ALSO BEEN DETERMINED.
DR PIR; A01908; KVM516.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 112 112
SQ SEQUENCE 112 AA; A58EDFD6404B9726 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 55 LMSTRAS 61

RESULT 2
KV2C_MOUSE STANDARD; PRT; 113 AA.
ID KV2C_MOUSE
AC P01628;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region WOPC 511.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=81052016; PubMed=6776396;
 RX Appella E.;
 RT "Amino acid sequence of the light chain variable region of Mb11, a
 RL phosphoricholine-binding murine myeloma protein."; Mol. Immunol. 17:711-718(1980).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS PHOSPHORYLCHOLINE.
 DR PIR; A01910; KWS51.
 DR HSP; P80362; IWT.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 KW Ig kappa chain V-II region VKAPPA167.
 FT CHAIN 21 120
 FT SIGNAL 1 20
 FT DOMAIN 21 43
 FT DOMAIN 44 59
 FT DOMAIN 60 74
 FT DOMAIN 75 81
 FT DOMAIN 82 113
 FT DOMAIN 114 120
 FT DISULFID 43 113
 SQ SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;
 Query Match 100.0%; Score 31; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 DB 75 LMSTRAS 81
 RESULT 4
 YHGB BACSU
 ID YHGB BACSU STANDARD; PRT; 104 AA.
 AC P38048;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical protein yhgB.
 GN YHGB OR BSU10090.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98240224; PubMed=9579061;
 RA Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R.,
 RA Wedler H., Venema G., Bron S.;
 RT "The 172 kb prkA-addAB region from 83 degrees to 97 degrees of the
 RT Bacillus subtilis chromosome contains several dysfunctional genes,
 RT the glyB marker, many genes encoding transporter proteins, and the
 RT ubiquitous hit gene."; Microbiology 144:859-875(1998).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Boursier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerth I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Etian K.D., Exington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogilwa A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

DR PIR; A01909; KWS67.
 DR HSP; P80362; IWT.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW Ig kappa chain V-II region VKAPPA167.
 FT CHAIN 21 120
 FT SIGNAL 1 20
 FT DOMAIN 21 43
 FT DOMAIN 44 59
 FT DOMAIN 60 74
 FT DOMAIN 75 81
 FT DOMAIN 82 113
 FT DOMAIN 114 120
 FT DISULFID 43 113
 SQ SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;
 Query Match 100.0%; Score 31; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 DB 75 LMSTRAS 81
 RESULT 4
 YHGB BACSU
 ID YHGB BACSU STANDARD; PRT; 104 AA.
 AC P38048;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical protein yhgB.
 GN YHGB OR BSU10090.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98240224; PubMed=9579061;
 RA Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R.,
 RA Wedler H., Venema G., Bron S.;
 RT "The 172 kb prkA-addAB region from 83 degrees to 97 degrees of the
 RT Bacillus subtilis chromosome contains several dysfunctional genes,
 RT the glyB marker, many genes encoding transporter proteins, and the
 RT ubiquitous hit gene."; Microbiology 144:859-875(1998).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Boursier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerth I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Etian K.D., Exington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogilwa A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

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RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Seaman E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi B., Takagi T., Takahashi H., Takenaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpestra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RT Nature 390:249-256(1997).
RN [3]
RN SEQUENCE OF 1-67 FROM N.A.
RP STRAIN=168;
RX MEDLINE=93328693; PubMed=8335642;
RA Popham D.L., Setlow P.;
RT "Cloning, nucleotide sequence, and regulation of the Bacillus
RT subtilis pbpF gene, which codes for a putative class A
RT high-molecular-weight penicillin-binding protein."
RL J. Bacteriol. 175:4870-4876(1993).
CC -----
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CC -----
DR EMBL; Y14083; CAA74515.1; -
DR EMBL; Z99109; CAB12849.1; -
DR EMBL; L10630; AAA71940.2; -
DR PIR; S69832; S69832.
DR Subtilisin; BG10426; yngB.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 104 AA; 11998 MW; 6B44CD77B52FDP968 CRC64;

Query Match      87.1%; Score 27; DB 1; Length 104;
Best Local Similarity 85.7%; Pred. No. 4.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 38 LMSTRCS 44

RESULT 5
YEKO YEAST      STANDARD;      PRT;      234 AA.
AC P40011;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 23.6 kDa protein in NTF2-SRPI intergenic region.
GN YEKO10C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313264; PubMed=9169868;
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
RA Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA Lin D., Mossdale D., Nakahara K., Namath A., Norgren R., Oeffner P.,
RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V."

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RL Nature 387:78-81(1997).
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CC -----
DR EMBL; U18778; AAB64543.1; -
DR PIR; S50468; S50468.
DR Germonline; 139090; -
DR SGD; S0000812; YER010C.
DR InterPro; IPR005493; Methyltransf_6.
DR Pfam; PF03737; Methyltransf_6; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25563 MW; EC109F224240F980 CRC64;

Query Match      87.1%; Score 27; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6
DB 102 LMSTRA 107

RESULT 6
MCM7 SCHPO      STANDARD;      PRT;      760 AA.
ID MCM7 SCHPO
AC O75001; P87302;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA replication licensing factor mcm7 (Minichromosome maintenance
DE protein 7).
GN MCM7 OR SPBC25D12.03C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RN SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RC STRAIN=SP011;
RX MEDLINE=21518581; PubMed=11606526;
RA Liang D.T., Forsburg S.L.;
RT "Characterization of Schizosaccharomyces pombe mcm7(+) and cdc23(+)
RT (MCM10) and interactions with replication checkpoints."
RL Genetics 159:471-486(2001).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Feat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

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RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Carutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Spakovski G.V., Usery D., Barrell B.G., Nurse P.,
 RA "The genome sequence of Schizosaccharomyces pombe.",
 RL Nature 415:871-880(2002).
 RN [3]
 RN SEQUENCE OF 367-466 FROM N.A.
 RP STRAIN=972;
 RC MEDLINE=98031880; PubMed=9366552;
 RX Adachi Y., Tsukura J., Yanagida M.,
 RA "A globular complex formation by Nda1 and the other five members of
 RT the MCM protein family in fission yeast.",
 RL Genes Cells 2:467-479(1997).
 CC -!- FUNCTION: Required for the progression of S phase.
 CC -!- SUBUNIT: Heterodimer. The heterodimers of mcm4/mcm6 and
 CC mcm3/mcm5 interact with mcm2 and mcm7.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the MCM family.
 CC -----
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 CC -----
 CC EMBL; AF070481; AAC23693.1; -;
 DR EMBL; AL031158; CAA20099.1; -;
 DR EMBL; AJ000065; CAA03898.1; -;
 DR PIR; T39991; T39991.
 DR GenBank_Spombe; SPBC25D12.03c; -;
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001208; MCM.
 DR InterPro; IPR008050; MCM.
 DR Pfam; PF00493; MCM; 1.
 DR PRINTS; PR01657; MCMFAMILY.
 DR PRINTS; PR01663; MCMFAMILY.
 DR ProDom; PD001041; MCM; 1.
 DR SMART; SM00382; AAA; 1.
 DR SMART; SM00350; MCM; 1.
 DR PROSITE; PS00847; MCM; 1.
 DR PROSITE; PS00501; MCM; 2; 1.
 DR Transcription regulation; DNA-binding; Nuclear protein;
 KW DNA replication; Cell cycle; ATP-binding.
 FT DOMAIN 353 559 MCM.
 FT NP_BIND 403 410 ATP (POTENTIAL).
 FT CONFLICT 457 457 V -> I (IN REF. 3).
 SQ SEQUENCE 760 AA; 85622 MW; 2141F8F9C80BAA34 CRC64;
 Query Match 87.1%; Score 27; DB 1; Length 760;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTRAS 7
 DB 243 MSTRAS 248
 RESULT 7
 CC47_YEAST STANDARD; PRT; 845 AA.
 AC P38132;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA replication licensing factor CDC47 (Cell division control protein
 DE 47).
 DE CDC47 OR YBR202W OR YBR1441.
 GN Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dalton S.,
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=93377417; PubMed=8368014;
 RA Bussereau F., Mallet L., Gaillon L., Jacquet M.,
 RT "A 12.8 kb segment, on the right arm of chromosome II from
 RT Saccharomyces cerevisiae including part of the DURI1,2 gene, contains
 RT five putative new genes.",
 RL Yeast 9:797-806(1993).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Belongs to the MCM family.
 CC -----
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 CC -----
 CC EMBL; U14730; AAA86309.1; -;
 DR EMBL; Z21487; CAA79689.1; -;
 DR EMBL; Z36071; CAA85166.1; -;
 DR PIR; S34027; S34027.
 DR GenOnline; 138745; -;
 DR GK; P38132; -;
 DR SGD; S0000406; CDC47.
 DR GO; GO:0005737; Cytoplasm; IDA.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0005656; C:pre-replicative complex; IDA.
 DR GO; GO:0005524; F:ATP binding; IDA.
 DR GO; GO:0006267; P:pre-replicative complex formation and maint. . .; IPI.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001208; MCM.
 DR InterPro; IPR008050; MCM.
 DR Pfam; PF00493; MCM; 1.
 DR PRINTS; PR01657; MCMFAMILY.
 DR PRINTS; PR01663; MCMFAMILY.
 DR ProDom; PD001041; MCM; 1.
 DR SMART; SM00382; AAA; 1.
 DR SMART; SM00350; MCM; 1.
 DR PROSITE; PS00847; MCM; 1; 1.
 DR PROSITE; PS00501; MCM; 2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein;
 KW DNA replication; Cell cycle; ATP-binding.
 FT DOMAIN 410 617 MCM.
 FT NP_BIND 460 467 ATP (POTENTIAL).
 FT CONFLICT 552 552 G -> V (IN REF. 2).
 FT CONFLICT 556 558 TLN -> NPG (IN REF. 2).
 FT CONFLICT 574 574 Y -> I (IN REF. 2).
 SQ SEQUENCE 845 AA; 94942 MW; ADA66C719D96DB4A CRC64;
 Query Match 87.1%; Score 27; DB 1; Length 845;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTRAS 7
 DB 300 MSTRAS 305
 RESULT 8
 WIS4_SCHPO STANDARD; PRT; 1401 AA.
 ID WIS4_SCHPO
 AC O14299; P87062; Q92384;
 DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE MAP kinase kinase kinase wis4 (EC 2.7.1.1-) (MAP kinase kinase kinase
 DE waki) (MAP kinase kinase kinase waki).
 GN WIS4 OR WAK1 OR WIK1 OR SPAC9G1.02.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC NCBI TaxID=4896;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98026892; PubMed=9321395;
 RX Samejima I., Mackie S., Fantes P.A.;
 RT "Multiple modes of activation of the stress-responsive MAP kinase
 RT pathway in fission yeast."
 RL EMBO J. 16:6162-6170(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,
 RA Mooney P., Moule S., Murgall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
 RA Welljens I., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:871-880(2002).
 RN [3]
 RP SEQUENCE OF 96-1401 FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=97282620; PubMed=9136929;
 RA Shieh J.C., Wilkinson M., Buck V., Morgan B., Makino K.,
 RA Willar J.B.A.;
 RT "The Mca4 response regulator coordinately controls the stress-
 RT activated Waki-Wisl-Styl MAP kinase pathway and fission yeast cell
 RT cycle."
 RL Genes Dev. 11:1008-1022(1997).
 RN [4]
 RP SEQUENCE OF 457-543 FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=97331752; PubMed=9188094;
 RA Shiozaki K., Shiozaki M., Russell P.;
 RT "Mca4 mitotic catastrophe suppressor regulates the fission yeast cell
 RT cycle through the Waki-Wisl-Spc1 kinase cascade."
 RL Mol. Biol. Cell 8:409-419(1997).
 CC -1- FUNCTION: Involved in a signal transduction pathway that is
 CC activated in under conditions of heat shock, oxidative stress or
 CC limited nutrition. Unlike wisk, it is not activated by changes in
 CC the osmolarity of the extracellular environment. Activates the
 CC wisk MAP kinase kinase by phosphorylation.
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. MAP
 CC kinase kinase subfamily.
 CC -----

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 CC -----
 DR EMBL; Z98763; CAB11500.1; -;
 DR EMBL; Y07750; CAA69030.1; ALT_INIT.
 DR EMBL; Y11989; CAA72718.1; -;
 DR EMBL; U1521; AAB39762.1; -;
 DR PIR; T39225; T39225.
 DR HSP; P24941; ICKP.
 DR GeneDB SPombe; SPAC9G1.02; -;
 DR GO; GO:0007049; P:cell cycle; ISS.
 DR GO; GO:0000165; P:MAPKK cascade; ISS.
 DR GO; GO:0007165; P:signal transduction; ISS.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SMO0220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW transferase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 1037 1306 PROTEIN_KINASE.
 FT NP_BIND 1043 1051 ATP (BY SIMILARITY).
 FT BINDING 1066 1066 ATP (BY SIMILARITY).
 FT ACT_SITE 1161 1161 RL -> SP (IN REF. 3).
 FT CONFLICT 484 485 D -> V (IN REF. 1).
 FT CONFLICT 1346 1346 D -> V (IN REF. 1).
 SQ SEQUENCE 1401 AA; 160537 MW; 529A989D2B627F3D CRC64;
 Query Match 87.1%; Score 27; DB 1; Length 1401;
 Best Local Similarity 85.7%; Pred.No. 72;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 DB 81 LMSTRTS 87
 RESULT 9
 RS3A_SULTO
 ID RS3A_SULTO STANDARD; PRT; 193 AA.
 AC Q95F8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S3Ae.
 GN RP3Ae OR ST0453.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankaï A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain7."
 RL DNA Res. 8:123-140(2001).

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CC -!- SIMILARITY: Belongs to the S3AE family of ribosomal proteins.
CC -----
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CC -----
CC EMBL; AF000982; BAB65443.1; -.
CC DR HAMAF; MF 00359; -.
CC DR InterPro; IPR001593; Ribosomal_S3AE.
CC DR Pfam; PF01015; Ribosomal_S3AE; 1.
CC DR ProDom; PD003035; Ribosomal_S3AE; 1.
CC DR PROSITE; PS01191; RIBOSOMAL_S3AE; FALSE NEG.
CC KW Ribosomal protein; Complete proteome.
CC SQ SEQUENCE 193 AA; 22180 MW; 78A94B87B961D751 CRC64;
CC -----
CC Query Match 83.9%; Score 26; DB 1; Length 193;
CC Best Local Similarity 71.4%; Pred. No. 15;
CC Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 1 LMSTRAS 7
CC : : : : :
CC Db 142 ILSTRAS 148
CC -----
CC RESULT 10
CC NU2M DROME
CC ID NU2M DROME STANDARD; PRT; 341 AA.
CC AC P03896;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
CC GN ND2.
CC OS Drosophila melanogaster (Fruit fly).
CC OG Mitochondrion.
CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC OC Ephydroidea; Drosophilidae; Drosophila.
CC OX NCBI_TaxID=7227;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=96423163; PubMed=8825764;
CC RA Lewis D.L., Farr C.L., Kaguni L.S.;
CC RT "Drosophila melanogaster mitochondrial DNA: completion of the
CC RT nucleotide sequence and evolutionary comparisons.";
CC RL Insect Mol. Biol. 4:263-278(1995).
CC RN [2]
CC RP SEQUENCE OF 56-341 FROM N.A.
CC RX MEDLINE=83245048; PubMed=6408489;
CC RA de Bruijn M.H.L.;
CC RT "Drosophila melanogaster mitochondrial DNA, a novel organization and
CC RT genetic code.";
CC RL Nature 304:234-241(1993).
CC CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC CC inner membrane.
CC CC -!- SIMILARITY: Belongs to the complex I subunit 2 family.
CC -----
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CC -----
CC EMBL; U37541; AAC47811.1; -.
CC DR EMBL; J01404; AAB59238.1; -.
CC PIR; A00419; QXFF2M.

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DR FlyBase; FBgn0013680; mt:ND2.
DR InterPro; IPR003917; NADHub_oxred2.
DR InterPro; IPR001750; Oxidored q1.
DR Pfam; PF00361; oxidored q1; 1.
DR PRINTS; PR01436; NADHDHGNASE2.
DR Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
DR SEQUENCE 341 AA; 39773 MW; 2B8E9528C28007D8 CRC64;
CC -----
CC Query Match 83.9%; Score 26; DB 1; Length 341;
CC Best Local Similarity 85.7%; Pred. No. 28;
CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC QY 1 LMSTRAS 7
CC : : : : :
CC Db 51 LMSTRAS 57
CC -----
CC RESULT 11
CC NU2M DROVA
CC ID NU2M DROVA STANDARD; PRT; 341 AA.
CC AC P03895;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
CC GN ND2.
CC OS Drosophila yakuba (Fruit fly).
CC OG Mitochondrion.
CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC OC Ephydroidea; Drosophilidae; Drosophila.
CC OX NCBI_TaxID=7245;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX STRAIN=2317.6 Ivory Coast;
CC RX MEDLINE=86089137; PubMed=3001325;
CC RA Clary D.O., Wolstenholme D.R.;
CC RT "The mitochondrial DNA molecular of Drosophila yakuba: nucleotide
CC RT sequence, gene organization, and genetic code.";
CC RN [2]
CC RP J. Mol. Evol. 22:252-271(1985).
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=84041489; PubMed=6314262;
CC RA Clary D.O., Wolstenholme D.R.;
CC RT "Genes for cytochrome c oxidase subunit I, URF2, and three tRNAs in
CC RT Drosophila mitochondrial DNA.";
CC RL Nucleic Acids Res. 11:6859-6872(1983).
CC RN [3]
CC RP SEQUENCE OF 1-56 FROM N.A.
CC RX MEDLINE=83090428; PubMed=6294611;
CC RA Clary D.O., Goddard J.M., Martin S.C., Fauron C.M.-R.,
CC RT "Drosophila mitochondrial DNA: a novel gene order.";
CC RN [4]
CC RP Nucleic Acids Res. 10:6619-6637(1982).
CC RP SEQUENCE OF 1-56 FROM N.A.
CC RX MEDLINE=88011348; PubMed=3116271;
CC RA Clary D.O., Wolstenholme D.R.;
CC RT "Drosophila mitochondrial DNA: conserved sequences in the A + T-rich
CC RT region and supporting evidence for a secondary structure model of the
CC RT small ribosomal RNA.";
CC RL J. Mol. Evol. 45:116-125(1987).
CC CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC CC inner membrane.
CC CC -!- SIMILARITY: Belongs to the complex I subunit 2 family.
CC -----
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CC -----
CC EMBL; U37541; AAC47811.1; -.
CC DR EMBL; J01404; AAB59238.1; -.
CC PIR; A00419; QXFF2M.

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CC -----
CC EMBL; X03240; CAA26985.1; -
CC EMBL; X05915; CAA29342.1; -
CC PIR; B93488; OXFERY.
CC FlyBase; FBgn0013184; Dyakmt.ND2.
CC InterPro; IPR003917; NADhub_oxred2.
CC Pflam; PF00361; oxidored_g1; 1.
CC PRINTS; PR01436; NADHDHGNASE2.
CC Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
CC KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
CC SQ SEQUENCE 341 AA; 39495 MW; E6117D5E0BE9D4AF CRC64;

Query Match 83.9%; Score 26; DB 1; Length 341;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LMSTRAS 7
Db 51 LMSTAS 57

RESULT 12
CALL_MOUSE
ID CALL_MOUSE STANDARD; PRT; 1453 AA.
AC P11067; G60635;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collagen alpha 1(I) chain precursor.
GN COL1A1 OR COL1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RX MEDLINE=96033240; PubMed=8535610;
RA Li S.W., Killian J., Prockop D.J.;
RT "The complete cDNA coding sequence for the mouse pro alpha 1(I) chain
RT of type I procollagen.";
RL Matrix Biol. 14:593-595 (1995).
RN [2]
RP SEQUENCE OF 518-1128 FROM N.A.
RX MEDLINE=86137403; PubMed=3841523;
RA French B.T., Lee W.-H., Maul G.G.;
RT "Nucleotide sequence of a cDNA clone for mouse pro alpha 1(I)
RT collagen protein.";
RL Gene 39:311-312 (1985).
RN [3]
RP SEQUENCE OF 735-1130 FROM N.A.
RX MEDLINE=83141374; PubMed=6298597;
RA Monson J.M., Friedman J., McCarthy B.J.;
RT "DNA sequence analysis of a mouse pro alpha 1(I) procollagen gene:
RT evidence for a mouse B1 element within the gene.";
RL Mol. Cell. Biol. 2:1362-1371 (1982).
RN [4]
RP SEQUENCE OF 735-878 AND 1005-1058 FROM N.A.
RX MEDLINE=83157109; PubMed=6219867;
RA Monson J.M., McCarthy B.J.;
RT "Identification of a Balb/c mouse pro alpha 1(I) procollagen gene:
RT evidence for insertions or deletions in gene coding sequences.";
RL DNA 1:59-69 (1981).
RN [5]
RP SEQUENCE OF 1442-1453 FROM N.A.
RX MEDLINE=88124276; PubMed=3340560;
RA Mooslechner K., Harbers K.;
RT "Two mRNAs of mouse pro alpha 1(I) collagen gene differ in the size
RT of the 3'-untranslated region.";
RL Nucleic Acids Res. 16:773-773 (1988).
CC -!- FUNCTION: Type I collagen is a member of group I collagen
CC (fibrillar forming collagen).

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CC -!- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
CC -!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and
CC bones. In bones the fibrils are mineralized with calcium
CC hydroxyapatite.
CC -!- PTM: Prolines at the third position of the tripeptide repeating
CC unit (G-X-Y) are hydroxylated in some or all of the chains.
CC -!- SIMILARITY: Contains 1 VWFC domain.
CC -----
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CC -----
CC EMBL; U08020; AAA88912.1; -
CC EMBL; X15896; CAA33904.1; -
CC EMBL; M14423; AAA37333.1; -
CC EMBL; M17491; AAA37334.1; -
CC EMBL; X06753; CAA29927.1; -
CC EMBL; X03036; AAA37332.1; -
CC EMBL; X03029; AAA37332.1; JOINED.
CC EMBL; X03030; AAA37332.1; JOINED.
CC EMBL; X03031; AAA37332.1; JOINED.
CC EMBL; X03032; AAA37332.1; JOINED.
CC EMBL; X03033; AAA37332.1; JOINED.
CC EMBL; X03034; AAA37332.1; JOINED.
CC EMBL; X03035; AAA37332.1; JOINED.
CC PIR; S57243; S21626.
CC MGD; MGI:88467; Colla1.
CC InterPro; IPR008161; C1g_helix.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR00885; Fib_collagen_C.
CC InterPro; IPR002181; Fibrinogen_C.
CC InterPro; IPR001007; VWFC.
CC Pfam; PF01410; COLFI; 1.
CC Pfam; PF01391; Collagen; 18.
CC ProDom; PD000007; C1g_helix; 1.
CC ProDom; PD002078; Fib_collagen_C; 1.
CC SMART; SM00038; COLFI; 1.
CC SMART; SM00214; VWFC; 1.
CC PROSITE; PS01208; VWFC_1; 1.
CC PROSITE; PS0184; VWFC_2; 1.
CC Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
CC Glycoprotein; Collagen; Signal.
FT SIGNAL 1 22
FT PROPEP 23 151 AMINO-TERMINAL PROPEPTIDE.
FT CHAIN 152 1207 COLLAGEN ALPHA 1(I) CHAIN.
FT PROPEP 1208 1453 CARBOXYL-TERMINAL PROPEPTIDE.
FT DOMAIN 29 87 VWFC.
FT DOMAIN 152 167 NONHELICAL REGION (N-TERMINAL).
FT DOMAIN 168 1181 TRIPLE-HELICAL REGION.
FT DOMAIN 1182 1207 NONHELICAL REGION (C-TERMINAL).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1354 1354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 734 736 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 1082 1084 CELL ATTACHMENT SITE (POTENTIAL).
FT CONFLICT 1450 1450 A -> V (IN REF. 5).
SQ SEQUENCE 1453 AA; 137944 MW; 3B802E53DF81808 CRC64;

Query Match 83.9%; Score 26; DB 1; Length 1453;
Best Local Similarity 85.7%; Pred. No. 144+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LMSTRAS 7
Db 1346 LMSTAS 1352

RESULT 13
CALL_CANFA
ID CALL_CANFA STANDARD; PRT; 1460 AA.

```

AC QXKSJ7;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Collagen alpha 1(I) chain precursor.
 GN COL1A1
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT OI ALA-208.
 RC TISSUE=Skin;
 RX MEDLINE=2103337; PubMed=11147834;
 RA Campbell B.G., Wootton J.A.M., Macleod J.N., Minor R.R.;
 RT "Sequence of normal canine COL1A1 cDNA and identification of a
 RT heterozygous alpha1(I) collagen Gly208Ala mutation in a severe case
 RT of canine osteogenesis imperfecta.";
 RL Arch. Biochem. Biophys. 384:37-46(2000).
 CC -1- FUNCTION: Type I collagen is a member of group I collagen
 CC (fibrillar forming collagen).
 CC -1- SUBUNIT: Trimer of one alpha 2(I) and two alpha 1(I) chains.
 CC -1- PTM: Prolines at the third position of the tripeptide repeating
 CC unit (G-X-Y) are hydroxylated in some or all of the chains.
 CC -1- DISEASE: Defects in COL1A1 are a cause of osteogenesis imperfecta
 CC (OI).
 CC -1- SIMILARITY: Contains 1 VWFC domain.
 CC
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF153062; AAD34619.1; -;
 DR InterPro; IPR008161; C1g helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR000885; Fib.collagen.C.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR InterPro; IPR001007; VWFC.
 DR Pfam; PF01410; COLFI; 1.
 DR ProDom; PD000007; C1g helix; 2.
 DR ProDom; PD002078; Fib.collagen_C; 1.
 DR SMART; SM00038; COLFI_1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS01208; VWFC_1; 1.
 DR PROSITE; PS0184; VWFC_2; 1.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 KW Glycoprotein; Collagen; Signal; Disease mutation.
 FT SIGNAL 1 22
 FT PROPEP 23 157 AMINO-TERMINAL PROPEPTIDE.
 FT CHAIN 158 1214 COLLAGEN ALPHA 1(I) CHAIN.
 FT PROPEP 1215 1460 CARBOXYL-TERMINAL PROPEPTIDE.
 FT DOMAIN 34 92 VWFC.
 FT DOMAIN 158 174 NONHELICAL REGION (N-TERMINAL).
 FT DOMAIN 175 1188 TRIPLE-HELICAL REGION.
 FT DOMAIN 1189 1214 NONHELICAL REGION (C-TERMINAL).
 FT SITE 741 743 CELL ATTACHMENT SITE (POTENTIAL).
 FT SITE 1089 1091 CELL ATTACHMENT SITE (POTENTIAL).
 FT CARBOHYD 1361 1361 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARIANT 208 208 G -> A (in OI; severe).
 SQ SEQUENCE 1460 AA; 138762 MW; 58E3674D2B570697 CRC64;

Query Match 83.9%; Score 26; DB 1; Length 1460;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LMSTRAS 7
 DB 1353 LMSTRAS 1359

RESULT 14
 CALL HUMAN STANDARD; PRT; 1464 AA.
 ID P02452; Q14037; Q15176;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Collagen alpha 1(I) chain precursor.
 GN COL1A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 1-472 FROM N.A.
 RX MEDLINE=89025644; PubMed=3178743;
 RA Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
 RA Jaenisch R., Prockup D.J.;
 RT "Structure of a full-length cDNA clone for the prepro alpha 1(I)
 RT chain of human type I procollagen.";
 RL Biochem. J. 253:919-922(1988).
 RN [2]
 RP SEQUENCE OF 1-181 FROM N.A.
 RX MEDLINE=84270697; PubMed=6462220;
 RA Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,
 RA Myers J., Williams C., Ramirez F.;
 RT "Human pro alpha 1(I) collagen gene structure reveals evolutionary
 RT conservation of a pattern of introns and exons.";
 RL Nature 310:337-340(1984).
 RN [3]
 RP SEQUENCE OF 162-301.
 RC TISSUE=Skin;
 RX MEDLINE=71038625; PubMed=5529814;
 RA Click E.M., Bornstein P.;
 RT "Isolation and characterization of the cyanogen bromide peptides from
 RT the alpha 1 and alpha 2 chains of human skin collagen.";
 RL Biochemistry 9:4699-4706(1970).
 RN [4]
 RP SEQUENCE OF 263-268.
 RC TISSUE=Skin;
 RX MEDLINE=71001508; PubMed=4319110;
 RA Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;
 RT "A comparative study of glycopeptides derived from selected
 RT vertebrate collagens. A possible role of the carbohydrate in fibril
 RT formation.";
 RL J. Biol. Chem. 245:5042-5048(1970).
 RN [5]
 RP SEQUENCE OF 425-1464 FROM N.A.
 RX MEDLINE=84080385; PubMed=6689127;
 RA Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F.,
 RA Prockup D.J.;
 RT "Nucleotide sequences of complementary deoxyribonucleic acids for the
 RT pro alpha 1 chain of human type I procollagen. Statistical evaluation
 RT of structures that are conserved during evolution.";
 RL Biochemistry 22:5213-5223(1983).
 RN [6]
 RP SEQUENCE OF 1229-1454 FROM N.A.
 RC TISSUE=Bone;
 RX MEDLINE=88124208; PubMed=3340531;
 RA Maskela J.K., Raasina M., Virta A., Vuorio E.;
 RT "Human pro alpha 1(I) collagen: cDNA sequence for the C-propeptide
 RT domain.";
 RL Nucleic Acids Res. 16:349-349(1988).
 RN [7]
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=88097389; PubMed=3480516;
 RA Bornstein P., McKay J., Morishima J.K., Devarayalu S., Gelinas R.E.;
 RT "Regulatory elements in the first intron contribute to
 RT transcriptional control of the human alpha 1(I) collagen gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8869-8873(1987).
 RN [8]

RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=85130970; PubMed=2857713;
 RA Chu M.-L., de Wet W.J., Bernard M.P., Ramirez F.;
 RT "Fine structural analysis of the human pro-alpha 1 (I) collagen gene.
 RT Promoter structure, Alu repeats, and polymorphic transcripts.";
 RL J. Biol. Chem. 260:2315-2320(1985).
 RN [9]
 RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=88033098; PubMed=2822714;
 RA Rossouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez F.,
 RA de Wet W.J.;
 RT "DNA sequences in the first intron of the human pro-alpha 1(I)
 RT collagen gene enhance transcription.";
 RL J. Biol. Chem. 262:15151-15157(1987).
 RN [10]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=91184577; PubMed=2010058;
 RA Kuivaniemi H., Tromp G., Prockop D.J.;
 RT "Mutations in collagen genes: causes of rare and some common diseases
 RT in humans.";
 RL FASEB J. 5:2052-2060(1991).
 RN [11]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=97255959; PubMed=9101290;
 RA Kuivaniemi H., Tromp G., Prockop D.J.;
 RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
 RT associated collagen (type IX), and network-forming collagen (type X)
 RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";
 RL Hum. Mutat. 9:300-315(1997).
 RN [12]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=91374476; PubMed=1895312;
 RA Evers P.H., Wallis G.A., Willing M.C.;
 RT "Osteogenesis imperfecta: translation of mutation to phenotype.";
 RL J. Med. Genet. 28:433-442(1991).
 RN [13]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=97169399; PubMed=9016532;
 RA Dalglish R.;
 RT "The human type I collagen mutation database.";
 RL Nucleic Acids Res. 25:181-187(1997).
 RN [14]
 RP VARIANT OI-II CYS-1166.
 RX MEDLINE=86287390; PubMed=3016737;
 RA Cohn D.H., Byers P.H., Steinmann B., Gelinas R.E.;
 RT "Lethal osteogenesis imperfecta resulting from a single nucleotide
 RT change in one human pro alpha 1(I) collagen allele.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6045-6047(1986).
 RN [15]
 RP VARIANT OI-II ARG-569.
 RX MEDLINE=8722295; PubMed=3108247;
 RA Bateman J.F., Chan D., Walkers I.D., Rogers J.G., Cole W.G.;
 RT "Lethal perinatal osteogenesis imperfecta due to the substitution of
 RT arginine for glycine at residue 391 of the alpha 1(I) chain of type I
 RT collagen.";
 RL J. Biol. Chem. 262:7021-7027(1987).
 RN [16]
 RP VARIANT OI-II CYS-926.
 RX MEDLINE=88033031; PubMed=3667599;
 RA Vogel B.E., Miror R.R., Freund M., Prockop D.J.;
 RT "A point mutation in a type I procollagen gene converts glycine 748
 RT of the alpha 1 chain to cysteine and destabilizes the triple helix in
 RT a lethal variant of osteogenesis imperfecta.";
 RL J. Biol. Chem. 262:14737-14744(1987).
 RN [17]
 RP VARIANT OI-II ARG-842.
 RX MEDLINE=88298628; PubMed=3403550;
 RA Bateman J.F., Lamané S.R., Dahl H.H., Chan D., Cole W.G.;
 RT "Substitution of arginine for glycine 664 in the collagen alpha 1(I)
 RT chain in lethal perinatal osteogenesis imperfecta. Demonstration of
 RT the peptide defect by in vitro expression of the mutant cDNA.";
 RL J. Biol. Chem. 263:11627-11630(1988).
 RN [18]

RP VARIANT OI CYS-1195.
 RX MEDLINE=89218628; PubMed=3244312;
 RA Lachard M.E., Wirtz M.K., Pope F.M., Nicholls A.C., Hollister D.W.;
 RT "A cysteine for glycine substitution at position 1017 in an alpha
 RT 1(I) chain of type I collagen in a patient with mild dominantly
 RT inherited osteogenesis imperfecta.";
 RL Mol. Biol. Med. 5:197-207(1988).
 RN [19]
 RP VARIANT OI-II VAL-434.
 RX MEDLINE=89255493; PubMed=2470760;
 RA Patterson E., Smiley E., Bonadio J.;
 RT "RNA sequence analysis of a perinatal lethal osteogenesis imperfecta
 RT mutation.";
 RL J. Biol. Chem. 264:10083-10087(1989).
 RN [20]
 RP VARIANT OI-IV SER-1010.
 RX MEDLINE=89308591; PubMed=2745420;
 RA Marini J.C., Grange D.K., Gottesman G.S., Lewis M.B., Koepf D.A.;
 RT "Osteogenesis imperfecta type IV. Detection of a point mutation in
 RT one alpha 1(I) collagen allele (COL1A1) by RNA/RNA hybrid analysis.";
 RL J. Biol. Chem. 264:11893-11900(1989).
 RN [21]
 RP VARIANTS OI-II ALA-1106; VAL-1151; ARG-1154 AND VAL-1184.
 RX MEDLINE=89380165; PubMed=277764;
 RA Lamané S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.;
 RT "Characterization of point mutations in the collagen COL1A1 and
 RT COL1A2 genes causing lethal perinatal osteogenesis imperfecta.";
 RL J. Biol. Chem. 264:15809-15812(1989).
 RN [22]
 RP VARIANT OI SER-1022.
 RX MEDLINE=90062068; PubMed=2511192;
 RA Pack M., Constantinou C.D., Kalia K., Nielsen K.B., Prockop D.J.;
 RT "Substitution of serine for alpha 1(I)-glycine 844 in a severe
 RT variant of osteogenesis imperfecta minimally destabilizes the triple
 RT helix of type I procollagen. The effects of glycine substitutions on
 RT thermal stability are either position of amino acid specific.";
 RL J. Biol. Chem. 264:19694-19699(1989).
 RN [23]
 RP VARIANT OI-II CYS-1082.
 RX MEDLINE=89109573; PubMed=2913053;
 RA Constantinou C.D., Nielsen K.B., Prockop D.J.;
 RT "A lethal variant of osteogenesis imperfecta has a single base
 RT mutation that substitutes cysteine for glycine 904 of the alpha 1(I)
 RT chain of type I procollagen. The asymptomatic mother has an
 RT unidentified mutation producing an overmodified and unstable type I
 RT procollagen.";
 RL J. Clin. Invest. 83:574-584(1989).
 RN [24]
 RP VARIANTS OI CYS-272; CYS-704 AND CYS-896.
 RX MEDLINE=90009313; PubMed=2794057;
 RA Staman B.J., Eyre D., Charbonneau H., Harrylock M., Weis M.A.,
 RA Weiss L., Graham J.M., Byers P.H.;
 RT "Osteogenesis imperfecta. The position of substitution for glycine by
 RT cysteine in the triple helical domain of the pro alpha 1(I) chains of
 RT type I collagen determines the clinical phenotype.";
 RL J. Clin. Invest. 84:1206-1214(1989).
 RN [25]
 RP VARIANT OI-II CYS-422.

Query Match 83.9%; Score 26; DB 1; Length 1464;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7

Db 1357 LMSTEAS 1363

RESULT 15

AGIL WHEAT

ID AGIL WHEAT STANDARD; PRT; 212 AA.

AC P10368;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Agglutinin isolectin 1 precursor (WGA1) (Isolectin A).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticaceae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91370843; PubMed=2491677;
 RA Smith J.J., Raikhel N.V.;
 RT "Nucleotide sequences of cDNA clones encoding wheat germ agglutinin
 RL isolectins A and D.";
 RL Plant Mol. Biol. 13:601-603(1989).
 RN [2]
 RP SEQUENCE OF 27-197.
 RC TISSUE=Germ;
 RX MEDLINE=89279931; PubMed=2499688;
 RA Wright C.S., Raikhel N.V.;
 RT "Sequence variability in three wheat germ agglutinin isolectins:
 RT products of multiple genes in polyploid wheat.";
 RL J. Mol. Evol. 28:327-336(1989).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=91039324; PubMed=2231724;
 RA Wright C.S.;
 RT "2.2-A resolution structure analysis of two refined
 RT N-acetylneuraminyllactose-wheat germ agglutinin isolectin
 RT complexes.";
 RL J. Mol. Biol. 215:635-651(1990).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=90064507; PubMed=2585496;
 RA Wright C.S.;
 RT "Comparison of the refined crystal structures of two wheat germ
 RT isolectins.";
 RL J. Mol. Biol. 209:475-487(1989).
 CC -1- FUNCTION: N-acetyl-D-glucosamine / N-acetyl-D-neuraminic acid
 CC binding lectin.
 CC -1- SUBUNIT: Homodimer, u-shaped.
 CC -1- MISCELLANEOUS: The 4 sites proposed for binding to carbohydrates
 CC (N-acetyl-D-glucosamine) of receptor molecules are on the surface
 CC of the agglutinin molecule.
 CC -1- SIMILARITY: THERE ARE THREE VARIANTS OF WGA; VARIABILITY AMONG
 CC THEM IS OBSERVED AT A TOTAL OF 10 POSITIONS.
 CC -1- SIMILARITY: Contains 4 chitin-binding domains.
 CC -1- SIMILARITY: Contains 4 chitin-binding type-1 domains.
 CC -----
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 CC -----
 DR EMBL: M25536; AAA34256.1; -;
 DR FAY: S09623; S09623.
 DR PDB: 7WGA; 15-OCT-90.
 DR PDB: 1WGC; 15-OCT-90.
 DR PDB: 2CWG; 31-JAN-94.
 DR InterPro: IPR001002; Chitin_binding_1.
 DR Pfam: PF00187; Chitin_bind_1; 4.
 DR PRINTS: PR00451; CHITINBINDING.
 DR ProDom: PD000609; Chitin_binding_1; 4.
 DR SMART: SM00270; ChEBD1; 4.
 DR PROSITE: PS00941; CHIT_BIND_1; 2; 4.
 DR PROSITE: PS00026; CHIT_BIND_1; 1; 4.
 KW Lectin; Repeat; Chitin-binding; 3D-structure; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 197 AGGLUTININ ISOLECTIN 1.
 FT PROPEP 198 212

| | | | |
|-------------|---------|-----------|--------------------------|
| FT DOMAIN | 27 | 68 | CHITIN-BINDING TYPE-1 1. |
| FT DOMAIN | 69 | 111 | CHITIN-BINDING TYPE-1 2. |
| FT DOMAIN | 112 | 154 | CHITIN-BINDING TYPE-1 3. |
| FT DOMAIN | 155 | 197 | CHITIN-BINDING TYPE-1 4. |
| FT DISULFID | 29 | 44 | |
| FT DISULFID | 38 | 50 | |
| FT DISULFID | 43 | 57 | |
| FT DISULFID | 61 | 66 | |
| FT DISULFID | 72 | 87 | |
| FT DISULFID | 81 | 93 | |
| FT DISULFID | 86 | 100 | |
| FT DISULFID | 104 | 109 | |
| FT DISULFID | 115 | 130 | |
| FT DISULFID | 124 | 136 | |
| FT DISULFID | 129 | 143 | |
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| FT CONFLICT | 63 | 63 | |
| FT STRAND | 30 | 30 | |
| FT HELIX | 31 | 33 | |
| FT TURN | 34 | 35 | |
| FT STRAND | 36 | 37 | |
| FT STRAND | 39 | 41 | |
| FT STRAND | 43 | 44 | |
| FT TURN | 46 | 47 | |
| FT STRAND | 50 | 52 | |
| FT HELIX | 54 | 57 | |
| FT TURN | 59 | 60 | |
| FT STRAND | 63 | 63 | |
| FT STRAND | 71 | 71 | |
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| FT TURN | 77 | 78 | |
| FT STRAND | 79 | 79 | |
| FT TURN | 83 | 84 | |
| FT STRAND | 86 | 87 | |
| FT TURN | 89 | 90 | |
| FT STRAND | 92 | 95 | |
| FT HELIX | 97 | 100 | |
| FT TURN | 102 | 103 | |
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| FT STRAND | 114 | 114 | |
| FT STRAND | 116 | 116 | |
| FT HELIX | 117 | 119 | |
| FT TURN | 120 | 121 | |
| FT STRAND | 122 | 122 | |
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| FT TURN | 132 | 133 | |
| FT STRAND | 135 | 138 | |
| FT HELIX | 140 | 143 | |
| FT TURN | 145 | 146 | |
| FT STRAND | 149 | 149 | |
| FT STRAND | 159 | 159 | |
| FT HELIX | 160 | 162 | |
| FT TURN | 163 | 164 | |
| FT STRAND | 165 | 165 | |
| FT HELIX | 168 | 170 | |
| FT STRAND | 172 | 173 | |
| FT TURN | 175 | 176 | |
| FT STRAND | 179 | 181 | |
| FT HELIX | 183 | 186 | |
| FT TURN | 188 | 189 | |
| FT STRAND | 192 | 192 | |
| FT SEQUENCE | 212 AA; | 21239 MW; | EC7B6F007DDC15EB CRC64; |

Query Match 80.6%; Score 25; DB 1; Length 212;
 Best Local Similarity 83.3%; Pred. No. 31;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Thu Sep 30 13:18:52 2004

Cy 1 LMSTRA 6
:|||||
Db 3 MMSTRA 8

Search completed: September 30, 2004, 06:01:16
Job time : 6.27119 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 22.8983 Seconds
(without alignments)
96.454 Million cell updates/sec

Title: US-09-674-716b-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$
Maximum Match 100\$
Listing first 45 summaries

Database :

- 1: sp_archaea:
- 2: sp_bacteria:
- 3: sp_fungi:
- 4: sp_human:
- 5: sp_invertebrate:
- 6: sp_mammal:
- 7: sp_mhc:
- 8: sp_organelle:
- 9: sp_phase:
- 10: sp_plant:
- 11: sp_rodent:
- 12: sp_virus:
- 13: sp_vertebrate:
- 14: sp_unclassified:
- 15: sp_rvirus:
- 16: sp_bacteriap:
- 17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 28 | 90.3 | 847 | 16 Q7UWT5 | Q7UWT5 rhodopirell |
| 2 | 27 | 87.1 | 124 | 15 Q8EEB9 | Q8EEB9 shewanella |
| 3 | 27 | 87.1 | 342 | 16 Q9P110 | Q9P110 campylobact |
| 4 | 27 | 87.1 | 409 | 16 Q8X5U5 | Q8X5U5 escherichia |
| 5 | 27 | 87.1 | 409 | 16 Q8FJ15 | Q8FJ15 escherichia |
| 6 | 27 | 87.1 | 505 | 16 Q7UQP6 | Q7UQP6 rhodopirell |
| 7 | 27 | 87.1 | 541 | 5 Q868T1 | Q868T1 anopheles g |
| 8 | 27 | 87.1 | 544 | 11 Q8BX14 | Q8BX14 mus musculu |
| 9 | 27 | 87.1 | 579 | 5 Q7YV69 | Q7YV69 cryptospori |
| 10 | 27 | 87.1 | 657 | 11 Q8BLC8 | Q8BLC8 mus musculu |
| 11 | 27 | 87.1 | 860 | 5 Q198S2 | Q198S2 caenorhabdi |
| 12 | 27 | 87.1 | 1024 | 11 Q9ESJ5 | Q9ESJ5 mus musculu |
| 13 | 27 | 87.1 | 1049 | 2 Q9XBP6 | Q9XBP6 myxococcus |
| 14 | 27 | 87.1 | 1141 | 10 Q8LJU7 | Q8LJU7 cryza sativ |
| 15 | 26 | 83.9 | 112 | 16 Q92W36 | Q92W36 rhizobium m |
| 16 | 26 | 83.9 | 114 | 6 Q862S4 | Q862S4 bos taurus |

| | | | | | |
|----|----|------|------|-----------|--------------------|
| 17 | 26 | 83.9 | 212 | 6 Q862R9 | Q862R9 bos taurus |
| 18 | 26 | 83.9 | 284 | 4 Q160S0 | Q160S0 homo sapien |
| 19 | 26 | 83.9 | 287 | 6 Q95ND8 | Q95ND8 bos taurus |
| 20 | 26 | 83.9 | 313 | 16 Q92TL9 | Q92TL9 rhizobium m |
| 21 | 26 | 83.9 | 325 | 11 Q60785 | Q60785 mus musculu |
| 22 | 26 | 83.9 | 338 | 8 Q9B2J6 | Q9B2J6 chrysomya c |
| 23 | 26 | 83.9 | 338 | 8 Q9MFQ0 | Q9MFQ0 cochliomyia |
| 24 | 26 | 83.9 | 340 | 8 Q9XMP1 | Q9XMP1 ceratitis c |
| 25 | 26 | 83.9 | 341 | 8 Q9MGL3 | Q9MGL3 drosophila |
| 26 | 26 | 83.9 | 341 | 8 Q9MGN7 | Q9MGN7 drosophila |
| 27 | 26 | 83.9 | 341 | 8 Q9MGN2 | Q9MGN2 drosophila |
| 28 | 26 | 83.9 | 341 | 8 Q9MDS9 | Q9MDS9 drosophila |
| 29 | 26 | 83.9 | 341 | 8 Q9MGP1 | Q9MGP1 drosophila |
| 30 | 26 | 83.9 | 341 | 8 Q9MD72 | Q9MD72 drosophila |
| 31 | 26 | 83.9 | 341 | 8 Q9MJC9 | Q9MJC9 drosophila |
| 32 | 26 | 83.9 | 341 | 8 Q9MD83 | Q9MD83 drosophila |
| 33 | 26 | 83.9 | 420 | 16 Q8E9A1 | Q8E9A1 shewanella |
| 34 | 26 | 83.9 | 437 | 16 Q7V3T8 | Q7V3T8 prochloroco |
| 35 | 26 | 83.9 | 481 | 13 Q90YJ1 | Q90YJ1 brachydanio |
| 36 | 26 | 83.9 | 531 | 10 Q8L4V1 | Q8L4V1 cryza sativ |
| 37 | 26 | 83.9 | 589 | 11 Q99LL6 | Q99LL6 mus musculu |
| 38 | 26 | 83.9 | 718 | 16 Q8D859 | Q8D859 vibrio vuln |
| 39 | 26 | 83.9 | 810 | 16 Q696S0 | Q696S0 mycobacteri |
| 40 | 26 | 83.9 | 810 | 16 Q7TVY3 | Q7TVY3 mycobacteri |
| 41 | 26 | 83.9 | 1453 | 11 Q63079 | Q63079 ratus norv |
| 42 | 26 | 83.9 | 1453 | 11 Q810J9 | Q810J9 mus musculu |
| 43 | 26 | 83.9 | 1461 | 4 Q76045 | Q76045 homo sapien |
| 44 | 26 | 83.9 | 1464 | 4 Q8N473 | Q8N473 homo sapien |
| 45 | 25 | 80.6 | 135 | 2 Q8RQ37 | Q8RQ37 bacillus ce |

ALIGNMENTS

RESULT 1
Q7UWT5 PRELIMINARY; PRT; 847 AA.
AC Q7UWT5; 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN R81802.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
RL EMEL; BX294135; CAD72277.1;
DR Hypothetical protein; Complete proteome.
KW Hypothetical protein; 89847 MW; 437EF2CED0B2812 CRC64;
SQ SEQUENCE 847 AA; 89847 MW; 437EF2CED0B2812 CRC64;

Query Match 90.3%; Score 28; DB 16; Length 847;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 177 LMSTRAS 183

RESULT 2
Q8EEB9 PRELIMINARY; PRT; 124 AA.
ID Q8EEB9

Q8EBB9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Adhesion-related protein.
 GN SO2467.
 OS Shewanella oneidensis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Alteromonadaceae; Shewanella.
 OX NCBI_TaxID=70863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NR-1;
 RX MEDLINE=2297686; PubMed=12368813;
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Brinkac L., Daugherty S.,
 RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
 RA Madupu R., Peterson J.D., Unayam L.A., White O., Wolf A.M.,
 RA Vamathevan J., Weidman J., Imprim M., Lee K., Berry K., Lee C.,
 RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., C.M.;
 RA Feldblyum T.V., Smith H.O., Venter J.C., Neelson K.H., Fraser C.M.;
 RA "Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT Shewanella oneidensis.";
 RL Nat. Biotechnol. 20:1118-1123 (2002).
 DR EMBL; AB015688; AAN55499.1; -.
 DR TIGR; SO2467; -.
 KW Complete proteome.
 SQ SEQUENCE 124 AA; 13061 MW; D77E2F6F42DEF735 CRC64;
 QY 1 LMSTRAS 7
 Db 83 LMSTRAS 89
 Query Match 87.1%; Score 27; DB 16; Length 124;
 Best Local Similarity 85.7%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 Db 83 LMSTRAS 89
 RESULT 3
 Q9PIIO PRELIMINARY; PRT; 342 AA.
 AC Q9PIIO;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Flagellar motor switch protein.
 GN FLIG OR CJ0319.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NTCT 11168;
 RX MEDLINE=20150912; PubMed=10688204;
 RA Parkhill J., Wren B.W., Mungall K., Kerley J.M., Church C.,
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtrold S.,
 RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajadream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrall B.G.;
 RA "The genome sequence of the food-borne pathogen Campylobacter jejuni
 RT reveals hypervariable sequences.";
 RL Nature 403:665-668 (2000).
 DR EMBL; AL139074; CAB72786.1; -.
 DR PIR; C81451; C81451.
 DR HSP; Q9WY63; 1QC7.
 DR GO; GO:0009288; C:flagellum (sensu Bacteria); IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0006935; P:chemotaxis; IEA.
 DR GO; GO:0001539; P:ciliary/flagellar motility; IEA.
 DR InterPro; IPR000090; Flg_Motor_Flg.
 DR Pfam; PF01706; Flig-C; 1.

DR PRINTS; PR00954; FLGMOTORFLIG.
 DR TIGRFams; TIGR00207; flig; 1.
 KW Complete proteome.
 SQ SEQUENCE 342 AA; 38429 MW; ED4D214417C1524C CRC64;
 Query Match 87.1%; Score 27; DB 16; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTRAS 7
 Db 289 MSTRAS 294
 RESULT 4
 Q8XSUS PRELIMINARY; PRT; 409 AA.
 ID Q8XSUS;
 AC Q8XSUS;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative beta-ketoacyl-ACP synthase (Putative 3-oxoacyl-(acyl-carrier-
 DE protein) synthase II).
 GN Z4866 OR EC34341.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.F., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
 RL Nature 409:529-533 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 050952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.,
 RA "Complete genome sequence of enterohaemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22 (2001).
 DR EMBL; AE005571; AAG58601.1; -.
 DR EMBL; AP002565; BAB37764.1; -.
 DR PIR; E86017; E86017.
 DR PIR; E91171; E91171.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro; IPR000794; Ketoacyl synth.
 DR Pfam; PF00109; ketoacyl-synt; 1.
 DR Pfam; PF02801; ketoacyl-synt C; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
 KW Complete proteome.
 SQ SEQUENCE 409 AA; 44148 MW; A4DAB0AFALIED883 CRC64;
 Query Match 87.1%; Score 27; DB 16; Length 409;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTRAS 7
 Db 77 MSTRAS 82

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RESULT 5
Q8FJ15 2 MSTRAS 7
ID Q8FJ15 PRELIMINARY; PRT; 409 AA.
AC Q8FJ15
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-ketoacyl-ACP synthase.
GN Cll86.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=06:HI / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RX "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AB016758; AAN79648.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0006533; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR000794; K:Ketoacyl_synth.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt C; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
KW Complete proteome.
SQ SEQUENCE 409 AA; 44133 MW; FEDAA0651B6E1239 CRC64;

Query Match 87.1%; Score 27; DB 16; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTRAS 7
Db 77 MSTRAS 82

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RESULT 6
Q7UQF6 2 MSTRAS 7
ID Q7UQF6 PRELIMINARY; PRT; 505 AA.
AC Q7UQF6
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Probable iron-sulfur protein.
GN RB6355.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR EMBL; BX294144; CAD74747.1; -.
KW Complete proteome.
SQ SEQUENCE 505 AA; 55984 MW; 22B90195A3E1D941 CRC64;

Query Match 87.1%; Score 27; DB 16; Length 505;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 MSTRAS 7
Db 1 MSTRAS 6

RESULT 7
Q868T1 2 MSTRAS 7
ID Q868T1 PRELIMINARY; PRT; 541 AA.
AC Q868T1
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gag-like protein (Fragment).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22531580; PubMed=12644555;
RA Kojima K.K., Fujiwara H.;
RT "Evolution of Target Specificity in R1 Clade Non-LTR
RT Retrotransposons.";
RL Mol. Biol. Evol. 20:351-361 (2003).
DR EMBL; AB090812; BAC57899.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_C2HC; 2.
DR PROSITE; PS50158; ZF_CCHC; 2.
FT NON_TER
SQ SEQUENCE 541 AA; 60221 MW; 6CB5F551260FDF55 CRC64;

Query Match 87.1%; Score 27; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTRAS 7
Db 37 MSTRAS 42

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RESULT 8
Q8BX14 2 MSTRAS 7
ID Q8BX14 PRELIMINARY; PRT; 544 AA.
AC Q8BX14
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RAP guanine nucleotide exchange factor homolog.
GN C030018K18RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK049228; BAC33622.1; -.
DR MGD; MGI:1924777; C030018K18RIK.
DR GO; GO:0005085; F:guanyl-nucleotide exchange factor activity; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR000651; RasGEFN.
DR InterPro; IPR008937; Ras_GEF.

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DR Pfam; PF00027; cNMP binding; 1.
 DR Pfam; PF00618; RasGEFN; 1.
 DR SMART; SM00100; cNMP; 1.
 DR SMART; SM00229; RasGEFN; 1.
 DR PROSITE; PS50042; cNMP BINDING_3; 2.
 DR PROSITE; PS50212; RasGEFN; 1.
 DR PROSITE; PS50212; RasGEFN; 1.
 SQ SEQUENCE 544 AA; 8225 MW; B8285479CB5ACEF5 CRC64;

Query Match 87.1%; Score 27; DB 11; Length 544;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6
 DB 48 LMSTRA 53

RESULT 9

Q7YV69
 ID Q7YV69 PRELIMINARY; PRT; 579 AA.
 AC Q7YV69;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN 56K.15.
 OS Cryptosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporidiidae; Cryptosporidium.
 OX NCBI_TaxID=5807;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=Iowa;
 RA Bankier A.T., Spriggs H.F., Partmann B., Konfortov B.A., Madera M.,
 RA Vogel C., Reichmann S.A., Ivens A., Dear P.H.,
 RT "Integrated mapping, chromosomal sequencing and sequence analysis of
 RT Cryptosporidium parvum."
 RL Genome Res. 0:0-0(2003).
 KW EMBL; BX538350; CAD98618.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 579 AA; 67569 MW; 3F153FD2678AEC75 CRC64;

Query Match 87.1%; Score 27; DB 5; Length 579;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 DB 393 LMSTRAS 399

RESULT 10

Q8BLC8
 ID Q8BLC8 PRELIMINARY; PRT; 657 AA.
 AC Q8BLC8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RAP guanine nucleotide exchange factor homolog (fragment).
 GN C030018K18RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Brain;
 RA MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).

DR EMBL; AK045540; BAC32411.1; -.
 DR MGD; MGI:1924777; C030018K18RIK.
 DR GO; GO:0005085; F:guanyl-nucleotide exchange factor activity; IEA.
 DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
 DR InterPro; IPR000595; cNMP_binding.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR000651; RasGEFN.
 DR InterPro; IPR008937; Ras GEF.
 DR Pfam; PF00037; cNMP binding; 1.
 DR Pfam; PF00595; PDZ_1.
 DR Pfam; PF00618; RasGEFN; 1.
 DR SMART; SM00100; cNMP; 1.
 DR SMART; SM00228; PDZ; 1.
 DR SMART; SM00229; RasGEFN; 1.
 DR PROSITE; PS50042; cNMP BINDING_3; 2.
 DR PROSITE; PS50106; PDZ_1.
 DR PROSITE; PS50212; RasGEFN; 1.
 DR PROSITE; PS50212; RasGEFN; 1.
 FT NON_TER 657
 SQ SEQUENCE 657 AA; 74726 MW; C531B0D1FB4E4D9A CRC64;

Query Match 87.1%; Score 27; DB 11; Length 657;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6
 DB 48 LMSTRA 53

RESULT 11

Q19852
 ID Q19852 PRELIMINARY; PRT; 860 AA.
 AC Q19852;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN F2884.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium."
 RL Science 282:2012-2018(1998).
 RN [2]
 RC SEQUENCE FROM N.A.
 RP STRAIN=Bristol N2;
 RA Leimbach D.;
 RT "The sequence of C. elegans cosmid F28B4."
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RC SEQUENCE FROM N.A.
 RP STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submission."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U42834; AAA83583.2; -.
 DR PIR; T16198; T16198.
 DR HSSP; Q61193; 18LF.
 DR WormPep; F2854.2; CE28222.
 DR GO; GO:0005085; F:guanyl-nucleotide exchange factor activity; IEA.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
 DR InterPro; IPR000651; RasGEFN.
 DR InterPro; IPR001895; RasGEFN.
 DR InterPro; IPR008937; Ras GEF.
 DR InterPro; IPR00159; RA_Domain.
 DR InterPro; IPR00159; RA_Domain.


```

DR Pfam; PF00788; RA; 1.
DR Pfam; PF00617; RasGEF; 1.
DR Pfam; PF00618; RasGEFN; 1.
DR SMART; SM00314; RA; 1.
DR SMART; SM00147; RasGEF; 1.
DR SMART; SM00229; RasGEFN; 1.
DR PROSITE; PS00300; RA; 1.
DR PROSITE; PS00720; RasGEF; 1.
DR PROSITE; PS00009; RasGEF_CAT; 1.
DR PROSITE; PS0212; RasGEF_NTER; 1.
KW Hypothetical protein.
SQ SEQUENCE 860 AA; 96122 MW; 16088524FBC65CA5 CRC64;

Query Match
Best Local Similarity 87.1%; Score 27; DB 5; Length 860;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTRAS 7
Db 668 MSTRAS 673

RESULT 12
Q9ESJ5 PRELIMINARY; PRT; 1024 AA.
AC Q9ESJ5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glur-delta2 philic-protein.
GN GRID2IP OR DELPHILIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Miyagi Y., Yamashita T., Okuda K., Mishina M., Kawamoto S.;
RT "Delphinin: A novel PDZ-containing protein associates with the Glur-
delta2 subunit."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; AF099933; AAG31020.1; -.
DR HSSP; P29476; IQAV.
DR MGD; MGI:2176213; Grid2ip.
DR GO; GO:0019717; C:synaptoosome; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR003104; FH2.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF02181; FH2; 1.
DR Pfam; PF00595; PDZ; 1.
DR SMART; SM00498; FH2; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS0106; PDZ; 1.
SQ SEQUENCE 1024 AA; 112578 MW; E318AFDE02F846A CRC64;

Query Match
Best Local Similarity 87.1%; Score 27; DB 11; Length 1024;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 53 LVSTRAS 59

RESULT 13
Q9XBP6 PRELIMINARY; PRT; 1049 AA.
AC Q9XBP6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

```

```

DE Serine/threonine kinase PKN8.
GN PKN8.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cytoobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DZFI;
RA Inouye S., Jain R., Ueki T., Nariya H., Xu C., Hsu M.,
RA Munoz-Dorado J., Farez-Vidal E., Inouye M.;
RT "Sequence Analysis of 13 Eukaryotic-like Protein Ser/Thr Kinases of
RT Myxococcus xanthus, a Developmental Bacterium and Significance of
RT Their Coexistence with Protein His Kinases."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159691; AAD42856.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001440; TPR-like.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00515; TPR; 5.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00028; TPR_3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 1049 AA; 114313 MW; 7752862DAA25338C CRC64;

Query Match
Best Local Similarity 87.1%; Score 27; DB 2; Length 1049;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1002 LMSTRAS 1008

RESULT 14
Q8LJJ7 PRELIMINARY; PRT; 1141 AA.
AC Q8LJJ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative chromodomain-helicase-DNA-binding protein.
GN P0018C10.33.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sakaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone: P0018C10."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003227; BAC06232.1; -.
DR Gramene; Q8LJJ7; -.
DR GO; GO:000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.
DR GO; GO:0003682; F:chromatin binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006333; P:chromatin assembly/disassembly; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000953; Chromo.

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DR InterPro; IPR001410; DEAD.
DR InterPro; IPR002464; DEAH_box.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR000330; SNF2_N.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00385; Chromo; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00176; SNF2_N; 1.
DR SMART; SM00298; CHROMO; 2.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS00013; CHROMO_2; 2.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
DR PROSITE; PS01359; ZF_PHD_1; 1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
KW ATP-binding; DNA-binding; Helicase; Hydrolase.
SQ SEQUENCE 1141 AA; 128517 MW; 47B812CC0ABC2649 CRC64;

Query Match      87.1%; Score 27; DB 10; Length 1141;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6
Db 908 LMSTRA 913

RESULT 15
Q92W36 PRELIMINARY; PRT; 112 AA.
AC Q92W36;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein RB0509.
GN RB0509 OR SMB20530.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymB (megaplasmid 2).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_taxid=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Gouzy J.,
RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puhler A.;
RT "The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
DR EMBL; AL603643; CAC48509.1; -.
DR FIR; E95905; E95905.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 112 AA; 11488 MW; 95FD54B0FC5CA90E CRC64;

Query Match      83.9%; Score 26; DB 16; Length 112;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 5 IMSTRSS 11

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2004, 05:55:56 ; Search time 34.1695 Seconds
(without alignments)
57.883 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 25Jan04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 31 | 100.0 | 7 | 2 AAW39825 | AAW39825 Light cha |
| 2 | 31 | 100.0 | 7 | 2 AAW39822 | AAW39822 Light cha |
| 3 | 31 | 100.0 | 7 | 2 AAW39819 | AAW39819 Light cha |
| 4 | 31 | 100.0 | 7 | 3 AAV32255 | AAV32255 Light cha |
| 5 | 31 | 100.0 | 100 | 4 AA06969 | AA06969 Mouse ger |
| 6 | 31 | 100.0 | 113 | 2 AAW39803 | AAW39803 Variable |
| 7 | 31 | 100.0 | 113 | 2 AAW39886 | AAW39886 Light cha |
| 8 | 31 | 100.0 | 113 | 2 AAW39802 | AAW39802 Variable |
| 9 | 31 | 100.0 | 113 | 2 AAW39882 | AAW39882 Light cha |
| 10 | 31 | 100.0 | 113 | 2 AAW39804 | AAW39804 Variable |
| 11 | 31 | 100.0 | 116 | 3 AAV32262 | AAV32262 Humanised |
| 12 | 31 | 100.0 | 145 | 3 AAV32261 | AAV32261 Mouse ant |
| 13 | 28 | 90.3 | 7 | 2 AAW39816 | AAW39816 Light cha |
| 14 | 28 | 90.3 | 113 | 2 AAW39801 | AAW39801 Variable |
| 15 | 28 | 90.3 | 274 | 2 AAW39899 | AAW39899 Single ch |
| 16 | 28 | 90.3 | 979 | 7 ADB64292 | ADB64292 Human pro |
| 17 | 27 | 87.1 | 7 | 2 AAW39876 | AAW39876 Light cha |
| 18 | 27 | 87.1 | 68 | 4 AAU54213 | AAU54213 Propionib |
| 19 | 27 | 87.1 | 68 | 6 ABM50732 | ABM50732 Propionib |
| 20 | 27 | 87.1 | 119 | 6 ABU00435 | ABU00435 Human nov |
| 21 | 27 | 87.1 | 123 | 4 AAU54742 | AAU54742 Propionib |
| 22 | 27 | 87.1 | 123 | 6 ABM51261 | ABM51261 Propionib |
| 23 | 27 | 87.1 | 131 | 2 AAR12232 | AAR12232 Mouse Mab |
| 24 | 27 | 87.1 | 132 | 2 AAR12354 | AAR12354 Light (ka |
| 25 | 27 | 87.1 | 140 | 4 AAM95756 | AAM95756 Human rep |

| | | | | | | |
|----|----|------|-----|---|----------|-----------|
| 26 | 27 | 87.1 | 218 | 5 | ABG77402 | Selected |
| 27 | 27 | 87.1 | 218 | 5 | ABJ11304 | Yeast sel |
| 28 | 27 | 87.1 | 342 | 6 | ABU26357 | Protein e |
| 29 | 27 | 87.1 | 409 | 4 | ABBS2717 | Escherich |
| 30 | 27 | 87.1 | 809 | 5 | ABP73372 | Candida a |
| 31 | 27 | 87.1 | 845 | 6 | ABR33640 | Protein s |
| 32 | 26 | 83.9 | 77 | 4 | AAU39838 | Propionib |
| 33 | 26 | 83.9 | 77 | 6 | ABM36357 | Propionib |
| 34 | 26 | 83.9 | 115 | 4 | AAU41133 | Peptide # |
| 35 | 26 | 83.9 | 115 | 4 | ABB33078 | Peptide # |
| 36 | 26 | 83.9 | 115 | 4 | AAW26539 | Peptide # |
| 37 | 26 | 83.9 | 115 | 4 | ABB27906 | Human pep |
| 38 | 26 | 83.9 | 115 | 4 | ABBI8546 | Protein # |
| 39 | 26 | 83.9 | 115 | 4 | AAW66263 | Human bon |
| 40 | 26 | 83.9 | 115 | 4 | AAW53875 | Human bra |
| 41 | 26 | 83.9 | 115 | 4 | ABG47927 | Human liv |
| 42 | 26 | 83.9 | 115 | 4 | AAU01871 | Peptide # |
| 43 | 26 | 83.9 | 115 | 5 | ABG35910 | Human pep |
| 44 | 26 | 83.9 | 133 | 7 | ADB64310 | Human pro |
| 45 | 26 | 83.9 | 134 | 4 | ABG10627 | Novel hum |

ALIGNMENTS

RESULT 1
AAW39825
ID AAW39825 standard; peptide; 7 AA.
XX
AC AAW39825;
XX
DT 16-JUN-1998 (first entry)
XX
DE Light chain CDR2 of catalytic antibody 12H1.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
PN WO9749800-A1.
XX
PD 31-DEC-1997.
XX
PF 25-JUN-1997; 97WO-US010965.
XX
PR 25-JUN-1996; 96US-00672345.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Laundry DW;
XX
DR WPI; 1998-077166/07.
XX
PT New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX
PS Claim 17; Page 83; 147pp; English.
XX
CC AAW39824-26 represent the sequences of the light chain complementarity
CC determining regions (CDRs) of the catalytic antibody 12H1, which is able
CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC were prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release 3H-
CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified
CC using TSA2, and has a per minute Kcat of 0.16. The antibodies reduce the
CC concentration of cocaine in a subject, and are used particularly for the
CC treatment of an overdose. They are also used for treating addiction (by
CC reducing the in vivo concentration that can be achieved)

SQ Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 Db 1 LMSTRAS 7
 |||||

RESULT 2
 AAW39822
 ID AAW39822 standard; peptide; 7 AA.
 XX AC AAW39822;
 XX DT 16-JUN-1998 (first entry)
 XX DE Light chain CDR2 of catalytic antibody 2A10.
 XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
 XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 XX KW overdose; addiction.
 XX OS Mus sp.
 XX PN WO9749800-A1.
 XX PD 31-DEC-1997.
 XX PF 25-JUN-1997; 97WO-US010965.
 XX PR 25-JUN-1996; 96US-00672345.
 XX PS (UYCO) UNIV COLUMBIA NEW YORK.
 XX PI Landry DW;
 XX DR WPI; 1998-077166/07.
 XX PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX PS Claim 15; Page 82; 147pp; English.

AAW39821-23 represent the sequences of the light chain complementarity
 determining regions (CDRs) of the catalytic antibody 2A10, which is able
 to degrade cocaine. A series of cocaine transition state analogues (TSAs)
 were prepared and used to immunise mice for production of hybridomas.
 Catalytic antibodies were identified by their capacity to release 3H-
 benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
 using TSA1, which is an immunogenic conjugate of a phosphate monoester
 transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
 The antibodies reduce the concentration of cocaine in a subject, and are
 used particularly for the treatment of an overdose. They are also used
 for treating addiction (by reducing the in vivo concentration that can be
 achieved)

SQ Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 Db 1 LMSTRAS 7
 |||||

RESULT 3
 AAW39822
 ID AAW39822 standard; peptide; 7 AA.
 XX AC AAW39822;
 XX DT 16-JUN-1998 (first entry)
 XX DE Light chain CDR2 of catalytic antibody 2A10.
 XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
 XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 XX KW overdose; addiction.
 XX OS Mus sp.
 XX PN WO9749800-A1.
 XX PD 31-DEC-1997.
 XX PF 25-JUN-1997; 97WO-US010965.
 XX PR 25-JUN-1996; 96US-00672345.
 XX PS (UYCO) UNIV COLUMBIA NEW YORK.
 XX PI Landry DW;
 XX DR WPI; 1998-077166/07.
 XX PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX PS Claim 15; Page 82; 147pp; English.

AAW39821-23 represent the sequences of the light chain complementarity
 determining regions (CDRs) of the catalytic antibody 2A10, which is able
 to degrade cocaine. A series of cocaine transition state analogues (TSAs)
 were prepared and used to immunise mice for production of hybridomas.
 Catalytic antibodies were identified by their capacity to release 3H-
 benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
 using TSA1, which is an immunogenic conjugate of a phosphate monoester
 transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
 The antibodies reduce the concentration of cocaine in a subject, and are
 used particularly for the treatment of an overdose. They are also used
 for treating addiction (by reducing the in vivo concentration that can be
 achieved)

AAW39819
 ID AAW39819 standard; peptide; 7 AA.
 XX AC AAW39819;
 XX DT 16-JUN-1998 (first entry)
 XX DE Light chain CDR2 of catalytic antibody 6A12.
 XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
 XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 XX KW overdose; addiction.
 XX OS Mus sp.
 XX PN WO9749800-A1.
 XX PD 31-DEC-1997.
 XX PF 25-JUN-1997; 97WO-US010965.
 XX PR 25-JUN-1996; 96US-00672345.
 XX PS (UYCO) UNIV COLUMBIA NEW YORK.
 XX PI Landry DW;
 XX DR WPI; 1998-077166/07.
 XX PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX PS Claim 13; Page 81; 147pp; English.

AAW39818-20 represent the sequences of the light chain complementarity
 determining regions (CDRs) of the catalytic antibody 6A12, which is able
 to degrade cocaine. A series of cocaine transition state analogues (TSAs)
 were prepared and used to immunise mice for production of hybridomas.
 Catalytic antibodies were identified by their capacity to release 3H-
 benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified
 using TSA1, which is an immunogenic conjugate of a phosphate monoester
 transition state analogue. Antibody 6A12 has a per minute Kcat of 0.072.
 The antibodies reduce the concentration of cocaine in a subject, and are
 used particularly for the treatment of an overdose. They are also used
 for treating addiction (by reducing the in vivo concentration that can be
 achieved)

SQ Sequence 7 AA;
 Query Match 100.0%; Score 31; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 Db 1 LMSTRAS 7
 |||||

RESULT 4
 AAW32255
 ID AAW32255 standard; peptide; 7 AA.
 XX AC AAW32255;
 XX DT 15-FEB-2000 (first entry)
 XX DE Light chain CDR L2 of mouse anti-CD23 MAb C11.
 XX KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
 XX KW monoclonal antibody; chimeric antibody; humanised antibody;
 XX KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic disease; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
KW therapy.
XX
XX
OS Mus musculus.
XX
PN WO958679-A1.
XX
XX
PD 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-GB001434.
XX
PR 09-MAY-1999; 98GB-00009839.
XX
XX (GLAX) GLAXO GROUP LTD.
XX
XX Bonnefoy JUMP, Crowe SJ, Ellis JH, Rapson NT, Sheariz J;
PI WPI; 2000-053101/04.
XX
DR N-PSDB; AAZ34749.
XX
XX
PT Cell receptor specific antibodies useful for treating e.g. arthritis,
PT diabetes, multiple sclerosis and psoriasis.
XX
XX
PS Claim 1; Page 40; 81pp; English.
XX
XX This sequence represents complementarity determining region 2 (CDR L2)
CC of the light chain of murine anti-CD23 (FCB2II) monoclonal antibody C11
CC (see also AAY32262). The invention provides altered antibodies, such as
CC chimeric or humanised antibodies, which comprise sufficient of the amino
CC acid residues of C11 light and heavy chain CDRs (see AAY32254-59) to
CC render them capable of binding to the CD23 type II molecule expressed on
CC haematopoietic cells. The antibodies are used to block soluble CD23
CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
CC are also useful for studying interactions between CD23 and various
CC ligands and determining the binding agents
XX
XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7
| | | | |
| | | | |

RESULT 5
ID AAE06969 standard; protein; 100 AA.
XX
XX AAE06969;
XX
XX 16-OCT-2001 (first entry)
XX
XX Mouse germline kappa light chain variable (VK) region, 167/24.
XX
XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KW neuroprotective; immunosuppressive; human immunodeficiency virus;
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;

KW multiple sclerosis; atherosclerosis; arteriosclerosis; restenosis; asthma;
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
KW inflammatory glomerulopathy; vascular intervention;
XX neointimal hyperplasia; VK; kappa light chain variable region.
XX
XX Mus sp.
XX
PN WO200157226-A1.
XX
XX 09-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US003537.
XX
XX 03-FEB-2000; 2000US-00497625.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
PI WPI; 2001-488888/53.
XX
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
PT disorder in a patient, comprises a binding specificity for CCR2, and a
PT non-human antigen binding region and human immunoglobulin.
XX
XX Disclosure; Page 151; 183pp; English.
XX
XX The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
CC comprising an antigen binding region of non-human origin and at least a
CC portion of an immunoglobulin of human origin. The humanised antibodies
CC are useful for inhibiting the interaction of a cell expressing CCR2. They
CC are useful for inhibiting or treating HIV infection. The proteins of the
CC invention are useful for inhibiting leukocyte trafficking, for treating
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
CC disorders such as rheumatoid arthritis and multiple sclerosis,
CC atherosclerosis and arteriosclerosis, and for inhibiting restenosis. They
CC are useful in therapy or diagnosis, and in the manufacture of a
CC medicament for treating CCR-2 mediated disease. They are also useful for
CC treating allergy, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and IgE-mediated allergic reaction, shock,
CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
CC associated with vascular intervention, including angioplasty and/or stent
CC placement in a mammal. Humanised antibodies are also useful for
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
CC neointimal hyperplasia of a vessel in a mammal, preferably associated
CC with vascular intervention. The present sequence is mouse germline kappa
CC light chain variable (VK) region, 167/24
XX
XX Sequence 100 AA;

Query Match 100.0%; Score 31; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61
| | | | |
| | | | |

RESULT 6
ID AAW39803
XX AAW39803 standard; protein; 113 AA.
XX
XX AAW39803;
XX
XX 16-JUN-1998 (first entry)
XX
XX Variable domain of the Kappa light chain of catalytic antibody 12H1.
DE
XX Variable domain; lambda light chain; catalytic antibody; degradation;
KW

KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addition.
 XX
 OS Mus sp.
 XX
 FN WO9749800-A1.
 XX
 XX 31-DEC-1997.
 PD
 XX
 XX 25-JUN-1997; 97WO-US010965.
 PF
 XX
 XX 25-JUN-1996; 96US-00672345.
 PR
 XX
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX Landry DW;
 XX
 XX WPI; 1998-077166/07.
 DR
 XX P-PSDB; AAV09802.
 XX
 XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 XX Claim 18; Page 73; 147pp; English.
 PS
 XX AAW39801-05 represent the amino acid sequences of the variable domain of
 CC the kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808
 CC represents the heavy chain) was identified using TSA2, and has a per
 CC minute Kcat of 0.016. The antibodies reduce the concentration of cocaine
 CC in a subject, and are used particularly for the treatment of an overdose.
 CC They are also used for treating addiction (by reducing the in vivo
 CC concentration that can be achieved)
 XX
 XX Sequence 113 AA;
 SQ
 Query Match 100.0%; Score 31; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 Db 55 LMSTRAS 61
 RESULT 7
 AAW39886
 ID AAW39886 standard; protein; 113 AA.
 XX
 AC AAW39886;
 XX
 XX 18-JUN-1998 (first entry)
 DT
 XX
 DE Light chain of the catalytic antibody 6A12.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addition.
 XX
 OS Mus sp.
 XX
 XX WO9749800-A1.
 FN
 XX 31-DEC-1997.
 PD
 XX
 XX 25-JUN-1997; 97WO-US010965.
 PF
 XX
 XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addition.
 XX
 OS Mus sp.
 XX
 XX WO9749800-A1.
 FN
 XX 31-DEC-1997.
 PD
 XX
 XX 25-JUN-1997; 97WO-US010965.
 PF
 XX

PR 25-JUN-1996; 96US-00672345.
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX Landry DW;
 XX
 XX WPI; 1998-077166/07.
 DR
 XX N-PSDB; AAV09793.
 DR
 XX
 XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 XX Disclosure; Fig 19; 147pp; English.
 XX
 XX The present sequence represents the light chain of a catalytic antibody
 CC which is capable of degrading cocaine. A series of cocaine transition
 CC state analogues (TSAs) were prepared and used to immunise mice for
 CC production of hybridomas. Catalytic antibodies were identified by their
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
 CC antibodies reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved)
 XX
 XX Sequence 113 AA;
 SQ
 Query Match 100.0%; Score 31; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 Db 55 LMSTRAS 61
 RESULT 8
 AAW39802
 ID AAW39802 standard; protein; 113 AA.
 XX
 AC AAW39802;
 XX
 XX 16-JUN-1998 (first entry)
 DT
 XX
 DE Variable domain of the kappa light chain of catalytic antibody 6A12.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addition.
 XX
 OS Mus sp.
 XX
 XX WO9749800-A1.
 FN
 XX 31-DEC-1997.
 PD
 XX
 XX 25-JUN-1997; 97WO-US010965.
 PF
 XX
 XX 25-JUN-1996; 96US-00672345.
 PR
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX Landry DW;
 XX
 XX WPI; 1998-077166/07.
 DR
 XX
 XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 XX Claim 14; Page 72; 147pp; English.
 PS
 XX

CC AAW39801-05 represent the amino acid sequences of the variable domain of
 CC the kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 6A12 antibody (AAW39807
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state analogue.
 CC Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the
 CC concentration of cocaine in a subject, and are used particularly for the
 CC treatment of an overdose. They are also used for treating addiction (by
 CC reducing the in vivo concentration that can be achieved)
 XX
 XX Sequence 113 AA;

Query Match 100.0%; Score 31; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 |||||
 Db 55 LMSTRAS 61

RESULT 9
 AAW39882
 ID AAW39882 standard; protein; 113 AA.

XX
 AC AAW39882;

XX
 DT 16-JUN-1998 (first entry)

XX
 DE Light chain of the catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX
 OS Mus sp.

XX
 PN WO9749800-A1.

XX
 PD 31-DEC-1997.

XX
 PF 25-JUN-1997; 97WO-US010965.

XX
 PR 25-JUN-1996; 96US-00672345.

XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.

XX
 PI Landry DW;

XX
 DR WPI; 1998-077166/07.

DR
 N-PSDB; AAV09789.

XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX
 PS Disclosure; Fig 21; 147pp; English.

XX The present sequence represents the light chain of a catalytic antibody
 CC which is capable of degrading cocaine. A series of cocaine transition
 CC state analogues (TSAs) were prepared and used to immunise mice for
 CC production of hybridomas. Catalytic antibodies were identified by their
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
 CC antibodies reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved)

XX
 XX Sequence 113 AA;

Query Match 100.0%; Score 31; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 |||||
 Db 55 LMSTRAS 61

RESULT 10
 AAW39804
 ID AAW39804 standard; protein; 113 AA.

XX
 AC AAW39804;

XX
 DT 16-JUN-1998 (first entry)

XX
 DE Variable domain of the kappa light chain of catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX
 OS Mus sp.

XX
 PN WO9749800-A1.

XX
 PD 31-DEC-1997.

XX
 PF 25-JUN-1997; 97WO-US010965.

XX
 PR 25-JUN-1996; 96US-00672345.

XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.

XX
 PI Landry DW;

XX
 DR WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX
 PS Claim 16; Page 73-74; 147pp; English.

XX AAW39801-05 represent the amino acid sequences of the variable domain of
 CC the kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AAW39809
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state analogue.
 CC Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the
 CC concentration of cocaine in a subject, and are used particularly for the
 CC treatment of an overdose. They are also used for treating addiction (by
 CC reducing the in vivo concentration that can be achieved)

XX
 SQ Sequence 113 AA;

Query Match 100.0%; Score 31; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 |||||
 Db 55 LMSTRAS 61

RESULT 11
 AAY32262

ID AAY32262 standard; protein; 116 AA.
 AC AAY32262;
 XX 15-FEB-2000 (first entry)
 DT
 XX Humanised anti-CD23 Mab C11 light chain variable region.
 DE
 XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Region 1. .23
 FT /note= "framework region 1"
 FT Region 24. .39
 FT /note= "CDR 1"
 FT Region 40. .54
 FT /note= "framework region 2"
 FT Region 55. .61
 FT /note= "CDR 2"
 FT Region 62. .93
 FT /note= "framework region 3"
 FT Region 94. .102
 FT /note= "CDR 3"
 FT Region 103. .113
 FT /note= "framework region 4"
 FT
 XX WO9958679-A1.
 XX
 XX 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-GB001434.
 XX
 XX 09-MAY-1998; 98GB-00009839.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 XX
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX
 XX WPI; 2000-053101/04.
 DR N-PSDB; AA234747.
 XX
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis.
 XX
 XX Claim 9; Fig 3; 81pp; English.
 PS
 XX This sequence represents the light chain variable region (VL) of
 CC humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human
 CC framework (H5IGKVII) and the light chain complementarity determining
 CC regions (see AAY32254-56) of murine antibody C11. The DNA was constructed
 CC by splice overlap PCR. The invention provides altered antibodies, such as
 CC chimeric or humanised antibodies, which comprise sufficient of the amino
 CC acid sequences of the C11 light and heavy chain complementarity
 CC determining regions to render them capable of binding to the CD23 type II
 CC molecule expressed on haematopoietic cells. The antibodies are used to
 CC block soluble CD23 formation in human therapy, for the treatment of
 CC arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-

CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX
 SQ Sequence 116 AA;
 Query Match 100.0%; Score 31; DB 3; Length 116;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 DB 55 LMSTRAS 61
 |||||
 |||||
 RESULT 12
 AAY32261
 ID AAY32261 standard; protein; 145 AA.
 XX
 AC AAY32261;
 XX
 XX 15-FEB-2000 (first entry)
 DT
 XX Mouse anti-CD23 Mab C11 light chain variable region.
 DE
 XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.
 XX
 XX Mus musculus.
 OS
 OS Key Location/Qualifiers
 FT Region 55. .70
 FT /note= "CDR L1"
 FT Region 83. .92
 FT /note= "CDR L2"
 FT Region 125. .134
 FT /note= "CDR L3"
 FT
 XX WO9958679-A1.
 XX
 XX 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-GB001434.
 XX
 XX 09-MAY-1998; 98GB-00009839.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 XX
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX
 XX WPI; 2000-053101/04.
 DR N-PSDB; AA234746.
 XX
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis.
 XX
 XX Claim 8; Fig 2; 81pp; English.
 PS
 XX This sequence represents the light chain variable region (VL) of murine
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies (see
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid
 CC sequences of the C11 light and heavy chain complementarity determining
 CC regions (see AAY32254-59) to render them capable of binding to the CD23

CC type II molecule expressed on haematopoietic cells. The antibodies are
 CC used to block soluble CD23 formation in human therapy, for the treatment
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 CC

SQ Sequence 145 AA;

Query Match 100.0%; Score 31; DB 3; Length 145;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

|||||

86 LMSTRAS 92

RESULT 13

AAW39816

ID AAW39816 standard; peptide; 7 AA.

XX AAW39816;

XX 16-JUN-1998 (first entry)

XX Light chain CDR2 of catalytic antibody 3B9.

XX Variable domain; lambda light chain; catalytic antibody; degradation;

KW cocaine; cocaine transition state analogue; TSA; benzoic acid;

KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;

KW overdose; addiction.

XX Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

PS Claim 11; Page 80; 147pp; English.

XX AAW39815-17 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.

CC Catalytic antibodies were identified by their capacity to release 3H-

CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified

CC using TSA1, which is an immunogenic conjugate of a phosphate monoester

CC transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11.

CC The antibodies reduce the concentration of cocaine in a subject, and are

CC used particularly for the treatment of an overdose. They are also used

CC for treating addiction (by reducing the in vivo concentration that can be

CC achieved)

SQ Sequence 7 AA;

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 7;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

|||||

1 LMSTRSS 7

RESULT 14

AAW39801

ID AAW39801 standard; protein; 113 AA.

XX AAW39801;

XX 16-JUN-1998 (first entry)

XX Variable domain of the Kappa light chain of catalytic antibody 3B9.

XX Variable domain; lambda light chain; catalytic antibody; degradation;

KW cocaine; cocaine transition state analogue; TSA; benzoic acid;

KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;

KW overdose; addiction.

XX Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX P-FSDB; AAW09791.

XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

PS Claim 12; Page 71-72; 147pp; English.

XX AAW39801-05 represent the amino acid sequences of the variable domain of
 CC the Kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.

CC Catalytic antibodies were identified by their capacity to release 3H-

CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806

CC represents the heavy chain) was identified using TSA1, which is an

CC immunogenic conjugate of a phosphate monoester transition state analogue.

CC Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the

CC concentration of cocaine in a subject, and are used particularly for the

CC treatment of an overdose. They are also used for treating addiction (by

CC reducing the in vivo concentration that can be achieved)

SQ Sequence 113 AA;

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 113;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

|||||

55 LMSTRSS 61

RESULT 15

AAW39899 standard; protein; 274 AA.

XX AC AAW39899;

XX DT 16-JUN-1998 (first entry)

XX DE Single chain Fv region of the catalytic antibody 3B9.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX OS Mus sp.

XX FH Key Location/Qualifiers

FT Region 32..37
 FT /note= "complementarity determining region 1 of the heavy
 chain"
 FT Region 52..67
 FT /note= "complementarity determining region 2 of the heavy
 chain"
 FT Region 99..106
 FT /note= "complementarity determining region 3 of the heavy
 chain"
 FT Region 120..134
 FT /note= "linker"
 FT Region 159..174
 FT /note= "complementarity determining region 1 of the light
 chain"
 FT Region 186..192
 FT /note= "complementarity determining region 2 of the light
 chain"
 FT Region 225..233
 FT /note= "complementarity determining region 3 of the light
 chain"
 FT Region 259..263
 FT /note= "Flag epitope sequence"

XX WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX DR WPI; 1998-077166/07.

XX PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS Disclosure; Fig 27; 147pp; English.

XX The present sequence represents the single chain Fv region of the
 CC monoclonal catalytic antibody 3B9, which is capable of degrading cocaine.
 CC A series of cocaine transition state analogues (TSAs) were prepared and
 CC used to immunise mice for production of hybridomas. Catalytic antibodies
 CC were identified by their capacity to release 3H-benzoic acid from 3H-
 CC phenyl cocaine. The antibodies reduce the concentration of cocaine in a
 CC subject, and are used particularly for the treatment of an overdose. They
 CC are also used for treating addiction (by reducing the in vivo
 CC concentration that can be achieved)

XX SQ Sequence 274 AA;

Query Match 90.3%; Score 28; DB 2; Length 274;
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMSTRAS 7
 |||||
 Db 186 LMSTRSS 192

Search completed: September 30, 2004, 06:06:12
 Job time : 37.1695 secs

| | | | | | | |
|----|----|-------|-----|----|----------------------|-------------------|
| 1 | 31 | 100.0 | 7 | 10 | US-09-940-727B-23 | Sequence 23, Appl |
| 2 | 31 | 100.0 | 7 | 10 | US-09-940-727B-26 | Sequence 26, Appl |
| 3 | 31 | 100.0 | 7 | 10 | US-09-940-727B-29 | Sequence 29, Appl |
| 4 | 31 | 100.0 | 100 | 9 | US-09-840-459-32 | Sequence 32, Appl |
| 5 | 31 | 100.0 | 100 | 16 | US-10-766-773-32 | Sequence 32, Appl |
| 6 | 31 | 100.0 | 100 | 16 | US-10-766-610-32 | Sequence 32, Appl |
| 7 | 31 | 100.0 | 100 | 16 | US-10-733-563-32 | Sequence 32, Appl |
| 8 | 31 | 100.0 | 100 | 16 | US-09-940-727B-6 | Sequence 6, Appl |
| 9 | 31 | 100.0 | 113 | 10 | US-09-940-727B-7 | Sequence 7, Appl |
| 10 | 31 | 100.0 | 113 | 10 | US-09-940-727B-8 | Sequence 7, Appl |
| 11 | 31 | 100.0 | 113 | 10 | US-09-940-727B-104 | Sequence 104, App |
| 12 | 31 | 100.0 | 113 | 10 | US-09-940-727B-108 | Sequence 108, App |
| 13 | 31 | 100.0 | 113 | 10 | US-09-940-727B-112 | Sequence 112, App |
| 14 | 29 | 93.5 | 63 | 12 | US-10-424-559-191879 | Sequence 191879, |
| 15 | 28 | 90.3 | 7 | 10 | US-09-940-727B-20 | Sequence 20, Appl |

; APPLICANT: Landry, Donald W
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 0575/51400-B
 ; CURRENT APPLICATION NUMBER: US/09/940,727B
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR APPLICATION NUMBER: 09/214,095
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965
 ; PRIOR FILING DATE: 1997-06-25
 ; PRIOR APPLICATION NUMBER: 08/672,345
 ; PRIOR FILING DATE: 1996-06-25
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 26
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: mouse
 US-09-940-727B-26

Query Match 100.0%; Score 31; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 Db 1 LMSTRAS 7

RESULT 3
 US-09-940-727B-29
 ; Sequence 29, Application US/09940727B
 ; Publication No. US2003007793A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald W
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 0575/51400-B
 ; CURRENT APPLICATION NUMBER: US/09/940,727B
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR APPLICATION NUMBER: 09/214,095
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965
 ; PRIOR FILING DATE: 1997-06-25
 ; PRIOR APPLICATION NUMBER: 08/672,345
 ; PRIOR FILING DATE: 1996-06-25
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 29
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: mouse
 US-09-940-727B-29

Query Match 100.0%; Score 31; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 Db 1 LMSTRAS 7

RESULT 4
 US-09-840-459-32
 ; Sequence 32, Application US/09840459
 ; Patent No. US20020150576A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Larosa, Gregory J.
 ; APPLICANT: Horvath, Christopher
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: O'Brien, Siobhan H.
 ; APPLICANT: O'Keefe, Theresa
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; TITLE OF INVENTION: METHODS OF USE THEREFOR
 ; FILE REFERENCE: 1855.1052-012
 ; CURRENT APPLICATION NUMBER: US/09/840,459
 ; CURRENT FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: PCT/US01/03537
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/497,625
 ; PRIOR FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/359,193
 ; PRIOR FILING DATE: 1999-07-22
 ; PRIOR APPLICATION NUMBER: 09/121,781
 ; PRIOR FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-840-459-32

Query Match 100.0%; Score 31; DB 9; Length 100;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 Db 55 LMSTRAS 61

RESULT 5
 US-10-766-773-32
 ; Sequence 32, Application US/10766773
 ; Publication No. US20040126851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Larosa, Gregory J.
 ; APPLICANT: Horvath, Christopher
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: O'Brien, Siobhan H.
 ; APPLICANT: O'Keefe, Theresa
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 ; TITLE OF INVENTION: METHODS OF USE THEREFOR
 ; FILE REFERENCE: 1855.1052-028
 ; CURRENT APPLICATION NUMBER: US/10/766,773
 ; CURRENT FILING DATE: 2004-01-27
 ; PRIOR APPLICATION NUMBER: 09/497,625
 ; PRIOR FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/359,193
 ; PRIOR FILING DATE: 1999-07-22
 ; PRIOR APPLICATION NUMBER: 09/121,781
 ; PRIOR FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-766-773-32

Query Match 100.0%; Score 31; DB 16; Length 100;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 Db 55 LMSTRAS 61

RESULT 6
 US-10-766-610-32
 ; Sequence 32, Application US/10766610
 ; Publication No. US20040132980A1
 ; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.
 ; APPLICANT: Horvath, Christopher
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: O'Brien, Siobhan H.
 ; APPLICANT: O'Keefe, Theresa
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 ; METHODS OF USE THEREFOR
 ; FILE REFERENCE: 1855-1052-029
 ; CURRENT APPLICATION NUMBER: US/10/766,610
 ; CURRENT FILING DATE: 2004-01-27
 ; PRIOR APPLICATION NUMBER: 09/840,459
 ; PRIOR FILING DATE: 2001-04-23
 ; PRIOR APPLICATION NUMBER: PCT/US01/03537
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/497,625
 ; PRIOR FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/359,193
 ; PRIOR FILING DATE: 1999-07-22
 ; PRIOR APPLICATION NUMBER: 09/121,781
 ; PRIOR FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-766-610-32

Query Match 100.0%; Score 31; DB 16; Length 100;
 Best Local Similarity 100.0%; Pred. NO. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
 Db 55 LMSTRAS 61

RESULT 7
 US-10-733-563-32
 ; Sequence 32, Application US/10733563
 ; Publication No. US20040151721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Keefe, Theresa
 ; APPLICANT: Ponath, Paul
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 ; METHODS OF USE THEREOF
 ; FILE REFERENCE: 10448-213001
 ; CURRENT APPLICATION NUMBER: US/10/733,563
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: US 10/272,899
 ; PRIOR FILING DATE: 2002-10-17
 ; PRIOR APPLICATION NUMBER: US 60/392,364
 ; PRIOR FILING DATE: 2002-06-26
 ; PRIOR APPLICATION NUMBER: US 60/350,166
 ; PRIOR FILING DATE: 2001-10-19
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 32
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-733-563-32

Query Match 100.0%; Score 31; DB 16; Length 100;
 Best Local Similarity 100.0%; Pred. NO. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
 Db 55 LMSTRAS 61

RESULT 8
 US-09-940-727B-6
 ; Sequence 6, Application US/09940727B
 ; Publication No. US2003007793A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald W
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 0575/51400-B
 ; CURRENT APPLICATION NUMBER: US/09/940,727B
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR APPLICATION NUMBER: 09/214,095
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965
 ; PRIOR FILING DATE: 1997-06-25
 ; PRIOR APPLICATION NUMBER: 08/672,345
 ; PRIOR FILING DATE: 1996-06-25
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 113
 ; TYPE: PRT
 ; ORGANISM: mouse
 US-09-940-727B-6

Query Match 100.0%; Score 31; DB 10; Length 113;
 Best Local Similarity 100.0%; Pred. NO. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
 Db 55 LMSTRAS 61

RESULT 9
 US-09-940-727B-7
 ; Sequence 7, Application US/09940727B
 ; Publication No. US2003007793A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald W
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 0575/51400-B
 ; CURRENT APPLICATION NUMBER: US/09/940,727B
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR APPLICATION NUMBER: 09/214,095
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: PCT/US97/10965
 ; PRIOR FILING DATE: 1997-06-25
 ; PRIOR APPLICATION NUMBER: 08/672,345
 ; PRIOR FILING DATE: 1996-06-25
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 113
 ; TYPE: PRT
 ; ORGANISM: mouse
 US-09-940-727B-7

Query Match 100.0%; Score 31; DB 10; Length 113;
 Best Local Similarity 100.0%; Pred. NO. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
 Db 55 LMSTRAS 61

RESULT 10
 US-09-940-727B-8
 ; Sequence 8, Application US/09940727B
 ; Publication No. US2003007793A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald W
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REFERENCE: 0575/51400-B
 CURRENT APPLICATION NUMBER: US/09/940,727B
 CURRENT FILING DATE: 2002-09-04
 PRIOR APPLICATION NUMBER: 09/214,095
 PRIOR FILING DATE: 1998-12-28
 PRIOR APPLICATION NUMBER: PCT/US97/10965
 PRIOR FILING DATE: 1997-06-25
 PRIOR APPLICATION NUMBER: 08/672,345
 PRIOR FILING DATE: 1996-06-25
 NUMBER OF SEQ ID NOS: 121
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 8
 LENGTH: 113
 TYPE: PRT
 ORGANISM: mouse
 US-09-940-727B-8

Query Match 100.0%; Score 31; DB 10; Length 113;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 DB 55 LMSTRAS 61

RESULT 11
 US-09-940-727B-104
 Sequence 104, Application US/09940727B
 Publication No. US2003007793A1
 GENERAL INFORMATION:
 APPLICANT: Landry, Donald W
 TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 FILE REFERENCE: 0575/51400-B
 CURRENT APPLICATION NUMBER: US/09/940,727B
 CURRENT FILING DATE: 2002-09-04
 PRIOR APPLICATION NUMBER: 09/214,095
 PRIOR FILING DATE: 1998-12-28
 PRIOR APPLICATION NUMBER: PCT/US97/10965
 PRIOR FILING DATE: 1997-06-25
 PRIOR APPLICATION NUMBER: 08/672,345
 PRIOR FILING DATE: 1996-06-25
 NUMBER OF SEQ ID NOS: 121
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 104
 LENGTH: 113
 TYPE: PRT
 ORGANISM: mouse
 US-09-940-727B-104

Query Match 100.0%; Score 31; DB 10; Length 113;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 DB 55 LMSTRAS 61

RESULT 12
 US-09-940-727B-108
 Sequence 108, Application US/09940727B
 Publication No. US2003007793A1
 GENERAL INFORMATION:
 APPLICANT: Landry, Donald W
 TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 FILE REFERENCE: 0575/51400-B
 CURRENT APPLICATION NUMBER: US/09/940,727B
 CURRENT FILING DATE: 2002-09-04
 PRIOR APPLICATION NUMBER: 09/214,095
 PRIOR FILING DATE: 1998-12-28
 PRIOR APPLICATION NUMBER: PCT/US97/10965
 PRIOR FILING DATE: 1997-06-25

PRIOR APPLICATION NUMBER: 08/672,345
 PRIOR FILING DATE: 1996-06-25
 NUMBER OF SEQ ID NOS: 121
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 108
 LENGTH: 113
 TYPE: PRT
 ORGANISM: mouse
 US-09-940-727B-108

Query Match 100.0%; Score 31; DB 10; Length 113;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 DB 55 LMSTRAS 61

RESULT 13
 US-09-940-727B-112
 Sequence 112, Application US/09940727B
 Publication No. US2003007793A1
 GENERAL INFORMATION:
 APPLICANT: Landry, Donald W
 TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 FILE REFERENCE: 0575/51400-B
 CURRENT APPLICATION NUMBER: US/09/940,727B
 CURRENT FILING DATE: 2002-09-04
 PRIOR APPLICATION NUMBER: 09/214,095
 PRIOR FILING DATE: 1998-12-28
 PRIOR APPLICATION NUMBER: PCT/US97/10965
 PRIOR FILING DATE: 1997-06-25
 PRIOR APPLICATION NUMBER: 08/672,345
 PRIOR FILING DATE: 1996-06-25
 NUMBER OF SEQ ID NOS: 121
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 112
 LENGTH: 113
 TYPE: PRT
 ORGANISM: mouse
 US-09-940-727B-112

Query Match 100.0%; Score 31; DB 10; Length 113;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 DB 55 LMSTRAS 61

RESULT 14
 US-10-424-599-191879
 Sequence 191879, Application US/10424599
 Publication No. US20040031072A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa Thomas J
 APPLICANT: Kovalic David K
 APPLICANT: Zhou Yihua
 APPLICANT: Cao Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO 191879
 LENGTH: 63
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_15287C.1.pep

US-10-424-599-191879

Query Match 93.5%; Score 29; DB 12; Length 63;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 24 LMSTRAS 30

RESULT 15

US-09-940-727B-20
; Sequence 20, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-20

Query Match 90.3%; Score 28; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRSS 7

Search completed: September 30, 2004, 06:54:51
Job time : 117.458 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 30, 2004, 08:41:28 ; Search time 32.6509 Seconds
(without alignments)
4221.672 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 2405

Sequence: 1 gaggtgcagctggggagtc.....ccctgtctcgggtaaatga 1335

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued_Patents_AA -QFWT=fastan -SUFFIX=ra1 -MINMATCH=0.1 -LOOPCTL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pcp:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------------------------------|
| 1 | 2161.5 | 89.9 | 478 | 3 | US-08-487-550-8 Sequence 8, Appli |
| 2 | 2161.5 | 89.9 | 478 | 3 | US-09-526-098-8 Sequence 8, Appli |
| 3 | 2151.5 | 89.5 | 453 | 3 | US-08-466-151-8 Sequence 8, Appli |
| 4 | 2151.5 | 89.5 | 453 | 4 | US-08-466-163B-8 Sequence 8, Appli |
| 5 | 2151.5 | 89.5 | 453 | 4 | US-09-802-096-8 Sequence 8, Appli |
| 6 | 2150.5 | 89.4 | 451 | 2 | US-08-887-352B-18 Sequence 18, Appl |
| 7 | 2150.5 | 89.4 | 451 | 3 | US-09-109-207C-18 Sequence 18, Appl |
| 8 | 2150.5 | 89.4 | 451 | 3 | US-09-282-505-2 Sequence 2, Appli |
| 9 | 2150.5 | 89.4 | 451 | 3 | US-09-054-255-2 Sequence 2, Appli |
| 10 | 2150.5 | 89.4 | 451 | 3 | US-09-296-005-18 Sequence 18, Appl |
| 11 | 2150.5 | 89.4 | 451 | 4 | US-09-282-846-2 Sequence 2, Appli |
| 12 | 2150.5 | 89.4 | 451 | 4 | US-09-680-145-2 Sequence 2, Appli |

| | | | | | |
|----|--------|------|-----|---|-------------------------------------|
| 13 | 2150.5 | 89.4 | 451 | 4 | US-09-920-171-18 Sequence 18, Appli |
| 14 | 2148 | 89.3 | 452 | 3 | US-09-027-449-71 Sequence 71, Appl |
| 15 | 2148 | 89.3 | 452 | 3 | US-09-026-985-71 Sequence 71, Appl |
| 16 | 2148 | 89.3 | 452 | 4 | US-09-121-952A-71 Sequence 71, Appl |
| 17 | 2148 | 89.3 | 452 | 4 | US-09-234-340A-71 Sequence 71, Appl |
| 18 | 2147.5 | 89.3 | 451 | 2 | US-08-887-352B-14 Sequence 14, Appl |
| 19 | 2147.5 | 89.3 | 451 | 2 | US-08-887-352B-16 Sequence 16, Appl |
| 20 | 2147.5 | 89.3 | 451 | 3 | US-08-466-151-65 Sequence 65, Appl |
| 21 | 2147.5 | 89.3 | 451 | 3 | US-09-109-207C-14 Sequence 14, Appl |
| 22 | 2147.5 | 89.3 | 451 | 3 | US-09-109-207C-16 Sequence 16, Appl |
| 23 | 2147.5 | 89.3 | 451 | 3 | US-09-296-005-14 Sequence 14, Appl |
| 24 | 2147.5 | 89.3 | 451 | 3 | US-09-296-005-16 Sequence 16, Appl |
| 25 | 2147.5 | 89.3 | 451 | 4 | US-09-920-171-14 Sequence 14, Appl |
| 26 | 2147.5 | 89.3 | 451 | 4 | US-09-920-171-16 Sequence 16, Appl |
| 27 | 2143 | 89.2 | 449 | 4 | US-08-679-397-2 Sequence 2, Appli |
| 28 | 2145 | 89.2 | 449 | 4 | US-09-680-148-2 Sequence 2, Appli |
| 29 | 2145 | 89.2 | 449 | 4 | US-09-304-465A-2 Sequence 2, Appli |
| 30 | 2144 | 89.1 | 459 | 1 | US-08-157-101A-7 Sequence 7, Appli |
| 31 | 2065.5 | 85.9 | 449 | 1 | US-08-458-516-13 Sequence 13, Appl |
| 32 | 2051 | 85.3 | 446 | 3 | US-08-397-411-7 Sequence 7, Appli |
| 33 | 2044.5 | 85.0 | 476 | 2 | US-08-378-939-10 Sequence 10, Appl |
| 34 | 2042.5 | 84.9 | 468 | 4 | US-09-485-737B-67 Sequence 67, Appl |
| 35 | 2042.5 | 84.9 | 711 | 4 | US-09-485-737B-90 Sequence 90, Appl |
| 36 | 2040 | 84.8 | 467 | 1 | US-08-704-744-81 Sequence 81, Appl |
| 37 | 2034 | 84.6 | 467 | 3 | US-09-049-672A-8 Sequence 8, Appli |
| 38 | 2033.5 | 84.6 | 476 | 3 | US-08-487-550-12 Sequence 12, Appl |
| 39 | 2033.5 | 84.6 | 476 | 4 | US-09-526-098-12 Sequence 12, Appl |
| 40 | 2029 | 84.4 | 473 | 3 | US-09-049-672A-4 Sequence 4, Appli |
| 41 | 2028.5 | 84.3 | 472 | 4 | US-08-793-450-8 Sequence 8, Appli |
| 42 | 2026 | 84.2 | 463 | 4 | US-09-472-087-4 Sequence 4, Appli |
| 43 | 2026 | 84.2 | 463 | 4 | US-09-472-087-68 Sequence 68, Appl |
| 44 | 2020.5 | 84.0 | 464 | 4 | US-09-472-087-2 Sequence 2, Appli |
| 45 | 2020.5 | 84.0 | 464 | 4 | US-09-472-087-66 Sequence 66, Appl |

ALIGNMENTS

RESULT 1

US-08-487-550-8

; Sequence 8, Application US/08487550

; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

TELEFAX: 703-836-2021
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 478 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-526-098-8

Alignment Scores:
 Pred. No.: 1,24e-152 Length: 478
 Score: 2161.50 Matches: 412
 Percent Similarity: 91.29% Conservative: 7
 Best Local Similarity: 89.76% Mismatches: 25
 Query Match: 89.88% Indels: 15
 DB: 4 Gaps: 1

US-09-674-716B-18 (1-1335) X US-09-526-098-8 (1-478)

QY 1 GAGGTGACAGTGGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGTCCCTTAGACTC 60
 DB 20 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuVal 39
 QY 61 TCCTGTGACGTAGCGGATTCATTTCAGTGGCTACTGATGTCCTGGTCCGCCAGCT 120
 DB 40 SerCysAlaValSerGlyPheThrPheSerAspHisTyrMetTyrTrpPheArgGlnAla 59
 QY 121 CCAGGAGGGGCTCGACTGGTCTGAAATTAGATTGAATCTGATAATTATGCAACA 180
 DB 60 ProGlyLysGlyProGluTrpValGlyPheLeuArgAsnLysProAsnGlyGlyThr 79
 QY 181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
 DB 80 GluTyrAlaAlaSerValLysAspArgPheThrLeuSerArgAspSerLysSerile 99
 QY 241 CTGATCTGCAATGAACAGCTGAAACCCAGGACACAGCCGTGATTACTGTACAGAT 300
 DB 100 AlaTyrLeuGlnMetSerSerLeuLysIleGluAspThrAlaValTyrTyrCysThr 119
 QY 301 -----TTCATAGACTGGGGC 315
 DB 120 SerTyrIleSerHisCysArgGlyGlyValCysTyrGlyGlyTyrPheGluPheTrpGly 139
 QY 316 CAGGAAACACTAGTCAACCGTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCGCTG 375
 DB 140 GlnGlyAlaLeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeu 159
 QY 376 GCACCTCTCTCAAGAGCACCTCTGGGGGCACAGGGCCCTGGGTGCTGCTCAAGGAC 435
 DB 160 AlaProSerSerLysSerThrSerGlyThrAlaAlaLeuGlyCysLeuValLysAsp 179
 QY 436 TACTTCCCGAACCCGGTGACGGTGTCTGGAACCTCAGCGCCCTGACAGCGGGGTGCAC 495
 DB 180 TyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHis 199
 QY 496 ACCTTCCCGGTCTCTACAGTCTCTCAGACTCTACTCCCTCAGCAGGGTGTGACCGTG 555
 DB 200 ThrPheProAlaValLeuGlnSerGlyLeuTyrSerLeuSerSerValValThrVal 219
 QY 556 CCCTCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAAGCAAC 615
 DB 220 ProSerSerSerLeuGlyThrGlnThrTyrLeuCysAsnValAsnHisLysProSerAsn 239
 QY 616 ACCAAGGTGGAAGAAGTGGAGGCCAAATTTGTGACAAACCTCACATATGCCACCG 675
 DB 240 ThrLysValAspLysLysAlaGluProLysSerCysAspLysThrHisThrCysProPro 259
 QY 676 TGCCAGACACCTGAACCTCGCGGGGCACCGTCAGTCTTCTCTCCCGCCCAAAACCCCAAG 735
 DB 260 CysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLys 279
 QY 736 GACACCTCATGATCTCCCGGACCCCTGAGGTACATCGTGGTGGTGGTGGTGGTGGTGGT 795

DB 280 AspThrLeuMetIleSerArgThrProGluValThrCysValValValAspValSerHis 299
 QY 796 GAAGACCTGAGGTCAAGTTCACTGGTACCTGGAGCGCGGTGAGGTGATATGCAAG 855
 DB 300 GluAspProGluValLysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLys 319
 QY 856 ACAAGCCCGGGAGGAGGAGTACACACAGTACCGTGTGGTCAAGCTCTCCACCGTTC 915
 DB 320 ThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValValSerValLeuThrVal 339
 QY 916 CTGCACAGGACTGGCTGAATGCAAGAGTCAAGTCAAGTCAAGTCTCCAAAGAGCCCTC 975
 DB 340 LeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeu 359
 QY 976 CCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCCACAGGTG 1035
 DB 360 ProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnProArgGluProGlnVal 379
 QY 1036 TACACCTCGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGTCAAGCTGACCTGCCTG 1095
 DB 380 TyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnValSerLeuThrCysLeu 399
 QY 1096 GTCAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGGCAATGGCGACCGGAG 1155
 DB 400 ValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGlu 419
 QY 1156 AACCACTACAAGACCAACGCTCCCGTGGTGGACTCCGAGCGGTCTCTTCTCTCTACAGC 1215
 DB 420 AsnAsnTyrLysThrThrProValLeuAspSerAspGlySerPheLeuTyrSer 439
 QY 1216 AAGCTCAGCGTGACAAAGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1275
 DB 440 LysLeuThrValAspLysSerArgTrpGlnGlnGlnValPheSerCysSerValMet 459
 QY 1276 CATGAGCTCTGCACAAACCACTACAGCAGAGAGCTCTCCCTGTCTCCGGGTAAA 1332
 DB 460 HisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 478

RESULT 3

US-08-466-151-8
 Sequence 8, Application US/08466151
 Patent No. 6037453
 GENERAL INFORMATION:
 APPLICANT: Jardieu, Paula M.
 APPLICANT: Presta, Leonard G.
 TITLE OF INVENTION: Immunoglobulin Variants
 NUMBER OF SEQUENCES: 65
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/466,151
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/466163
 FILING DATE: 06-Jun-1995
 APPLICATION NUMBER: 08/405617
 FILING DATE: 15-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/185899
 FILING DATE: 26-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/879495

FILING DATE: 07-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/744768
 FILING DATE: 14-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REGISTRATION NUMBER: 39,044
 REFERENCE/DOCKET NUMBER: P0718P2C1D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1489
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-466-151-8

Alignment Scores:
 Pred. No.: 6,77e-152 Length: 453
 Score: 2151.50 Matches: 410
 Percent Similarity: 92.76% Conservative: 13
 Best Local Similarity: 89.91% Mismatches: 18
 Query Match: 89.46% Indels: 15
 DB: 3 Gaps: 4

US-09-674-716b-18 (1-1335) x US-08-466-151-8 (1-453)

QY 1 GAGGTGACGCTGGTGGAGCTCGGGAGGCTTGGTAAAGCCGGGGGGTCCCTTAGACTC 60
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
 QY 61 TCCTGTGCGAGTAGCGGATCTCTTC---AGTGGCTACTGATCTCTGGTCCGCCAG 117
 Db 21 SerCysAlaValSerGlyThrSerIleThrSerGlyThrSerTrpAsnTrpIleArgGln 40
 QY 118 GTCCAGGGAAGGGGCTCGAGTGGGTGTGTAATAGATTGAAATCTGATAATTATGCA 177
 Db 41 AlaProGlyGlyGlyLeuGluTrpValAlaSerIleThrTyAspGly-----Ser 57
 QY 178 ACACATTATGCGAGTCTGTGAAGGGGAATTCACATCTCAAGAGATGATTCAAATCT 237
 Db 58 ThrAsnTyAlaAspSerValIysGlyArgPheThrIleSerArgAspSerIysAsn 77
 QY 238 AGACTGTATCTGCAATGAACAGCTGAAACCGAGGACACAGCGCTGTATTACTGTACA 297
 Db 78 ThrPheTyLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyThrCysAla 97
 QY 298 -----GATTTCTAGACTGGGCGCAGGGAACACTAGTC 330
 Db 98 ArgGlySerHisTyThrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117
 QY 331 ACGTCTCTCGCTCCACCC-----AAGGCCCATCGTCTCCCTCCCTGGCACCCTCC 384
 Db 118 ThrValSerSerAlaSerThrIysGlyIysGlyProSerValPheProLeuAlaProSer 137
 QY 385 TCCAGAGCACCTCTGGGGGCGACAGCGCCCTGGCTCGCTGGTCAAGGACTTACTTCCC 444
 Db 138 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValIysAspTyPhePro 157
 QY 445 GAACCGGTACGGTGTCTGGAACTCAGCGCCCTGACACAGCGGGGTGCACACCTTCCG 504
 Db 158 GluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhePro 177
 QY 505 GTGTCTCTCAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGGTGCCCTCCAGC 564
 Db 178 AlaValLeuGlnSerSerGlyLeuTyThrSerLeuSerSerValValThrValProSerSer 197
 QY 565 AGCTGGGACCCAGACCTACATCTGCAACGTGAATCAACGCCCAAGCAACCCAGGTG 624
 Db 198 SerLeuGlyThrGlnThrTyIleCysAsnValAsnHisLysProSerAsnThrIysVal 217
 QY 625 GACAAGAAAGTGAGGCCCAAAATCTTGTGCAAAACTCACAATGCCACCGTCCGCCAGCA 684

Db 218 AspLysValGluProLysSerCysAspLysThrHisThrCysProCysProAla 237
 QY 685 CCTGAACCTCGCGGGGACCGTCTTCCTTCTCCCTCCCAAAACCCCAAGACACCTTC 744
 Db 238 ProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeu 257
 QY 745 ATGATCTCCCGACCCCTGAGTCAATCGGTGGTGGTGGAGCTGAGCCAGCAAGACCTC 804
 Db 258 MetIleSerArgThrProGluValThrCysValValValAspValSerHisGluAspPro 277
 QY 805 GAGTCAAGTTCACTGACGTGGACGGGTGAGGTGCATAATCCCAAGCAAAAGCCG 864
 Db 278 GluValIysPheAsnTrpTyValAspGlyValGluValHisAsnAlaIysThrIysPro 297
 QY 865 CGGAGGAGCAGTACCAACAGCAGTACCGTGTGGTGGTGGTCTCACCCTCTGACCCAG 924
 Db 298 ArgGluGluGlnTyAsnSerThrTyArgValValSerValLeuThrValLeuHisGln 317
 QY 925 GACTGCTGATGGCAAGGAGTACAGTCTCCCAAGAGCCCTCCAGCCGCC 984
 Db 318 AspTrpLeuAsnGlyIysGluTyIysCysLysValSerAsnLysAlaLeuProAlaPro 337
 QY 985 ATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAGAACCAAGGTGTACACCTG 1044
 Db 338 IleGluLysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyThrLeu 357
 QY 1045 CCCCCTATCCCGGATGAGTGCACCAAGAACAGGTGAGGTGAGTCTGCTGCTGCTCAAGGC 1104
 Db 358 ProProSerArgGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGly 377
 QY 1105 TTCTATCCAGCACATCGCGTGGAGTGGGAGACAAATGGGCGAGCCGAGAACCAACTAC 1164
 Db 378 PheTyProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTy 397
 QY 1165 AAGACACGCTCCCGTGTGGTGGTCCGACGGTCTCTTCTCTTACAGCAGGTCACTCACC 1224
 Db 398 LysThrThrProProValLeuAspSerAspGlySerPhePheLeuTySerLysLeuThr 417
 QY 1225 GTGCAAGAGCAGGTGGCAGCAGGGAACGCTCTCTCATGTCTCGTGTATGATGAGGCT 1284
 Db 418 ValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMethHisGluAla 437
 QY 1285 CTGCACACCACTACAGCAGAGAGCCCTCTCCCTCTCTCCGGGTAAA 1332
 Db 438 LeuHisAsnHisTyThrGlnLysSerLeuSerLeuSerProGlyLys 453

RESULT 4

US-08-466-163B-8
 ; Sequence 8, Application US/08466163B
 ; Patent No. 6329509
 ; GENERAL INFORMATION:
 ; APPLICANT: Jardiou, Paula M.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Immunoglobulin Variants
 ; FILE REFERENCE: P0718P2C1D1
 ; CURRENT APPLICATION NUMBER: US/08/466,163B
 ; CURRENT FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: US 08/405,617
 ; PRIOR FILING DATE: 1995-03-15
 ; PRIOR APPLICATION NUMBER: US 08/185,899
 ; PRIOR FILING DATE: 1994-01-26
 ; PRIOR APPLICATION NUMBER: US 07/879,495
 ; PRIOR FILING DATE: 1992-05-07
 ; PRIOR APPLICATION NUMBER: US 07/744,768
 ; PRIOR FILING DATE: 1991-08-14
 ; NUMBER OF SEQ ID NOS: 64
 ; SEQ ID NO 8
 ; LENGTH: 453
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: humanized mae11, version 1 heavy chain

US-08-466-163B-8

Alignment Scores:

Pred. No.: 6,77e-152 Length: 453
Score: 2151.50 Matches: 410
Percent Similarity: 92.76% Conservative: 13
Best Local Similarity: 89.91% Mismatches: 18
Query Match: 89.46% Indels: 15
DB: 4 Gaps: 4

US-09-674-716B-18 (1-1335) x US-08-466-163B-8 (1-453)

QY 1 GAGGTGCAGCTGCTGAGTCTGGGAGGCTGTGTAAAGCCGGGGTCCCTAGACTC 60
DB 1 GluValGlnLeuValGlnSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCTGTGCAGCTAGCGGATCTCACTTC---AGTGCTACTGGATGCTCGGTGGTCCGAG 117
DB 21 SerCysAlaValSerGlyTyrSerIleThrSerGlyTyrSerTrpAsnTrpIleArgGln 40
QY 118 GCTCCAGGGAAGGGCTGAGTGGTGTCTGTAATAGATTGAATCTGATAATTATGCA 177
DB 41 AlaProGlyLysGlyLeuGlnTrpValAlaSerIleThrTyrAspGly-----Ser 57
QY 178 ACACATTATGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCT 237
DB 58 ThrAsnTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspSerLysAsn 77
QY 238 AGACTGTATCTCAATGAACAGCTGAAACCCGAGGACACAGCCGTGTATTACTGTACA 297
DB 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAla 97
QY 298 -----GATTTCATAGACTGGGGCCAGGGACACTAGTC 330
DB 98 ArgGlySerHisTyrPheClyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117
QY 331 ACCGTCTCTAGCTCCACCC-----AAGGCCCATCGTCTTCCCGCTGGCCACCTCC 384
DB 118 ThrValSerSerAlaSerThrLysGlyLysGlyProSerValPheProLeuAlaProSer 137
QY 385 TCCAGAGACACTCTGGGGGCACGGCCCTGGCTGCTGGTCAAGACTACTTCC 444
DB 138 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 157
QY 445 GAACCGGTGACGGTGTCTGGAACTCAGCGCCCTGACAGCGGGGTGCACACTTCCG 504
DB 158 GluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhePro 177
QY 505 GCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGGGTGTGACCGTCCCTCCAGC 564
DB 178 AlaValLeuGlnSerSerGlyLeuTyrSerLeuSerValValThrValProSerSer 197
QY 565 AGCTTGGGCACCCAGACCTTACATCTGCAACGTGAATCAAGCCCAAGCAACACCAAGTG 624
DB 198 SerLeuGlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysVal 217
QY 625 GACAGAAAGTGGAGCCCAAACTTGTGTGACAAACTCACATGCCCGCTGGCCAGCA 684
DB 218 AspLysLysValGluProLysSerCysAspLysThrHisThrCysProProCysProAla 237
QY 685 CTTGAACCTCGGGGCGCACCGTCAGTCTTCTTCCCGCCCAAAACCAAGGACACCTC 744
DB 238 ProGluLeuLeuGlyLysProSerValPheLeuPheProProLysProLysAspThrLeu 257
QY 745 ATGATCTCCGGACCCCTGAGTGCATCATCGTGGTGGAGTGTGAGCAGCAGCAAGACCT 804
DB 258 MetIleSerArgThrProGluValThrCysValValValAspValSerHisGluAspPro 277
QY 805 GAGGTCAAGTTCACCTGTACGTGACGGCGGTGGAGTGCATTAATGCCAAGCAACAGCG 864
DB 278 GluValLysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysPro 297
QY 865 CGGGAGGACGAGTACAAACAGCAGTACCGTGGTGGTCAAGCTCTCAGCGTCTCAGCACC 924

DB 298 ArgGluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGln 317
QY 925 GACTGGCTGAATGCGCAAGAGTAGTACAAAGTGTCAAGGTCTCCAACAAGCCCTCCAGCCCC 984
DB 318 AspTrpLeuAsnGlyLysGlnTyrLysCysLysValSerAsnLysAlaLeuProAlaPro 337
QY 985 ATGAGAAACCATCTCCAAAGCCAAAGGCGACCCCGAGAACACACAGGTGTACACCTG 1044
DB 338 IleGluLysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeu 357
QY 1045 CCCCCATCCCGGATGAGTGCACCAAGAACCAAGTCAAGCTCAGCTCCCTGCTGGTCAAGGC 1104
DB 358 ProProSerArgGluGlnMetThrLysAsnGlnValSerLeuThrCysLeuValLysGly 377
QY 1105 TTCTATCCCGAGCAGATCGCCGTGGAGTGGAGAGCAATGGGAGCGGAGACAACACTAC 1164
DB 378 PheTyrProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyr 397
QY 1165 AAGACACAGCTCCCGTGTGGACTCCGACGGGTCTCTCTCTCTACAGCAAGCTCAC 1224
DB 398 LysThrThrProProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThr 417
QY 1225 GTGCACAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCCGTCATGAGGCT 1284
DB 418 ValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAla 437
QY 1285 CTGCACACCACTACACGACAGAGAGCCCTCTCCCTGCTCTCCGGGTAAA 1332
DB 438 LeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 453
RESULT 5
US-09-802-096-8
; Sequence 8, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mael1, version 1 heavy chain
US-09-802-096-8
Alignment Scores:
Pred. No.: 6,77e-152 Length: 453
Score: 2151.50 Matches: 410
Percent Similarity: 92.76% Conservative: 13
Best Local Similarity: 89.91% Mismatches: 18
Query Match: 89.46% Indels: 15
DB: 4 Gaps: 4
US-09-674-716B-18 (1-1335) x US-09-802-096-8 (1-453)
QY 1 GAGGTGCAGCTGCTGAGTCTGGGAGGCTGTGTAAAGCCGGGGTCCCTAGACTC 60

1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
 61 TCCTGTGCGAGTACGGATCTACTTTC---ATGGCTACTGATGTCCTGGTCCGCCAG 117
 21 SerCysAlaValSerGlyThrSerIleThrSerGlyTyrSerTrpAsnTrpIleArgGln 40
 118 GCTCCAGGAAGGGCTCCAGTGGTGTCTGAAATAGATTGAATCTCATTAATTATGCA 177
 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleThrTyrAspGly-----Ser 57
 178 ACATATTCCGGAGTCTGTGAAGGGGAAATTCACATCTCAAGAGATGATCAAAATCT 237
 58 ThrAsnTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspSerLysAsn 77
 238 AGACTATCTGCAATGACACCTGAAACCGGAGGACACAGCGTGTATTACTGTACA 297
 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAla 97
 298 -----GATTTTCATAGACTGGGGCCAGGGAACACTAGTCT 330
 98 ArgGlySerHisTyrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117
 331 ACGTCTCTCTAGCTCCACC-----AAGGCCCATCGGTCTTCCCTGGCACCCTCC 384
 118 ThrValSerSerAlaSerThrLysGlyLysGlyProSerValPheProLeuAlaProSer 137
 385 TCCAAGACACCTCTCGGGGACAGCGGCTGGTCTGCTCAAGACTACTTCCCC 444
 138 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 157
 445 GAACCGGTCAACGGTGTCTGGAACCTAGCGGCCCTGACAGCGGCTGCACACCTTCCCG 504
 158 GluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhePro 177
 505 GCTGTCTCAGTCTCAGACCTCTACTCCCTCAGCAGCGTGTGTCAGCGTCCCTCAGC 564
 178 AlaValLeuGlnSerSerGlyLeuTyrSerLysSerValValThrValProSerSer 197
 565 AGCTGGGACCCAGACCTACATCTGCAACGTGAATCAAGCCAGCCAGCAACCAAGGTG 624
 198 SerLeuGlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysVal 217
 525 GACAAAGAGTGGAGCCCAAACTGTGTGACAAACTCAGATGCCACCGCTGCCACGA 684
 218 AspLysLysValGluProLysSerCysAspLysThrHisThrCysProProCysProAla 237
 685 CTTGAATCTCGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 744
 238 ProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeu 257
 745 ATGATCTCCGGACCCCTCAGTCTCAGTCTGCTGGTGGAGTGGAGTGGAGTGGAGTGG 804
 258 MetIleSerArgThrProGluValThrCysValValValValValValValValValVal 277
 305 GAGTCAAGTCAACTGAGTACGTCGACGCGCGTGGAGTGCATAATGCCAAGCAAGCCG 864
 278 GluValLysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysPro 297
 865 CGGAGGAGCAGTACCAACGACGCTACCGTGTGGTCAAGCTCTCAGCTCTCAGCTCTC 924
 298 ArgGluGluGlnTyrAsnSerThrTyrArgValValValValValValValValValVal 317
 925 GACTGCTCAATGGACGAGTACAGTCAAGTCAAGTCTCCCAAGAGCCCTCCAGCCCCC 984
 318 AspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaPro 337
 985 ATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGACCAACAGGTGTACACCTG 1044
 338 IleGluLysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeu 357
 1045 CCCCCTCCCGGATGAGTGTACCAAGACCAAGTGTACCGTGTACCGTGTGTGTGTGTGT 1104
 358 ProProSerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGly 377

1105 TTCTATCCAGCACATCCCGCTGGTGGAGCAATGGGAGCGCGGAGCAACTAC 1164
 378 PheTyrProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyr 397
 1165 AAGACACACCGCTCCGCTGGTGGACTCCGACGGTCTCTCTCTCTCTCTCTCTCTCTCT 1224
 398 LysThrThrProProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThr 417
 1225 GTGACACAGAGAGTGGGAGCGAGGAGGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1284
 418 ValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMethHisGluAla 437
 1285 CTCACACACCACTACACGACGAGAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
 438 LeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 453

RESULT 6

US-08-887-352B-18
 ; Sequence 18, Application US/08887352B
 ; Patent No. 5994511
 ; GENERAL INFORMATION:
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 ; TITLE OF INVENTION: Improved Anti-IGE Antibodies and Method of
 ; TITLE OF INVENTION: Improving Polypeptides
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 03-Jul-1997
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Svoboda, Craig G.
 ; REGISTRATION NUMBER: 39,044
 ; REFERENCE/DOCKET NUMBER: P1123
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1489
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 451 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-887-352B-18
 Alignment Scores:
 Pred. No.: 8,02e-152 Length: 451
 Score: 2150.50 Matches: 408
 Percent Similarity: 92.51% Conservative: 12
 Best Local Similarity: 89.87% Mismatches: 21
 Query Match: 89.42% Indels: 13
 DB: 2 Gaps: 3

US-09-674-716B-18 (1-1335) x US-08-887-352B-18 (1-451)
 QY 1 GAGTGTGAGTGTGGAGTCTGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 60
 DB 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
 QY 61 TCCTGTGAGTACCGGATTCATTTC---AGTGGCTACTGGATGTCCTGGGTCCGCCAG 117
 DB 21 SerCysAlaValSerGlyThrSerIleThrSerGlyTyrSerTrpAsnTrpIleArgGln 40


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391 AGCACCTCTGGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGCAACG 450
138 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValIysAspThrPheProGluPro 157
451 GTGACGGTGTGGAACTCAGCGCCCTGACAGCGGGTGCACACCTTCCCGGTGTC 510
158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177
511 CTACAGTCTCAGGACTACTCTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCGCTGG 570
178 LeuGlnSerGlyLeuThrSerLeuSerValValThrValProSerSerLeu 197
571 GGCACCCAGCAGCTACATCTGCAACGTAATCAACAGCCCAAGCAACCAAGGTGCAAG 630
198 GlyThrGlnThrTrpIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217
631 AAAGTGGAGCCCAATCTGTGACAAACTCACACATGCCACCTGCCAGCAGCTGAA 690
218 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237
691 CTCGCGGGGCGCACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 750
238 LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIle 257
751 TCCCGGACCCCTGAGGTACATGCTGTGAGCGTGTGGAGCTGAGCCACGAGCCTGAGTGC 810
258 SerArgThrProGluValThrCysValValAspValSerHisGluAspProGluVal 277
811 AAGTCAACCTGCTGACGAGCGGTGGAGTGCATATGCAAGCAAGCAAGCGGGGAG 870
278 LysPheAsnTrpTrpValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297
871 GAGCAGTACAAAGCAGTACCTGCTGTGTGAGCGTCTCACCCTGCTGACCAAGACTGG 930
298 GluGlnTrpAsnSerThrTrpArgValValSerValLeuThrValLeuHisGlnAspTrp 317
931 CTCAATGGCAAGGAGTACAGTACAGTCTCAACAAAGCCCTCCAGCCCGCTCGAG 990
318 LeuAsnGlyLysGluTrpLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 337
991 AAAACCATCTCCAAAGCCAAAGGCGCCCGGAGCAACCAAGCAACCAAGCAACCAAG 1050
338 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValThrLeuProPro 357
1051 TCCCGGAGTGTGACCAAGACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1110
358 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTrp 377
1111 CCCAGCGCATCCCGTGGAGTGGAGAGCAATGGCGAGCGGAGCAACCAAGCAACCAAG 1170
378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnThrLysThr 397
1171 AGCCTCCCGTGTGACGCGCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230
398 ThrProValLeuAspSerAspGlySerPhePheLeuThrSerLysLeuThrValAsp 417
1231 AAGAGCAGGTGGCAGCAGGAGCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1290
418 LysSerArgTrpGlnGlnGlnValPheSerCysSerValMetHisGluAlaLeuHis 437
1291 AACCATACAGCAGGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
438 AsnHisThrThrGlnLysSerLeuSerLeuSerProGlyLys 451

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RESULT 8

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US-09-282-505-2
; Sequence 2, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A

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; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-2

Alignment Scores:
Pred. No.: 8,02e-152 Length: 451
Score: 2150.50 Matches: 408
Percent Similarity: 92.51% Conservativeness: 12
Best Local Similarity: 89.87% Mismatches: 21
Query Match: 89.42% Indels: 13
DB: 3 Gaps: 3

US-09-674-716B-18 (1-1335) x US-09-282-505-2 (1-451)

QY 1 GAGTTCAGCTGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCCGTGTGAGTACGCGGATTCACCTTTC--AGTGGCTACTGGATGCTCTGGTCCGCCAG 117
Db 21 SerCysAlaValSerGlyTrpSerIleThrSerGlyTrpSerTrpAsnThrIleArgGln 40
QY 118 GCTCCAGGGAAGGGCTCGAGTGGGTGCTGAAATAGATTGAAATCTGATAATTATGCA 177
Db 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysTrpSerGlyGlu-----57
QY 178 ACATATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCT 237
Db 58 ThrLysTrpAsnProSerValLysGlyArgIleThrIleSerArgAspSerLysAsn 77
QY 238 AGACTGTATCTGCAATGAACAGCTGAAACCCAGAGACACACCGCTGTATTACTGTACA 297
Db 78 ThrPheTrpLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTrpCysAla 97
QY 298 -----GATTTCATAGACTGGGGCCAGGGAACACTAGTC 330
Db 98 ArgGlySerHisTrpPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117
QY 331 ACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCCTCTCCAAG 390
Db 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 137
QY 391 AGACCTCTGGGGGCACAGCGCCCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 450
Db 138 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTrpPheProGluPro 157
QY 451 GTGACGGTGTGGAACTCAGCGCCCTCAGCAGCGGGTGCACACCTTCCCGGTGTC 510
Db 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177
QY 511 CTACAGTCTCAGGACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 570
Db 178 LeuGlnSerSerGlyLeuTrpSerLeuSerValValThrValProSerSerLeu 197
QY 571 GGCACCCAGCAGCTACATCTGCAACGTAATCAACAGCCCAAGCAACCAAGGTGCAAG 630
Db 198 GlyThrGlnThrTrpIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217
631 AAAGTGGAGCCCAATCTGTGACAAACTCACACATGCCACCTGCCAGCAGCTGAA 690
218 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237
691 CTCGCGGGGCGCACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 750

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|--|------|---|------|
| Db | 238 | LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetile | 257 |
| Qy | 751 | TCCCGGACCCCTGAGGTCAATCGTGGTGGACGTGAGCCACGAGACCCCTGAGGTC | 810 |
| Db | 258 | SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal | 277 |
| Qy | 811 | AAGTTCAACTGGTACGTGGAGCGCGTGGAGGTGCATAATGCCAAGACAAAGACCGCGGAG | 870 |
| Db | 278 | LysPheAsnTrpYrValAspGlyValGluValHisAenAlaLysThrLysProArgGlu | 297 |
| Qy | 871 | GAGCAGTACAAACAGCAGCTACCGGTGGTGGTCCAGCGTCTCTCCCGTCCCTGCACCAAGACTGG | 930 |
| Db | 298 | GluGlnTyrsnSerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrp | 317 |
| Qy | 931 | CTGAATGGCAAGAGTAGTCAAGTCAAGGTCTTCCAAACAAAGCCCTCCAGCCCCCATCGAG | 990 |
| Db | 318 | LeuAsnGlyLysGluTyLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu | 337 |
| Qy | 991 | AAACACCATCTCCAAAGCCAAAGGCGACCCCGAGAACACACAGGTGTACACCTGCCCCCA | 1050 |
| Db | 338 | LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyThrLeuProPro | 357 |
| Qy | 1051 | TCCCGGAGTGACTGACCAAGAACACCGGTGAGCTGAGCTGCTCTGGTCAAGGGCTTCTAT | 1110 |
| Db | 358 | SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTy | 377 |
| Qy | 1111 | CCCAGCGACATCCCGTGGAGTGGGAGCAATGGCGAGCGGAGAACCACTACAAGACC | 1170 |
| Db | 378 | ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyLysThr | 397 |
| Qy | 1171 | ACGCTCCCGTGTGGACTCCGAGCGGTCTCTTCTTCTTACAGCAAGCTCACCGTGGAC | 1230 |
| Db | 398 | ThrProProValLeuAspSerAspGlySerPhePheLeuTySerLysLeuThrValAsp | 417 |
| Qy | 1231 | AAGAGCAGTGGCAGCAGGGGAAGCTTCTTCATGCTCCGTGATGATGAGGCTCTGCAC | 1290 |
| Db | 418 | LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis | 437 |
| Qy | 1291 | AACCATACACGCAAGAGAGCTCTCCTGTCTCCGGGTAAA | 1332 |
| Db | 438 | AsnHisTyThrGlnLysSerLeuSerLeuSerProGlyLys | 451 |
| RESULT 9 | | | |
| US-09-054-255-2 | | | |
| ; Sequence 2, Application US/09054255 | | | |
| ; Patent No. 6242195 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Esche Ekinaduese Idusogie et al. | | | |
| ; TITLE OF INVENTION: Polypeptide variants | | | |
| ; FILE REFERENCE: P1266 | | | |
| ; CURRENT APPLICATION NUMBER: US/09/054.255 | | | |
| ; CURRENT FILING DATE: 1998-04-02 | | | |
| ; NUMBER OF SEQ ID NOS: 2 | | | |
| ; SEQ ID NO 2 | | | |
| ; LENGTH: 451 | | | |
| ; TYPE: PRT | | | |
| ; ORGANISM: Artificial Sequence | | | |
| ; FEATURES: | | | |
| ; OTHER INFORMATION: E27 anti-IgE antibody heavy chain | | | |
| US-09-054-255-2 | | | |
| Alignment Scores: | | | |
| Pred. No.: 8.02e-152 Length: 451 | | | |
| Score: 2150.50 Matches: 408 | | | |
| Percent Similarity: 92.51% Conservative: 12 | | | |
| Best Local Similarity: 89.87% Mismatches: 21 | | | |
| Query Match: 89.42% Indels: 13 | | | |
| DB: 3 Gaps: 3 | | | |
| US-09-674-716B-18 (1-1335) x US-09-054-255-2 (1-451) | | | |
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QY 1111 CCAGCGACATCCCGTGGAGTGGAGCAATGGCGGAGGAGCAACTACAGACC 1170
 Db 378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTrpLysThr 397
 QY 1171 ACGCCTCCCGTGGACTCCGACGGCTCTTCTCTCTACAGCAAGTCCACCGTGGAC 1230
 Db 398 ThrProValLeuAspSerAspGlySerPhePheLeuTrpSerLysLeuThrValAsp 417
 QY 1231 AAGAGCGTGGCAGCAGGGAACGGTCTTCTCTATGCTCCGTGATGATGAGGCTTCGCAC 1290
 Db 418 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 437
 QY 1291 AACCACTACAGCAGAGACCTCTCCCTGCTCCCGGTAAA 1332
 Db 438 AsnHisTrpThrGlnLysSerLeuSerLeuSerProGlyLys 451
 RESULT 10
 US-09-296-005-18
 ; Sequence 18, Application US/09296005
 ; Patent No. 6290957
 ; GENERAL INFORMATION:
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 ; TITLE OF INVENTION: Improved Anti-IGe Antibodies and Method of Improving Polypeptides
 ; FILE REFERENCE: P1123C1r
 ; CURRENT APPLICATION NUMBER: US/09/296,005
 ; CURRENT FILING DATE: 1999-04-21
 ; EARLIER APPLICATION NUMBER: US 08/887,352
 ; EARLIER FILING DATE: 1997-07-02
 ; NUMBER OF SEQ ID NOS: 26
 ; SEQ ID NO 18
 ; LENGTH: 451
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Artificial
 ; LOCATION: 1-451
 ; OTHER INFORMATION: Heavy chain sequence derived from MAB11
 US-09-296-005-18
 Alignment Scores:
 Pred. No.: 8,02e-152 Length: 451
 Score: 2150.50 Matches: 408
 Percent Similarity: 92.51% Conservative: 12
 Best Local Similarity: 89.87% Mismatches: 21
 Query Match: 89.42% Indels: 13
 DB: 3 Gaps: 3
 US-09-674-716b-18 (1-1335) x US-09-296-005-18 (1-451)
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 Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
 QY 61 TCCTGTGCAGTACGAGTTCACATTC---AGTGGCTACTGGATGTCCTGGGTCCGCGCAG 117
 Db 21 SerCysAlaValSerGlyrSerIleThrSerGlyrSerTrpAsnTrpIleArgGln 40
 QY 118 GCTCCAGGGAAGGGTTCGAGTGGTGTCTGAAATPAGATTGAAATCTGATTAATTATGCA 177
 Db 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysrSerGlyGlu----- 57
 QY 178 ACACATTATCGGAGTCTGTGAGGGGAATTCACCATCTCAGAGATGATTCAAATCT 237
 Db 58 ThrLysrTrpAsnProSerValLysGlyrGlyrIleThrSerArgAspSerLysAsn 77
 QY 238 AGACTATCTGCAATGAACAGCTGAAACCGAGGACACAGCGGTGTATTACTGTACA 297
 Db 78 ThrPheTyLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTrpTrpCysAla 97
 QY 298 -----GATTTTCATAGACTGGGCGCAGGAAACATAGTC 330
 Db 98 ArgGlySerHisTrpPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117

QY 331 ACCGTCTCTCAGGCTCCACCAAGGGCCCATCGGTCTTCCCTCTGGACCCCTCTCTCCAG 390
 Db 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 137
 QY 391 AGCACCTCTGGGGCAGCAGCGCCCTGGGTGCTCTCAAGGACTACTTCCCGGAACCG 450
 Db 138 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTrpPheProGluPro 157
 QY 451 CTGACGGTGTCTGGAACCTCAGCGCCCTGCACAGCGCGGTGCACACCTTCCCGGTGTC 510
 Db 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177
 QY 511 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGTCACCGCTCCCTCAGCGCTTG 570
 Db 178 LeuGlnSerSerGlyLeuTrpSerLeuSerSerValValThrValProSerSerSerLeu 197
 QY 571 GGCACCCAGACCTACATCTGCACAGTGAATCACAAGCCCAAGCCCAACCAAGGTGGACAAG 630
 Db 198 GlyThrGlnThrTrpIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217
 QY 631 AAAGTGGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGTCCCGACCTGAA 690
 Db 218 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237
 QY 691 CTCGGGGGGCACCGTCT 750
 Db 238 LeuLeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIle 257
 QY 751 TCCCGGACCCCTGAGGTACATGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 810
 Db 258 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 277
 QY 811 AAGTTCAACTGTTACGTGGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 870
 Db 278 LysPheAsnTrpTrpValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297
 QY 871 GAGCAGTACAACAGCAGTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 930
 Db 298 GluGlnTrpAsnSerThrTrpArgValValSerValLeuThrValLeuHisGlnAspTrp 317
 QY 931 CTGATGCGCAGGAGTACAAAGTCTCCCAAGAGCCCTCCCAAGAGCCCTCCCAAGAGCC 990
 Db 318 LeuAsnGlyLysGluTrpLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 337
 QY 991 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCCAGAGTGTACACCTGCCCCCA 1050
 Db 338 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTrpThrLeuProPro 357
 QY 1051 TCCCGGATGAGTGCACCAAGAACCCAGGTGAGTGCCTGACCTGCTGTCTCAAGGCTTCTAT 1110
 Db 358 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTrp 377
 QY 1111 CCCAGCCACATCCCGTGGAGTGGAGAGCAATGGCGGAGGAGCAACTCAAGAGCC 1170
 Db 378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTrpLysThr 397
 QY 1171 ACGCCTCCCGTGTGAGTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230
 Db 398 ThrProValLeuAspSerAspGlySerPhePheLeuTrpSerLysLeuThrValAsp 417
 QY 1231 AAGAGCAGTGGCAGCAGGGAACGGTCTTCTCTATGCTCCGTGATGATGAGGCTCTGCAC 1290
 Db 418 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 437
 QY 1291 AACCACTACAGCAGAGACCTCTCCCTGCTCCCGGTAAA 1332
 Db 438 AsnHisTrpThrGlnLysSerLeuSerLeuSerProGlyLys 451

RESULT 11

US-09-282-846-2

; Sequence 2, Application US/09282846

; Patent No. 6528624

; GENERAL INFORMATION:
 ; APPLICANT: Esche Ekinaduse Idusogie et al.
 ; TITLE OF INVENTION: Polypeptide Variants
 ; FILE REFERENCE: P1266R2
 ; CURRENT APPLICATION NUMBER: US/09/282,846
 ; CURRENT FILING DATE: 1999-03-31
 ; NUMBER OF SEQ ID NOS: 2
 ; SEQ ID NO 2
 ; LENGTH: 451
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Artificial Sequence
 ; LOCATION: 1-451
 ; OTHER INFORMATION: Sequence is completely synthesized
 ; Patent No. 6528624
 US-09-282-846-2

Alignment Scores:
 Pred. No.: 8,02e-152 Length: 451
 Score: 2150.50 Matches: 408
 Percent Similarity: 92.5% Conservatives: 12
 Best Local Similarity: 89.8% Mismatches: 21
 Query Match: 89.42% Indels: 13
 DB: 4 Gaps: 3

US-09-674-716b-18 (1-1335) x US-09-282-846-2 (1-451)

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QY 1 GAGGTGACCTGCTGGAGTCTGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCTGTGACGCTAGCGGATTCACTTTC---AGTGGCTACTGGATGCTCTGGTCCGCCAG 117
DB 21 SerCysAlaValSerGlyTyrSerIleThrSerGlyTyrSerTrpAsnTrpIleArgGln 40
QY 118 GTCCAGGAAGGGCTCGAGTGGTGTGCTGAAATAGATTGAATCTGAATATTATGCA 177
DB 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysTyrSerGlyGlu-----57
QY 178 ACACATTATCGGAGTCTCTGAGGGGAATTCACCATCTCAAGAGATGATTCAAAATCT 237
DB 58 ThrLysTyrAsnProSerValLysGlyArgGileThrIleSerArgAspSerLysAsn 77
QY 238 AGACTGTATCTGCAATGAACCCCTGAAACCCAGGACACAGCCCGTGTATTACTGTACA 297
DB 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAla 97
QY 298 -----GATTCATAGACTGGGCCAGGACACACTAGTC 330
DB 98 ArgGlySerHisTyrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117
QY 331 ACCGTCTCTCCAGCTCCACCAAGGGCCCATCGTCTTCCCTCGGCACCCCTCTCCAG. 390
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QY 391 AGACCTCTGGGGGCACAGCGGCCCTGGGTGCTGCTCAAGACTACTTCCCGGACCG 450
DB 138 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 157
QY 451 GTGACGGTGTCTGGAACTCAGCGCCCTGACAGCGGGTGCACACCTTCCCGGCTGTC 510
DB 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177
QY 511 CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCTGCCCTCCAGCAGCTTG 570
DB 178 LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeu 197
QY 571 GGACCCAGACCTACATCTCAAGCTGAATCAAGCCCGACACACCCAGGTGGACAG 630
DB 198 GlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217
QY 631 AAAGTGGAGCCCAATCTTGTGCAAAAACCTCACACATGCCCGCCAGCTGGCCAGCACCTGAA 690
  
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DB 218 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237
QY 691 CTCGGGGGACACCGTCAGTCTTCTTCCCCCAAAACCCAGGACACCCCTCATGATC 750
DB 238 LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetIle 257
QY 751 TCCGGACCCCTCAGGTTCACATCGTGGTGGTGGAGCTGAGCCACGAGACCCCTGAGGTC 810
DB 258 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 277
QY 811 AAGTTCAACTGGTAGCGCGGTGGAGGTGCATAATGCCAAGACAAAGCCCGGGGAG 870
DB 278 LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297
QY 871 GAGCAGTACACAGCAGTACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 930
DB 298 GluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrp 317
QY 931 CTGAATGGCAAGGAGTACAAAGTCTCAAAAGCCCTCCAGCCCTCCAGCCCTCATCGAG 990
DB 318 LeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 337
QY 991 AAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTACACCTGCCCCCA 1050
DB 338 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProPro 357
QY 1051 TCCCGGATCAGTTCACCAAGAACCCAGGTTCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCT 1110
DB 358 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr 377
QY 1111 CCCAGGACATCGCGGTGGAGTGGGAGCAATGGGCGAGCGGAGAACCACTACAGACC 1170
DB 378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr 397
QY 1171 ACGCTCCCGTGGGACTCCGACGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1230
DB 398 ThrProProValLeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAsp 417
QY 1231 AAGACGAGTGGGACGAGGGGAACGTCTTCTCATGCTCCGTGATGATGATGATGATGATGAT 1290
DB 418 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 437
QY 1291 AACCATACACGACGAGAGCGCTCTCCCTGTCCTCGGGGTAAA 1332
DB 438 AsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 451
  
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RESULT 12
 US-09-680-145-2
 ; Sequence 2, Application US/09680145
 ; Patent No. 6538124
 ; GENERAL INFORMATION:
 ; APPLICANT: Esche Ekinaduse Idusogie et al.
 ; TITLE OF INVENTION: Polypeptide Variants
 ; FILE REFERENCE: P1266R1
 ; CURRENT APPLICATION NUMBER: US/09/680,145
 ; CURRENT FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 09/282,505
 ; PRIOR FILING DATE: 1999-03-13
 ; NUMBER OF SEQ ID NOS: 2
 ; SEQ ID NO 2
 ; LENGTH: 451
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Artificial Sequence
 ; LOCATION: 1-451
 ; OTHER INFORMATION: Sequence is completely synthesized
 ; Patent No. 6538124
 US-09-680-145-2

Alignment Scores:
 Pred. No.: 8,02e-152 Length: 451

Score: 2150.50 Matches: 408
Percent Similarity: 92.51% Conservative: 12
Best Local Similarity: 89.87% Mismatches: 21
Query Match: 89.42% Indels: 13
DB: 4 Gaps: 3

US-09-674-716B-18 (1-1335) x US-09-680-145-2 (1-451)

QY 1 GAGGTGAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCCTGTGACACTAGCGATTCACTTTC---AGTGGCTACTGGATGTCCTGGGTCCGCCAG 117
Db 21 SerCysAlaValSerGlyTyrSerIleThrSerGlyTyrSerTrpAsnTrpIleArgGln 40
QY 118 GCTCCAGGGAAGGGCTCGAGTGGTTCCTGAAATAGATTGAAATCTGATATTATGCA 177
Db 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysTyrSerGlyGlu-----57
QY 178 ACACATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATCAAAATCT 237
Db 58 ThrLysTyrAsnProSerValLysGlyArgIleThrIleSerArgAspSerLysAsn 77
QY 238 AGACTGTATCTGCAAAATGAACAGCCTGAAACCGAGACACAGCCGCTGTATTACTGTACA 297
Db 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAla 97
QY 298 -----GATTTCATAGACTGGGCGGAGGAGAACTAGTGC 330
Db 98 ArgGlySerHisTyrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117
QY 331 ACCGTCTCCCTCAGCTCCACCAAGGCCATCGTCTCCCTGGACCCCTCCCTCCAG 390
Db 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 137
QY 391 AGCACTCTGGGGGCACAGGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCG 450
Db 138 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 157
QY 451 GTACGGTGTCTGGACTCAGGCGCCCTGACAGCGGGGTGACACCTTCCGGCTGTC 510
Db 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177
QY 511 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGCACCGTGGCTCCCTCCAGCAGTGTG 570
Db 178 LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerLeu 197
QY 571 GGCACCCAGACTACATCTGCAAGCGTAATCAAGCCCGAGCAACACCAAGTGGACAG 630
Db 198 GlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217
QY 631 AAAGTGGAGCCCAAAATCTTGTGACAAACTCACAATGCCACCGCCCGCCAGCACTGAA 690
Db 218 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237
QY 691 CTCGGGGGCGACCGTCACTGCTTCTTCTTCCCGCAAAACCAAGGACACCTCATGATC 750
Db 238 LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetile 257
QY 751 TCCCGGACCCCTGAGTGCATCGGTGGTGGTGGACGTGAGCCAGAGACCTCAGTGC 810
Db 258 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 277
QY 810 AAGTTCACCTGAGTACGTGACCGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAG 870
Db 278 LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297
QY 371 GAGCACTACAAGCAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 930
Db 298 GluGlnTyrAsnSerThrTyrArgValValValValValValValValValValValVal 317
QY 931 CTGAATGGCAAGGAGTACAAGTGCAGAGGTCTCCAAAGCCCTCCCGAGCCCGCCATCGAG 990

318 LeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 337
QY 991 AAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTTGACACCTGCCCCCA 1050
Db 338 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProPro 357
QY 1051 TCCCGGATGAGCTGACCAAGAACAGGTGACCTGACCTGCTCGTCAAGGCTTCTAT 1110
Db 358 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr 377
QY 1111 CCCAGCACATCCGCTGGAGTGGAGAGCATATGGGAGCGCGAGACAACTACAAGACC 1170
Db 378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr 397
QY 1171 ACGCTCCCGTGGTGGACTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230
Db 398 ThrProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAsp 417
QY 1231 AAGAGCGAGTGGACAGCGGGAACGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1290
Db 418 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 437
QY 1291 AACCACTACAGCAGAAAGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
Db 438 AsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 451

RESULT 13
US-09-920-171-18
; Sequence 18, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-18

Alignment Scores:
Pred. No.: 8.02e-152 Length: 451
Score: 2150.50 Matches: 408
Percent Similarity: 92.51% Conservative: 12
Best Local Similarity: 89.87% Mismatches: 21
Query Match: 89.42% Indels: 13
DB: 4 Gaps: 3

US-09-674-716B-18 (1-1335) x US-09-920-171-18 (1-451)

QY 1 GAGGTGAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCCTGTGACACTAGCGATTCACTTTC---AGTGGCTACTGGATGTCCTGGGTCCGCCAG 117
Db 21 SerCysAlaValSerGlyTyrSerIleThrSerGlyTyrSerTrpAsnTrpIleArgGln 40
QY 118 GCTCCAGGGAAGGGCTCGAGTGGTTCCTGAAATAGATTGAAATCTGATATTATGCA 177
Db 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysTyrSerGlyGlu-----57
QY 178 ACACATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATCAAAATCT 237
Db 58 ThrLysTyrAsnProSerValLysGlyArgIleThrIleSerArgAspSerLysAsn 77
QY 238 AGACTGTATCTGCAAAATGAACAGCCTGAAACCGAGACACAGCCGCTGTATTACTGTACA 297
Db 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAla 97
QY 298 -----GATTTCATAGACTGGGCGGAGGAGAACTAGTGC 330
Db 98 ArgGlySerHisTyrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117
QY 331 ACCGTCTCCCTCAGCTCCACCAAGGCCATCGTCTCCCTGGACCCCTCCCTCCAG 390
Db 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 137
QY 391 AGCACTCTGGGGGCACAGGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCG 450
Db 138 SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 157
QY 451 GTACGGTGTCTGGACTCAGGCGCCCTGACAGCGGGGTGACACCTTCCGGCTGTC 510
Db 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177
QY 511 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGCACCGTGGCTCCCTCCAGCAGTGTG 570
Db 178 LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerLeu 197
QY 571 GGCACCCAGACTACATCTGCAAGCGTAATCAAGCCCGAGCAACACCAAGTGGACAG 630
Db 198 GlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217
QY 631 AAAGTGGAGCCCAAAATCTTGTGACAAACTCACAATGCCACCGCCCGCCAGCACTGAA 690
Db 218 LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 237
QY 691 CTCGGGGGCGACCGTCACTGCTTCTTCTTCCCGCAAAACCAAGGACACCTCATGATC 750
Db 238 LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetile 257
QY 751 TCCCGGACCCCTGAGTGCATCGGTGGTGGTGGACGTGAGCCAGAGACCTCAGTGC 810
Db 258 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 277
QY 810 AAGTTCACCTGAGTACGTGACCGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAG 870
Db 278 LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297
QY 371 GAGCACTACAAGCAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 930
Db 298 GluGlnTyrAsnSerThrTyrArgValValValValValValValValValValValVal 317
QY 931 CTGAATGGCAAGGAGTACAAGTGCAGAGGTCTCCAAAGCCCTCCCGAGCCCGCCATCGAG 990

Db 41 AlaProGlyLysGlyLeuGluTrpValAlaSerIleLysTyrSerGlyGlu----- 57
 QY 178 ACACATTATGCGAGTCTGTAAGGGAAATCCACATCTCAAGAGATGATTCAAAATCT 237
 Db 58 ThrLysTyrAsnProSerValLysGlyArgIleThrIleSerArgAspSerLysAsn 77
 QY 238 AGACTGTATCTGCAATGAACAGCCTGAAACCCGAGGACACAGCCGTGTATTACTGTACA 297
 Db 78 ThrPheTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAla 97
 QY 298 -----GATTTCATAGACTGGGCCAGGACACACTAGTC 330
 Db 98 ArgGlySerHisTyrPheGlyHisTrpHisPheAlaValTrpGlyGlnGlyThrLeuVal 117
 QY 331 ACCGTCCTCTCAGCCTCCACCAAGGCCCATCGGTCTTCCCTCCGACACCTCTCTCCCAAG 390
 Db 118 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 137
 QY 391 AGCACTCTGGGGGACAGCGCCCTGGCGTCCCTGTCAGGACTACTTCCCGAACCG 450
 Db 138 SerThrSerGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 157
 QY 451 GTGACGGTCTGTAACCTCAGCGCCCTGACAGCGCGTGCACACCTTCCCGCTGTC 510
 Db 158 ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 177
 QY 511 CTACAGTCTCTCAGGACTCTACTCTCAGCAGCGGTGAGCGTCCCTCCAGCAGCTTG 570
 Db 178 LeuGlnSerSerGlyLeuTyrSerLeuSerValValThrValProSerSerSerLeu 197
 QY 571 GCAACCCAGACTACATCTGCACTGATCAACAGCCAGCAGCAACCAACCAAGGTGACAA 630
 Db 198 GlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys 217
 QY 631 AAAGTGGACCCAAATCTTGTGACAAACTCACATGCCACCGTCCCGCCAGCACTGAA 690
 Db 218 LysValGluProLysSerCysAspLysThrHisThrCysProCysProAlaProGlu 237
 QY 691 CTCGCGGGGACCGTCAGTCTTCTCTTCCCGCCAAACCCCAAGCACCTCATGTC 750
 Db 238 LeuLeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIle 257
 QY 751 TCCGAGACCCCTGAGTCACTGCGTGGTGGAGCTGAGCAGCAGCAACCAACCTCAGTGC 810
 Db 258 SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal 277
 QY 811 AAGTTCACCTGTTACTGACGCGGTGGAGGTGCATATGCAAGACAAAGCCGCGGAG 870
 Db 278 LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu 297
 QY 871 GAGCCTCAACAGCAGCTACGTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 930
 Db 298 GluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrp 317
 QY 931 CTGAATGGCAAGGAGTACAGTCAAGTCTCCAAAGCCCTCCACCAAGCCCTCCACCCCAATCGAG 990
 Db 318 LeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu 337
 QY 991 AAAACATCTCCAAAGCCAAAGGGAGCCCGGAGACCAACCAAGTGTACACCTGCCCCCA 1050
 Db 338 LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProPro 357
 QY 1051 TCCCGGATGAGTGCACCAAGAACCAAGGTGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCT 1110
 Db 358 SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr 377
 QY 1111 CCAGCGACATCCCGGTGGAGTGGAGAGCAATGGCGAGCCGAGAACCAACTACAGACC 1170
 Db 378 ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr 397
 QY 1171 ACCCTCCCTGCTGACTCCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230
 Db 398 ThrProProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAsp 417

QY 1231 AAGAGCAGGTGGCAGCAGCGGAAACGTTCTCTCATGCTCCGTGATGATGAGGCTTGAC 1290
 Db 418 LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis 437
 QY 1291 AACCACTACACGACAGAGCCCTCTCCCTGCTCCCGGTAAA 1332
 Db 438 AsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 451
 RESULT 14
 US-09-027-449-71
 ; Sequence 71, Application US/09027449
 ; Patent No. 6025158
 ; GENERAL INFORMATION:
 ; APPLICANT: Gonzalez, Tania R.
 ; APPLICANT: Leong, Steven R.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
 ; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
 ; NUMBER OF SEQUENCES: 72
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/027,449
 ; FILING DATE: 20-Feb-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/074,330
 ; FILING DATE: 22-Jan-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/038,664
 ; FILING DATE: 21-Feb-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Love, Richard B.
 ; REGISTRATION NUMBER: 34,659
 ; REFERENCE/DOCKET NUMBER: P1085R3-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-5530
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 71:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 452 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-09-027-449-71
 Alignment Scores:
 Pred. No.: 1,23e-151 Length: 452
 Score: 2148.00 Matches: 407
 Percent Similarity: 92.73% Conservative: 14
 Best Local Similarity: 89.65% Mismatches: 21
 Query Match: 89.31% Indels: 12
 DB: 3 Gaps: 3
 US-09-674-716B-18 (1-1335) x US-09-027-449-71 (1-452)
 QY 1 GAGGTGACGTGGTGGAGTCTGGGGAGGCTGTGTAAGCCCGGGGGTCCCTTAGACTC 60
 Db 1 GluValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
 QY 61 TCCTGTGACGTAGCGGATTCACATTTCAGTCCGTACTGATGCTCTGGGTCCGCGAGCT 120
 Db 21 SerCysAlaAlaSerGlyTyrSerPheSerSerHisTyrMetHisTrpValArgGlnAla 40

121 CCAGGGAAGGGCTCGAGTGGTGTGCTGAATAGATTGAATCTGATATATTATCAACA 180
Db |||||ProGlyLysGlyLeuGluTrpValGlyTyrile-----AspProSerAsnGlyGluThr 58
181 CATTTATCGGAGTGTGTAAGGGGAATTCACCATCTCAAGAGATGATTCAMAATCTAGA 240
Db |||||ProGlyLysGlyLeuGluTrpValGlyTyrile-----AspProSerAsnGlyGluThr 78
59 ThrTyrAsnGlnLysPheLysGlyArgPheThrLeuSerArgAspAsnSerLysAsnThr 78
241 CTGTATCTGCAATGAAACACCTGAAACCGAGACACACCGCTGTATTACTGTACAGAT 300
Db |||||ProGlyLysGlyLeuGluTrpValGlyTyrile-----AspProSerAsnGlyGluThr 98
79 AlaTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98
301 -----TTCATAGAC---TGGGGCCAGGGAACACTAGTC 330
Db |||||GlyAspTyrArgTyrAsnGlyAspTyrPhePheAspValTyrGlyGlnGlyThrLeuVal 118
331 ACCGTCTCTCAGCTCCACCAAGGGCCGATCGGTCTTCCCTCGGACCCCTCTCCAAG 390
Db |||||ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 138
391 AGCACCTCTCGGGGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGCAACCG 450
Db |||||SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 158
451 GTACGGTGTGTGGAACCTCAGCGCCCTGACAGCGGGCTGCACACCTTCCCGGCTGTC 510
Db |||||ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal 178
511 CTACAGTCTCAGGACTACTCTCCCTCAGCAGGGTGTGACCGTGCCTCCAGCAGCTTG 570
Db |||||LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerLeu 198
571 GGCACCCAGACCTACATCTGCAACGTGAATCAAGCCCAAGCAACCAAGGTGACCAAG 630
Db |||||GlyThrGlnThrTyrileCysAsnValAsnHisLysProSerAsnThrLysValAspLys 218
631 AAGTGGAGCCCAATCTTGTGACAAACTCAGATGCCCGGCTGCCAGCAGCTGAA 690
Db |||||LysValGluProLysSerCysAspLysThrHisThrCysProProCysProAlaProGlu 238
691 CTCGGGGGSCACCGTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 750
Db |||||LeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThrLeuMetile 258
751 TCCCGGACCCCTGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 810
Db |||||SerArgThrProGluValThrCysValValValValValValValValValValVal 278
311 AAGTTCACCTGTTACGTGACCGGCTGAGGTGCATATGTCACCAAGCAAGCGCGGAG 870
Db |||||LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProGlu 298
371 GAGCAGTACAACGACGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 930
Db |||||GluGlnTyrAsnSerThrTyrArgValValValValValValValValValValVal 318
931 CTGAATGGCAAGGAGTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 990
Db |||||LeuAsnGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 338
991 AAAACCATCTCCAAAGCCCAAGGGCCCGGAGAACCCAGAGGTGTACACCTGCCCCCA 1050
Db |||||LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProPro 358
1051 TCCCGGATGAGTCAAGCAAGGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1110
Db |||||SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr 378
1111 CCCAGCAGCATCCCGTGGAGTGGGAGAGCAATGGCGAGCCCGGAGAACCACTACAAGACC 1170
Db |||||ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr 398

1171 AGCCTCCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1230
Db |||||ThrProProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAsp 418
1231 AAGAGCAGTGGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1290
Db |||||LysSerArgTyrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 438
1291 AACCACTACACGACGAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
Db |||||AsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys 452
RESULT 15
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026, 985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34, 659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-026-985-71
Alignment Scores:
Pred. No.: 1-23e-151 Length: 452
Score: 2148.00 Matches: 407
Percent Similarity: 92.73% Conservative: 14
Best Local Similarity: 89.65% Mismatches: 21
Query Match: 89.31% Indels: 12
DB: 3 Gaps: 3
US-09-674-716B-18 (1-1335) x US-09-026-985-71 (1-452)
QY 1 GAGTGCAGCTGGTGGAGTCTGGGGAGGCTGGTAAAGCCCGGGGGCTCCCTTAGACTC 60
Db 1 GluValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyLysLeuArgLeu 20
QY 61 TCCTGTGCTGACGTAGCGGATTCAGTTTCAGTGGCTACTGATGCTCTGGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyTyrSerPheSerSerHisTyrMetHisTrpValArgGlnAla 40
QY 121 CGAGGGAAGGGCTCGAGTGGGTGCTGGAATAGATTGAATCTGATATATTATCAACA 180
Db |||||

| | | | |
|----|------|---|------|
| Db | 41 | ProGlyLysGlyLeuGluTrpValGlyTyrIle-----AspProSerAsnGlyGluThr | 58 |
| Qy | 181 | CATATGCGGAGTGTGTCAGAGGGAATTCACCATCTCAGAGATGATTCAAAATCTAGA | 240 |
| Db | 59 | ThrTyrAsnGlnLysPheLysGlyArgPheThrLeuSerArgAspAsnSerLysAsnThr | 78 |
| Qy | 241 | CTGTATCTGCAATCAACAGCCTCAAAACCGAGGACACAGCCGTGTTATTACTGTACAGAT | 300 |
| Db | 79 | AlaTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAlaArg | 98 |
| Qy | 301 | -----TTCATAGAC---TGGGGCCAGGGACACACTGTC | 330 |
| Db | 99 | GlyAspTyrArgTyrAsnGlyAspTrpPheAspValTrpGlyGlnGlyThrLeuVal | 118 |
| Qy | 331 | ACCGTCTCCTCAGCCTCCACCAAGGCCCATCGGTCTTCCCTCCGCGCACCCCTCCTCCAAG | 390 |
| Db | 119 | ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys | 138 |
| Qy | 391 | AGCACCTCTGGGGGACACAGCGGCCCTGGGCTGCTGTCAGAGACTACTTCCCGCAACCG | 450 |
| Db | 139 | SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro | 158 |
| Qy | 451 | GTGAGCGTGTCTGGAACCTCAGCGGCCCTGACGCGCGTGCACACCTTCCCGCTGTC | 510 |
| Db | 159 | ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal | 178 |
| Qy | 511 | CTACAGTCTCCTCAGGACTCTACTCCTCAGACGCGTGTGACCGTCCCTCCAGCAGCTTG | 570 |
| Db | 179 | LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeu | 198 |
| Qy | 571 | GGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAACACCAAGTGGACACAAG | 630 |
| Db | 199 | GlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLys | 218 |
| Qy | 631 | AAAGTGGAGCCCAAAATCTTGTGACAAAACCTCACACATGCCACCGTCCCGCACCTGAA | 690 |
| Db | 219 | LysValGluProLysSerCysAspLysThrHisThrCysProCysProAlaProGlu | 238 |
| Qy | 691 | CTCGGGGGGACCGTCACTGTCATCGTGTGGTGGACGTGAGCCACGAGACCCCTCAGGTC | 750 |
| Db | 239 | LeuLeuGlyGlyProSerValPheLeuPheProLysProLysAspThrLeuMetIle | 258 |
| Qy | 751 | TCCCGGACCCCTGAGTGCATCGTGTGGTGGACGTGAGCCACGAGACCCCTCAGGTC | 810 |
| Db | 259 | SerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal | 278 |
| Qy | 811 | AAAGTCAACTGGTACCTGACCGCGTGGAGTGCATATGCCAAGAACAGCCCGGGAG | 870 |
| Db | 279 | LysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlu | 298 |
| Qy | 871 | GAGCAGTCAACAGCAGCTACCGTGTGTCAGCGTCTCACCCTGCTGACCCAGGACTGG | 930 |
| Db | 299 | GluGlnTyrAsnSerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrp | 318 |
| Qy | 931 | CTGAATGGCAAGGAGTACAAAGTCTCCACAAAGCCCTCCAGCCCGCCCATCGAG | 990 |
| Db | 319 | LeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGlu | 338 |
| Qy | 991 | AAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACCCAGAGTGTACACCTGCCCCCA | 1050 |
| Db | 339 | LysThrIleSerLysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProPro | 358 |
| Qy | 1051 | TCCCGGATGAGTGCATCCAGACCAAGTCCAGCTCAGCTGCTGCTCAAGGCTTCTAT | 1110 |
| Db | 359 | SerArgGluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyr | 378 |
| Qy | 1111 | CCAGCGACATCCCGTGGAGTGGGAGCAATGGCGAGCCCGAGAACCAACTACAGACC | 1170 |
| Db | 379 | ProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr | 398 |
| Qy | 1171 | ACGCTCCCGTGTGAGTCCGAGCGCTCTCTCTCTCTACAGAGCTCACCGTGGAC | 1230 |
| Db | 399 | ThrProProValLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAsp | 418 |

| | | | |
|----|------|--|------|
| Qy | 1231 | AAAGCAGGTGGCAGCAGGGGAACGTTCTTCTCATGCTCGTATCATGAGGCTCTGCAC | 1290 |
| Db | 419 | LysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHis | 438 |
| Qy | 1291 | AACCACTACACGAGAGAGACCTCTCCCTGTCTCCGGGTAAA | 1332 |
| Db | 439 | AsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys | 452 |

Search completed: September 30, 2004, 09:32:00
Job time : 54.6509 secs

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